STIC-Biotech/ChemLib	E	155312	~6/7 06h+C
From: Sent: To: Subject: From: Sepps-Ford, Jan Thursday, June STIC-Biotech/C 09/155,676	02, 2005 5:21 PM		6/8 8 (40 h.
Please search			
SEQ ID NOs: 1, 3, 4, and 6 in all pending ar in all amino acid pending and commercial da	nd commercial nucleic acid atabases	sequence databases. Rev	erse translation search
SEQ ID NO: 2, 5, 7 in all pending and comm	nercial amino acid database	es.	1
Thanks, Janet L. Epps-Ford, Ph.D. Ant Unit 1635 Mailbox: Remsen 2C18 Office: Remsen 2C05 Phone: 571-272-0757 Fax: 571-273-0757	1 ma 3 ma 4 ma 6 ma 2 aa 5 aa 7 aa	1906 2631 1253 4596 604 417 941	UI) - 3 2005 STIC)

STAFF USE ONLY

Type of Search NA#: _____ AA#: 3
Interference: ____ SPDI:
S/L: ____ Oligomer: ___
Encode/Transi: ____ Text:
Inventor: ____ Litigation: ___

Vendors and cost where applicable STN:______DIALOG:_____QUESTEL/ORBIT:_ LEXIS/NEXIS:______SEQUENCE SYSTEM:_______ WWW/Internet:_ Other(Specify):_

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STIC Search Report Biotech-Chem Library

STIC Database Track

TO: Janet Epps-Ford

Location: rem/2C05/2C18

Art Unit: 1635

Tuesday, June 14, 2005

Case Serial Number: 09/155676

From: Toby Port

Location: Biotech-Chem Library

REM1-A59

Phone: 272-2523

toby.port@uspto.gov

Searen Nores

Dear Examiner Epps-Ford,

Here are the results of your search. Please feel free to contact me if you have any questions.

Toby Port



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STIC SEARCH RESULTS FEEDBACK FORM

tech-		

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor Remsen Bldg. 01 D86 571-272-2507

Vol	luntary Results Feedback Form
>	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found , search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
×	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Co	mments:

Drop off-or send completed forms to STIC-Biotech-Chem library Remsen Bidg



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Run on:

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AAV03323 standard; cDNA; 1906 BP
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Aak67282 Human imm
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Ab67233 Human gen
Ach75347 Human gen
Ach89047 Human gen
Ach892200 DNA encod
Aa673549 DNA encod
Aa673549 DNA encod Ach75141 Human gen Ach88841 Human gen Aas6411 DNA encod Aac12137 Human sec Abl09365 Drosophil AAS92200 AAS73549 AAC11927 ACH75141 ACH88841 AAD04335 AAD04334 AAH15665 AAH18235 AAH04973 AAK67282 AAS64410 ACH75347 ACH89047 AAS64411 AAC12137 ABL09365 1782 2873 3139 2248 6045 730

Abl09364 Drosophil	Aba09172 Human BG3	Aav03325 Sequence	Ada71938 Rice gene	Adl13471 Osteoarth	Abl86718 Human ova	Aac59953 Human sec	Abz73290 Secreted	Abz66903 Human sec	Adf81729 Leukaemia	Adq53383 Novel can	Ade07225 Novel cod	Ach37072 Human end	Abn95020 Gene #151	Aai95747 Human neu	Aas85362 DNA encod	Ach27965 Human adu	Ads31085 Human gen	Aad04332 Human IRE	Aba21208 Human ner	Aba21210 Human ner	Adl12492 Human ste	Adr07577 Full leng	Abal4117 Human ner	Abz35416 Human gen	
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66.8	63.8	61.6	61	9	59.6	59.4	59.4	59.4	59	58.4	9.95	54.6	54.6	54.6	54.4	54	53.2	53	52.2	52.2	52.2	52.2	51.8	50.4	
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ALIGNMENTS

DNA encoding tumour necrosis factor receptor-associated factor binding molecule - used for modulation or mediation in cells of the activity of NF-kB. Human tumour necrosis factor receptor-associated factor 2; TRAF2; TRAF-2 binding protein; NF-kappaB activity; NF-kappaB induction; intracellular signalling activity; acute hepatitis; autoimmune-induced call death; 88. /*tag= a /codon= 127-129, aa:Ser /note= "no ATG start or STOP codon given" 5' end of clone 9, which encodes a TRAF2 binding protein. Mett I; Kovalenko A, Location/Qualifiers 94. .1906 /*tag= a Boldin M, 96IL-00117800. 96IL-00119133. YEDA) YEDA RES & DEV CO LTD 97WO-IL000117. Wallach D, Malinin N, WPI; 1997-503101/46. P-PSDB; AAW42400. 01-APR-1997; 02-APR-1996; 26-AUG-1996;

> Result Š

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The present sequence represents the 5' end of clone 9, which encodes a TRAF2 binding protein. Clone 9 is a partial clone, which lacks most of TRAF2 binding protein. Clone 9 is a partial clone, which lacks most of the 5' end of the coding DNA sequence. A cDNA library prepared from B-c cells was screened for proteins that associate with TRAF2, and the call be actived as screened for proteins the clone 9 protein is capable of binding to at least amino acids 222-501 of TRAF2. The TRAF-2 binding proteins can be comediated or mediated or mediated by cany other intracellular signalling activity modulated or mediated by TRAF2. TRAF-binding proteins are especially used for prevention or TRAF2. TRAF-binding proteins are especially used for prevention or CC treatment of pathological conditions associated with NF-kB induction, c.g. acute hepatitis, autoimmune-induced cell death, e.g. death of the beta Langarhans cells or the pancreas that results in diabetes, the death of collection of graft rejection, the death of oligodendrocytes in the brain of multiple sclerosis, and AlDS-inhibited T cell suicide which causes C proliferation of the AlDS virus and hence the AlDS disease. The proteins are also useful for modulating cellular activity modulated/mediated by manch 3; 127pp; English Claim 4; Fig

Sequence 1906 BP; 482 A; 492 C; 547 G; 378 T; 0 U; 7 Other;

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1020 1080 1200 1200 1260 1380 1380 1440 1500 1500 1680 1560 1560 1620 1680 1800 1800 780 780 840 840 900 900 960 960 TIGAACGGCAGAGATAAGTTIGCTCCCACCGTTICAGACCTCTTAAAGGAGTCAACGCAG AACGTGACCTCCTTGCTGAAGGAGTCCACGCAAGGAGTGAGCAGCCTGTTCAGGGAGATC TTAAAAAAGACACCTGGGGCAGGGGAGGGCTCAGAGGACAACTCCGACCGCTCCTCTGTCA ATATCATGTCCGCCTTTGAAAGCCCCTTCGGGCCTAACTCCAATGGAATCAGAGCAGCAA ATATCATGTCCGCCTTTGAAAGCCCCTTCGGGCCTAACTCCAATGGAATCAGAGCAGCAA CAGGGCATGAAGGTCCAGGCGCTGGCCAGCTATCTTTGCTATTTTGTGAGGAGAGTTCTAA TCGTGTCCAGGAATGTCAGTGCTGATGCCAAATGCAAAAAGGAGGGGGAAGAAGAAAAAGA AAGTGACCAACATAATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGGACGTGT TTAAAAAGACACCTGGGGCAGGGGAGAGCTCAGAGGACAACTCCGACCGCTCCTCTGTCA CTCATGGAAAATTGATTCCCTGTCTTTGAACGGGGAGTTTGGGTACCAGAAGCTTGATGT GAAAAGCATCGATGAAGATGTGGATGAAAACGAAGATGACGTGTATGGAAACTCATC GAAAAGCATCGATGAAGATGTGGATGAAAACGAAGATGACGTGTATGGAAACTCATC AGGAAGGAAGCACACAGGGGCCACTCGGAGTCGCCCGAGAAGCCACTGGAAGGGGAACACCTG CCTCTCCCAGATGCACAGCTGGGCTCCGCTGAAGGTGCTGCACAATGACTCCGACATCCT CCTCTCCCAGATGCACAGGTGGGCTCCGCTGAAGGTGCTGCACAATGACTCCGACATCCT CTTCCCTGTCAGTGGCGTGGGCTCCTACAGCCCAGCAGATGCCCCCCTCGGAAGCCTGGA crrcccrercagreecerecereceracaececaecagarececereceaagecreea GAACGGGACAGGACCAGAGGACCACGTTCTCCCGGATCCTGGACTTCGGTACAGTGTGGA GAACGGGACCAGGACCAGGACCACGTTCTCCCCGGATCCTGGACTTCGGTACAGTGTGGA GAGTCCATGACAATTAGTGAACTGCGCCAGGCCACTGTGGCCCATGATGAACAGGAT GAGCTGGAGGAGGAGAACAGATCACTGCGAAACCTGCTCGACGGTGAGATGGAGCACTCA AGCCAGCTCTCCAGGCCACGGAAGTCCTCTGAGCAGCCTGTTACTTCTGCCTCAGTGCCA GAGCTGGAGGAGAGAGATCACTGCGAAACCTGCTCGACGGTGAGATGGAGCACTCA CAGGGCATGAAGGTCCAGGCGCTGGCCAGCTATCTTTGCTATTTTTGTGAGGAGATTCTAA 721 1021 1081 661 721 781 781 841 841 901 901 961 196 1021 1081 1141 1141 1201 1201 1261 1321 1321 1381 1381 1441 1441 1501 1501 1561 1561 1681 1741 1261 1621 1681 q ò ò 엄 셤 d g οp ò ð ò 8 ò d ò 셤 g ò ð 셤 à ద ò g ò g ò g ò g 원 ò 원 Dp ò ò

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receptor-associated factor (TRAP2) binding protein, IREN. A fragment of
this IREN molecule is capable of binding protein, IREN. A fragment of
this IREN molecules to human tumour necrosis factor (TNF)
501. The invention relates to human tumour necrosis factor (TNF)
receptor- associated factor (TRAP2) binding protein designated as IREN
(IKAPPAB REGULACO, its isoforms IREN-108, IREN-E and their
corresponding cDNA molecules. IREN is useful for modulating/mediating the
activity of transcription factor NF (Nuclear Factor)-kappaB or any other
intracellular signalling activity mediated by TRAP2. IREN is useful in
the prevention and treatment of a pathological condition associated with
NF-kappaB induction (abnormal) e.g. AIDS (acquired immune deficiency
syndrome), autoimmune diseases, tumours, rheumatic diseases, anorexia,
coeptic shock and graft-ve-host reactions IREN also plays an important
coll in the control of inflammation and other non-apoptocic effects of
TNF as well as in the control of apoptosis. The invention also relates to
method for screening, identifying and producing a molecule capable of
modulating activities mediated by IREN. IREN antibodies are useful for
the purification of new proteins from different sources, including cell
                      Human; Tumour Necrosis Factor; TNF; TNP Receptor Associated Factor; TRAF2; TRAF2 binding protein; IREN; IkappaB Regulator; immunosuppressive; nuclear factor-kappaB; NF-kappaB; cytostatic; tumour; AIDS; acquired immune deficiency syndrome; rheumatic disease; apoptosis; autoimmune disease; septic shock; graft-vs-host reaction; inflammation; anorexia; anti-HIV; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                           Human TNF receptor-associated factor (TRAF2) binding protein, IREN cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA sequence encoding Tumor Necrosis Factor receptor associated factor (TRAF) binding proteins (IREN) for treatment or prevention of pathological conditions associated with NF-kappaB induction.
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| /product= "Human TRAF2-binding protein, IREN"
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extracts or transformed cell lines, in addition IREN can be used ir diagnostic purposes for identifying disorders related to abnormal functioning of cellular effects mediated directly by TRAF proteins
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                                                                                              Sequence 1782 BP; 456 A; 458 C; 504 G; 364 T; 0 U; 0 Other;
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                                                                                                                                           Score 1742;
Pred. No. 0;
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Matches 1775; Conservative
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anorexia; anti-HIV; therapy;

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                                                                                                                                                                                                                                                                                                           Human; Tumour Necrosis Factor; TNF; TNF Receptor Associated Factor; TRAF2; TRAF2 binding protein; IREN, IkappaB Regulator; IREN-E; immunosuppressive; nuclear factor-KappaB; NF-KappaB; vytostatic; tumour; AIDS; acquired immune deficiency syndrome; rheumatic disease; apoptosis; autoimmune disease; septic shock; graft-vs-host reaction; inflammation;
                                                                                                                                                                                                                                                           Human TNF receptor-associated factor binding protein, IREN-E cDNA.
                                                                                                                   ВР
                                                                                                                AAD04335 standard; cDNA; 2873
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04-JUL-2001

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AADO4335
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AC AAL
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DT 04XX
XX
CW Hun
KW Hun
KW TRI
KW AII
KW AIII

<u>ب</u>

Gaps 3;

Indels

4;

DB 4; Length 2873;

120 297 180 357

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The present cDNA sequence encodes human tumour necrosis factor (TNF)
receptor-associated factor (TRAF2) binding protein isoform, IREN-E. A
fragment of this IRRN-E molecule is capable of binding protein
at position 225-501. The invention relates to human tumour necrosis
factor (TNF) receptor- associated factor (TRAF2) binding protein

CG designated as IREN (IRappaB REGulator), its isoforms IREN-10B, IREN-E and

CC designated as IREN (IRappaB REGulator), its isoforms IREN-10B, IREN-E and

CC their corresponding the activity of transcription factor NF (Nuclear

CC Factor) KappaB or any other intracellular signalling activity mediated by

CC TRAF2. IREN is useful in the prevention and treatment of a pathological

CO CONDITION (IRAPPAB PROVINCE), autoimmune diseases, tumours,

CC TRAF2. IREN is useful in the prevention and treatment of a pathological

CO CONDITION (IRAPPAB PROVINCE), autoimmune diseases, tumours,

CR CACQUIRED (IRAPPAB PROVINCE), autoimmune diseases, tumours,

CR CACQUIRED (IRAPPAB PROVINCE), and CALOR (IRAPPAB PROVINCE)

CR CONDITION (IRAPPAB PROVINCE), and CALOR (IRAPPAB PROVINCE)

CR Mediated by IREN IREN antibodies are useful for the purification of new

CC mediated by IREN IREN antibodies are useful for the purification of new

CC proteins from different sources, including cell extracts or transformed

CC mediated directly by TRAF proteins
                                                                                                                                  "Human TRAF2-binding protein isoform, IREN-E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA sequence encoding Tumor Necrosis Factor receptor associated factor (TRAF) binding proteins (IREN) for treatment or prevention of pathological conditions associated with NF-kappaB induction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2873 BP; 756 A; 736 C; 806 G; 575 T; 0 U; 0 Other;
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P-PSDB; AAE00685.
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                                    Homo sapiens
                                                                          Key
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1614

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AAGGATGAGCTGGAGGAGGAGAACAGATCACTGCGAAACCTGCTCGACGGTGAGGATGGAG 1500
                                                                                                                                                                                                   The present cDNA sequence encodes human tumour necrosis factor (TNF) receptor-associated factor (TRAF2) binding protein isoform, IREN-10B. A fragment of this IREN-10B molecule is capable of binding to TRAF2 protein at position 225-501. The invention relates to human tumour necrosis factor (TMF) receptor- associated factor (TRAF2) binding protein designated as IREN (IkappaB REgulator), its isoforms IREN-10B, IREN-E and
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Tumour Necrosis Factor; TNF; TNF Receptor Associated Factor; TRAF2; TRAF2 binding protein; IkappaB Regulator; IREN-10B; immunosuppressive; nuclear factor-kappaB; NF-kappaB; oytostatic; tumour; AIDS; acquired immune deficiency syndrome; rheumatic disease; apoptosis; autoinmune disease; septic shock; graft-vs-host reaction; inflammation; anorexia; anti-HIV; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human TRAF2-binding protein isoform, IREN-10B"
                                                                                                                            <u> AAGGATGAGCTGGAGGAGAACAGATCACTGCGAAACCTGCTCGACGGTGAGATGGAG</u>
                                                                                       GTGCCAGAGTCCATGACAATTAGTGAACTGCGCCAGGCCACTGTGGCCATGATGAACAGG
                               GTGGAAGCCAGCTCTCCAGGCCACGGAAGTCCTCTGAGCAGCCTGTTACCTTCTGCCTCA
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       modulating/mediating the activity of transcription factor NF (Nuclear Factor)-kappaB or any other intracellular signalling activity mediated by TRAF2. IREN is useful in the prevention and treatment of a pathological condition associated with NF-kappaB induction (abnormal) e.g. AIDS (acquired immune deficiency syndrome), autoimmune diseases, tumours, rheumatic diseases, anortain septic shock and graft-vs-host reactions. IREN also plays an important role in the control of inflammation and apportoric effects of TNF as well as in the control of apportoric. The invention also relates to method for screening, identifying and producing a molecule capable of modulating activities including by IREN. IREN antibodies are useful for the purification of new proteins from different sources, including cell extracts or transformed cell lines, in addition IREN can be used in diagnostic purposes for indentifying disorders related to abnormal functioning of cellular effects
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1016 1075 1375 1440 1320 1494 1554 1500 1674 1560 88 GTGTTTAAAAAGACACCTGGGGCAGGGGAGAGCTCAGAGGACAACACCGGACCGCTCCT GATGTGAAAAGCATCGATGATGAAGATGTGGATGAAAACGAAGATGACGTGTATGGAAAC CCTGTCGTGTCCAGGAATGTCAGTGCTGATGCCAAATGCAAAAAGGAGCGGAAGAAGAAA AAGAAAGTGACCAACATAATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGAC GTGTTTAAAAAGACACCTGGGGCAGGGAGAGCTCAGAGGACAACTCCGACCGCTCCTCT GTCAATATCATGTCCGCCTTTGAAAGCCCCTTCGGGCCTAACTCCAATGGAA-TCAGAGC AGCAACTCATGGAAAATTGATTCCTGTCTTTGAACGGGGGGTTTGGGTACCAGAAGCTT GATGTGAAAAGCATCGATGATGAGATGTGGATGAAAACGAAGATGACGTGTATGGAAAC ACCTGCCTCTCCCAGATGCACAGCTGGGCTCCGCTGAAGGTGCTGCACAATGACTCCCGAC AGCAACTCATGGAAAATTGATTCCCTGTCTTTGAACGGGGAGTTTGGGTACCAGAAGCTT TCATCAGGAAGGAAGCACAGGGGCCACTCGGAGTCGCCCGAGAAGGCACTGGAAGGGAAC ACCTGCCTCTCCCAGATGCACAGCTGGCCTCGAAGGTGCTGCACAATGACTCCGAC 1316. ATCCTCTTCCCTGTCAGTGGCGTGGGCTCCTACAGCCCAGCAGATGCCCCCCCTCGGAAGC CTGGAGAACGGGACAGGACCAGAGCACGTTCTCCCGGATCCTGGACTTCGGTACAGT CTGGAGAACGGGACAGGACCAGGACCACGTTCTCCCCGGATCCTGGACTTCGGTACAGT GTGGAAGCCAGCTCTCCAGGCCACGGAAGTCCTCTGAGCAGCCTGTTA-CTTCTGCCTCA GregaAGCCAGCTCTCCAGGCCACGGAAGTCCTCTGAGCAGCCTGTTACCTTCTGCCTCA GTGCCAGAGTCCATGACAATTAGTGAACTGCGCCAGGCCACTGTGGCCATGATGAACAGG AAGGATGAGCTGGAGGAGGAGAACAGATCACTGCGAAACCTGGTCGACGGTGAGATGGAG Human; primer; detection; diagnosis; antisense therapy; gene therapy; GTGCCAGAGTCCATGACAATTAGTGAACTGCGCCAGGCCACTGTGGCCATGATGAACAGG **AAGAAAGTGACCAACATAATCTCATTTGATGATGAGGAAGATGAGCAGAACT** GAGCGCCAGGCCATGAAGGTCCAGGCGCTGGCCAG 1709 GAGCGCAGGCATGAAGGTCCAGGCGCTGGCCAG Human cDNA sequence SEQ ID NO:14016. BP AAH15665 standard; cDNA; 2248 (first sapiens. 26-JUN-2001 1017 721 897 781 957 1076 1136 1081 1256 1201 841 901 961 1021 1196 1141 1376 1261 1436 1321 1495 1381 1555 1441 1615 1675 AAH15665

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  CGGCAGCGATCAAGCAGGCAGCGGGCTTTGCCAGCAAAACCGAAACAGAGCCCGTGTTCT 321
                                                            GGTACTACGTGAAGGAGGTCCTCAACAAGCACGAGCTGCAGCGCGTTCTACTCCCTGCGCC
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                                        GGTACTACGTGAAGGAGGTCCTCAACAAGCACGAGCTGCAGCGCTTCTACTCCCTGCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprisentary to the
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polynucleotides, or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises at least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in the
specification. The primer sets can be used in antisense therapy and in
specification and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
CDNAs easily without any specialised methods. AAH13612 to AAH13623 represent
the mann amino acid sequences; and AAH13629 to AAH13622 represent
configuration of the the complemences; AAH3622 represent
configuration of the which are used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCAGTTTGAAGCCGTCCTGCAGCATGGCTTGAAGAGAGTCGAGGGTTGGCACTCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 14016; 2537pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65; Indels
                                                                                                                                                                                                                                                                          Saito K, Y. Otsuki T;
                                                                                                                                                                                                                                                                          hikawa T, Hayashi K, S<sup>,</sup>
Wakamatsu A, Nagai K,
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                                                                                                                                  27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
                                                                                                                                                                                                                                                                      Isogai T, Nishikawa
Sugiyama T, Wakama
                                                                             2000EP-00116126
                                                                                                                 99JP-00248036
                                                                                                                                                                                            09-JUN-2000; 2000JP-00241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 59.7%;
Best Local Similarity 94.7%;
Matches 1195; Conservative
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EP1074617-A2
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID NO 18174; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                hikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                    Human cDNA sequence SEQ ID NO:18174
                                                                                                                                                                                                                             sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
AAH18235 standard; cDNA; 6045
                                                                                                                                                                  27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
09-JUN-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                        28-JUL-2000; 2000EP-00116126
                                                                                                                                                           99JP-00248036
                                    entry)
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                                                                                                                                                                                                                               Isogai
                                                                                                       EP1074617-A2
                                                                                                                                                            29-JUL-1999;
                                  26-JUN-2001
                                                                                                                        07-FEB-2001
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Ishii S,
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Yamamoto J;

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Saito K, , Otsuki

The present invention describes primer sets for synthesising 5602 full[angth cDNAs defined in the specification, where a primer set comprises.
[a) an oligo-dr primer and an oligonucleotide complementary to the
complementary strand of a polynucleotide which comprises one of the 5602
[a) complementary strand of a polynucleotide which comprises one of the 5602
[c) ligonucleotide comprises at least 15 nucleotides, or (b) a combination
[c) of an oligonucleotide comprising a sequence complementary to the
[c) sequence and an oligonucleotide comprising a sequence complementary to a
[c) complementary strand of a polynucleotide which comprises a 3'-end sequence (c)
[c) complementary strand of a polynucleotide comprises a 0-end sequence (c)
[c) complementary strand of a polynucleotide comprises a 1'-end sequence (c)
[c) complementary strand of a polynucleotide on in oligonucleotide which comprises a 1'-end sequence (c)
[c) complementary strand of a polynucleotide on in an oligonucleotide which comprises at least 15 nucleotides and the combination of
[c) c) complementary strand of a polynucleotides and the comprises at least 15 nucleotides and the comprises
[c) c) dispuncleotide which comprises at least 15 nucleotides and the comprise of the primers are useful for synthesising polynucleotides,
[c) particularly full-length cDNAs. The primers are also useful for the
[c) complementary strbout any specialised methods. AAH13613 to AAH13628 and
[c) AAH13613 to AAH18742 represent human cDNA sequences; AAB92446 to AAH13628
[c) complementary strand and or dissequences, and AAH13629 to AAH13632 represent
[c) complementary strand and confidence used in the exemplification of the
[c) complementary strand and confidence used in the exemplification of the

Sequence 6045 BP; 1561 A; 1493 C; 1427 G; 1564 T; 0 U; 0 Other; 9 41.6%; Score 792.8; DB 4; Length 6045; 96.8%; Pred. No. 4.6e-205; Live 0; Mismatches 22; Indels 6; Conservative Best Local Similarity Matches 852; Conserv Query Match Best Local S

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1171 1231 1408 1528 1292 ATGTGA---CCTTGCTGAAGGAGTCCACGCAAGGAGTGAGCAGCGTGTTCAGGGAGATCA 1348 1079 1648 992 TCTACTCCCTGCGCCACATCGCCTCAGACGTGGGCCGGGGCCGCACCTGGCTGCGCTGTG 1051 1232 TGAACGGGCAGATAAGTTTGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGA 1291 1409 regretecaggaargreagrecrgargeeaaargeaaaaggageggaagaagaaaaage 1468 1139 1768 601 661 721 840 TTAAAAAAGACACCTGGGGCAGGGAGAGCTCAGAGGACAACTCCGACCGCTCCTCTGTCA 1020 TGAAAAGCATCGATGAAGATGTGGATGAAAACGAAGATGACGTGTATGGAAACTCAT 1199 781 TCGTGTCCAGGAATGTCAGTGCTGATGCCAAATGCAAAAAGGAGCGGAAGAAGAAAAAGA 900 960 Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss. 1052 CCCTCAACGAACACTCCCTGGAGCGCTACCTGCACATGCTCCTGGCCGGAGCGCTGCAGGC 1172 CTACCATGGCAGCAGGTCCGAACTCCATACTCTTTGCGATTAACATTGACAACAAGGATT TGAGCACTTTTTATGAAGACTGGTCTTTTGTGATGGATGAAGAAGGTCCAGTATGCTTC 1112 TCAGTACTITITATGAAGACTGGTCTTTTGTGATGGATGAAGAGGGTCCAGTATGCTTC CTACCATGGCAGCAGGTCTGAACTCCATACTCTTTGCGATTAACATCGACAACAAGGATT CCCTCAACGAACACTCCCTGGAGCGCTACCTGCACATGCTCCTGGCCGACCGGTGCAGGC ACTCGTGGAAAATTGATTCCCTGTCTTTGAACAGGGAGTTTGGGTACCAGAAGCTTGATG TGAACGGGCAGAGTTTGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGA 722 ACGIGACCICCITGCIGAAGGAGICCACGCAAGGAGIGAGCAGCCIGIICAGGGAGAICA 782 CAGCCTCCTCTGCCGTCTCCATCCTCAAACCTGAACAGGAGACCGA-CCCTTGCCTG 901 AAGTGACCAACATAATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGACGTGT 1469 AAGTGACCAACATTATCTCATTTGATGATGAGGAAGATGAGCAGGACATGT ATATCATGTCCGCCTTTGAAAGCCCCTTCGGGCCTAACTCCAATGGAA-TCAGAGCAGCA ACTCATGGAAAATTGATTCCCTGTCTTTGAACGGGGAGTTTGGGTACCAGAAGCTTGATG TGAAAAGCATCGATGATGATGTGGATGAAAACGAAGATGACGTGTATGGAAACTCAT 1200 CAGGAAGGACACAGGGCCACTCGGAGTCGCCCGAGAA 1239 CAGGACGGAAGCACACGCCCACTCAGAGTCGCCCCGAGAA 1808 Human cDNA clone (5'-primer) SEQ ID NO:1808. AAH04973 standard; cDNA; 730 (first entry) EP1074617-A2 26-JUN-2001 07-FEB-2001. 542 602 662 482 1769 841 961 1529 1021 1589 1080 1140 1709 1649 Ношо AAH04973 RESULT ò q Dp a δ ò ò d ò g g Dp à ò ò g ò 셤 à d 쉱 ò 셤 ò 원 ò

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32 GGTACTACGTGAAGGAGGTCCTCAACAAGCACGAGCTGCAGGGGCTTCTACTCCCTGCGCC 381
                                                           CCCTGGAGCGCTACCTGCACATGCTCCTGGCCGACCGCTGCAGGCTGAGCACTTTTATG
                                                                       CCCTGGAGCGCTACCTGCACATGCTCCTGGCCGACCGCTGCAGGCTGAGGCACTTTTTATG
                              AAGACTGGTCTTTTGTGATGGATGAAGAAAGGTCCAGTATGCTTCCTACCATGGCAGCAG
                                                                                                                 AAGACTGGTCTTTTGTGATGGATGGATGAAAGGTCCAGTATGCTTCCTACCATGGCAGGAG
                                                                                                                                            GTCTGAACTCCATACTCTTTGCGATTAACATCGACAACAAGGATTTGAACGGGCAGAGTA
                                                                                                                                                     AGTITGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCCAGAACGTGACCTCCTTGC
                                                                                                                                                                                                      AGTITIGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCANAACGTGA-CTNCTTGC
                                                                                                                                                                                                                                                                                                                                                                                Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                    <u> ACATCGCCTCAGACGTGGGCCGGGGTCGCGCTTGGCTGCGCTGTGCCCTCAACGAACACT</u>
                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22094.
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16-MAR-2000;
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                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGCAGCGATCAAGCAGCCAGCGGGCTTTGCCAGCAAAACCGAAACAGAGCCCGTGTTCT
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                                                                                                                                                                                                      Claim 1; SEQ ID NO 1808; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 730 BP; 173 A; 200 C; 217 G; 137 T; 0 U; 3 Other;
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                                                                                                    Saito K,
Otsuki
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Pred. No. 1.3e-172;
0; Mismatches 13;
                                                                                                   ogai T, Nishikawa T, Hayashi K, Sa
Sugiyama T, Wakamatsu A, Nagai K,
                            27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
                                                02-MAY-2000; 2000JP-00183767.
28-JUL-2000; 2000EP-00116126.
                    99JP-00248036
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Best Local Similarity 97.9%;
Matches 696; Conservative (
                                                                               (HELI-) HELIX RES INST
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                                                                                                   Isogai T,
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      14-AUG-2000;
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08-NOV-2000; 2000US-024653BP.
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08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0249611P.
17-NOV-2000; 2000US-024920BP.
17-NOV-2000; 2000US-024920BP.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-024921BP.
17-NOV-2000; 2000US-024926FP.
17-NOV-2000; 2000US-024926PP. 2000US-0250160P. 2000US-0251988P 2000US-0256719P 2000US-0251030P 05-JAN-2001; 2001US-0259678P 05-DEC-2000; 05-DEC-2000; 06-DEC-2000;

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 22094; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
broteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or delations in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
co supplement the patients own production of (I). Additionally, (I)
co polymucleotides may be used to produce the secreted (I), by inserting the
mucleic acids into a host cell and culturing the cell to express the
concers and creat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic antigen genomic
co AAK87F094 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK84950 and AAM82169
corporation in the exemplification of the present invention

Sequence 33147 BP; 8370 A; 7682 C; 8382 G; 8713 T; 0 U; 0 Other;

1; Gaps 18.5%; Score 352.2; DB 4; Length 33147; llarity 96.4%; Pred. No. 1.8e-84; Conservative 0; Mismatches 13; Indels 1; Query Match Best Local Similarity Matches 371; Conserv

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genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences. AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGACAAAAGACAATTTCTGCTGGAGCGACTGCTGGATGCAGTGAAACAGTGCCAGATCC
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                                                                                                                                                                                                                                                                           Sequence 454 BP; 107 A; 110 C; 151 G; 86 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                        Ouery Match 14.4%; Score 274.6; DB 5; Best Local Similarity 96.2%; Pred. No. 3.3e-64; Matches 277; Conservative 0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oilgomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed
                                                                                                     TTGATGATGAGGAAGATGAGCAGAACTCTGGGGACATGTTTAAAAAGACACTGGGGCAG
                                                                                                                                                GGGAGAGCTCAGAGGACAACTCCGACCGCTCCTCTGTCAATATCATGTCCGCCTTTGAAA
                                                                                                                                                                                                              GCCCCTTCGGGCCTAACTCCAATGGAA-TCAGAGCAGCAACTCATGGAAAATTGATTCCC
                                                                                 TTGATGATGAGGAAGATGAGCAGAACTCTGGGGACGTGTTTAAAAAGACACCTGGGGCAG
                                                                                                                                                                                                                              GCCCCTTCGGGCCAAACTCCAATGGAAGTCAGAGCAGCAACTCGTGGAAAATTGATTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #214.
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                                                                                                                                                                                                                                                                                                                                                                                                          ACTCGGAGTCGCCCGAGAAGCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                      Acreagagregecegagagagagr
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2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS64410 standard; cDNA; 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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P-PSDB; ABG00223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     food supplement;
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Length 454;

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614 CAGGICIGAACTCCATACTCTTTGCGATTAACATCGACAACAAGGATTTGAACGGCAGA 673
Human genome derived single exon probe #8542.
                                                                                                                                                                                                                                                                                           Penn SG,
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                                                                                                                                                                                                                                           correspond to human gene trapped sequences (GTSS). The human GTSS are useful for gene discovery and as markers for gene expression analysis, for identifying and mapping the coding regions of the mammalian, particularly human, genome, for forensic analysis, and for determining the genetic basis of human disease. The peptides and proteins encoded by the genetic basis of human disease. The peptides and proteins encoded by the polynucleotides are useful for generating antibodies, as reagents in diagnostic assays and in identifying other cellular gene products involved in the regulation of development and cellular differentiation of various cell types. The peptides are also useful as reagents in assays for screening of compounds used in treating disorders affecting evelopment and cellular differentiation. The GTSs are also useful in treating or ameliorating disease associated with the expression of mutant or normal variants of the GTSs, e.g. cancer, autoimmune disease, lupus, scleroderma, Crohn's disease, multiple sclerosis, inflammatory bowel disease, immune disorders, schizophrenia, psychosis, inflammatory disorders, diabetes, skin disorders such as ache or eczema, cardiovascular disease, Alzheimer's disease, parkinson's disease, cardiovascular disease, Alzheimer's disease, parkinson's disease, batterial infections. This sequence represents a human GTS of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ACACCTTGAAAAGGAAGGTGGCTGAACAGGAGGAGCGGCAGGGCATGAAGGTCCAGGCGC 240
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                                                                                                                           New isolated or purified human gene trapped sequences, useful for gene
                                                                                                                                           discovery, as markers for gene expression analysis, identifying and mapping the coding regions of human genome, or determining the genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCCTATGAGCAGCCTGNTACCTTCTGCTCAGTGCCAGAGTCCATGACAATTAGTGAAC
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                                                                                                                                                                                                                                  The invention relates to isolated or purified polynucleotides that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 263.8; DB 6; Length 280; Pred. No. 2.38-61; 0; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1703 TGGCCAGCTATCTTTGCTATTTTGTGAGGAGATTCTAACC 1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 280 BP; 71 A; 66 C; 91 G; 51 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TGGCCAGCTATCTTTGCTATTTTGTGAGGAGATTCTAACC 280
                                                                                                                                                                                                     Claim 1; SEQ ID NO 201; 36pp; English.
                                                                Sands AT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.8%;
98.6%;
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Matches 276; Conservative
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                                                                Zambrowicz
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                                                                                           WPI; 2002-656030/70.
   (XAMB/) NEHLS M C.
(ZAMB/) ZAMBROWICZ
(SAND/) SANDS A T.
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                                                                Nehls MC,
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially.

CC addressable set of single exon nucleic acid probes for measuring human cells a purality of single exon nucleic acid probes for measuring human gene expression, a method of comprising a plurality of single exon microarray for measuring human gene expression, a wector comprising the single exon probes cited above, an ORF-encoded peptide comprising at least 8

CC exon microarray for measuring human gene expression, a method of solid above.

CC exon microarray for measure gene expression, a method of solid any of the above- mentioned amino acid solid any of single exon probes of selling and/or licensing single exon probes or microarrays to sequences (optionally with conservative amino acid substitutions), an order desiring to measure gene expression, a method of providing any or sequence desiring to measure gene expression of a single exon probe created antibody that binds specifically to a peptide cited above.

CC a customer desiring to measure gene expression of a single exon probe created method of selling and on the expression of a single exon probe created and a by subscription, and a computer-readable created accorage medium which contains a database having a plurality of records (extression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed measures are useful in gene attentions in the genomic alterations in the genomic alterations in the genomic learned by probes or the inventor services of maller geno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Human, probe, ss, gene expression, single exon probe, microarray, alternative splicing event, genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 215.8; DB 12; Length 542;
Pred. No. 4e-48;
); Mismatches 7; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 542 BP; 135 A; 143 C; 129 G; 135 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR, Hanzel DK;
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95.7%;
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-119264/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surveying tissues.
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                                                                                                                                                   Homo sapiens
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences (ully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule cypressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
CAGGTCCGAACTCCATACTCTTTGCGATTAACATTGACAACAAGGATTTGAACGGGCAGA 436
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                                                                                                            TGCTGAAGGAGTCCACGCAAGGAGTGAGCAGCCTGTTCAGGGAGATCACAGCCTCCTCTG 793
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                                                          GTAAGTTTGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGAATGTGA ---CCT
                                                                                                                                           TECTGAAGGAGTCCACGCAAGGAGTGAGTGATTCAGGGAGATCACAGCCTCCTCTG
                                                                                                                                                                                    CCGTCTCCATCCTCAAACCTGAACAGGAGACCGA-CCCTTGCCTGTCGTGTCCAGGA
                                    GTAAGTTTGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGAACGTGACCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; probe; ss; gene expression; single exon probe; microarray;
alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome derived single exon probe #22242.
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                                                                                                                                                                                                                                                                                                                                                                                              ACH89047 standard; DNA; 284 BP.
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                                                                                                                                                                                                                                                                ATGTCAGTGCTGATG
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records card including data on the expression of a single exon probe cited above. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-enceded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this caingle controlic form part of the printed specification, but was obtained in electronic format directly from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 Greccaacrecaracretrigegarraacarreacaacaagarrigaacegegagra 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              617 AGTITIGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGAACGTGACCTCCTTGC 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         797 TCTCCATCCTCATCAAACCTGAACAGGAGACCGA-CCCTTGCCTGTCGTGTCCAGGAATG 855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 TCTCCATCCTCATCAAACCTGAACAGGAGACCGACCCCTTGCCGGTGTCCAGGAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 212.8; DB 12; Length 284; Pred. No. 1.9e-47; 0; Mismatches 7; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 284 BP; 60 A; 78 C; 74 G; 72 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #28004
                                                                                                                                                                                                                                                                                                                                                                                      seqdata.uspto.gov/sequence.html?DocID=20030194704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS92200 standard; cDNA; 463 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.2%;
Best Local Similarity 95.6%;
Matches 241; Conservative
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Best Local Similarity
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        BXBXBXBXBXSXXXXXBXBXBX
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WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1334 GGCGTGGGCTCCTACAGCCCAGCAGATGCCCCCTCGGAAGCCTGGAGAACGGGACAGGA 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCACGGAAGTCCTCTGAGCAGCCTGTTA-CTTCTGCCTCAGTGCCAGAGTCCATGACA 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGAGGACCACGTTCTCCCGGATCCTGGACTTCGGTACAGTGTGGAAGCCAGCTCTCCA 1453
                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 CCAGAGGACCACGTTCTCCCAGATCCTGGACTTCGGTACAGTGTGGAAGCCAGCTCTCCA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 GGCCACGGAAGTCCTCTGAGCAGCTGTTACCTTCTGCCTCAGTGCCAGGGTCCATGACA 413
                                                                                                                                                                                                                                                                                                                                                                                       diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIDO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 GTCCTCAGCCCTGGCTGAACAAAGATGCCCCCCTCGGAAGCCTGGAGAAGCGGGACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, chromosome mapping, gene mapping; gene therapy, forensic; food supplement, medical imaging; diagnostic; genetic disorder; ss.
                                                                                     New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.3%; Score 195.6; DB 5; Length 463; 93.5%; Pred. No. 1.2e-42; tive 0; Mismatches 14; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 463 BP; 124 A; 133 C; 122 G; 84 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            novel human diagnostic protein #9353.
                                                                                                                                                              Claim 1; SEQ ID NO 28004; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS73549 standard; cDNA; 474 BP.
               Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity 93.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
               Liu C,
                                         WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                       P-PSDB; ABG28013
                                                                                                                                  biodiversity.
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             Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 215;
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AAS73549/c
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cartivity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food polypeptide in tissue, as molecular weight markers and as a food of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations capponable for genetic disorders or other traits to assess produces ity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and to produce other types of data and products dependent on DNA and amino acid sequencee. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AGGGTCACCTGTCTGTGTGCCCCAGTTTGAAGCCGTCCTGCAGCATGGCTTGAAGAGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGGTCACCTGTCTGTGTGCCCCAGTTTGAAGCCGTCCTGCAGCATGGCTTGAAGAAGAGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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79.6%; Pred. No. 3.2e-26;
tive 0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 9353; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCTTCTACTCCCTGCGCCAC 438
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                                                                 30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                    Tang YT;
                                                                                                                                          31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; ABG09362.
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                                                                                                                                                                                                                                                                                                                    RT,
11-0CT-2001
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(first entry)

06-OCT-2000

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The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are defived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                 numan; s' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 16002; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 190 BP; 47 A; 42 C; 73 G; 28 T; 0 U; 0 Other;
                                                      Human secreted protein 5' EST, SEQ ID NO: 16002.
                                                                                                                                                                                                                                                                                                                                                                           Giordano J;
                                                                                                                                                                                                                                                                                                                                                                           Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression and secretion vectors
                                                                                                                                                                                                                                                           21-FEB-2000; 2000EP-00200610.
                                                                                                                                                                                                                                                                                                  99US-0122487P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.3
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                     (GEST ) GENSET
                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                  26-FEB-1999;
                                                                                                                                                                                    EP1033401-A2
                                                                                                                                                                                                                        06-SEP-2000.
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79 GGTGGACACCTTGAAAAGGAAGGTGGCTGAACAGGAGGAGGAGGGCAGGAGGATGAAGGTCCA 138 1698 GGCGCTGGCCAGCTA 1712 139 GCCCTGCCCAGGTA 153 셤 ò δ

1578 CAGATCACTGCGAAACCTGCTCGACGGTGAGATGGAGCACTCAGCCGCGCTCCGGCAAGA 1637

Gaps ö

Score 133.4; DB 3; Length 190; Pred. No. 7.2e-26; 0; Mismatches 1; Indels 0;

7.0%;

19 CAGATCACTGCGAAACCTGCTCGACGGGGATGGAGCACTCAGCCGCGCGCCTCGGCAAGA 78

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Search completed: June 10, 2005, 06:10:07 Job time : 655.812 secs

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Perfect score:

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Scoring table:

Minimum DB s Maximum DB s

Database

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Sequence 1518, Ap Sequence 118, App Sequence 118, App Sequence 118, App Sequence 527, App Sequence 10243, App Sequence 102953, Sequence 102953, Sequence 6278, App Sequence 6278, App Sequence 6278, App Sequence 6278, App Sequence 2201, App Sequence 2463, App Sequence 24633, App Sequence 246
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US-09-563-817-201

US-09-563-817-201

Sequence 201, Application US/09563817

Patent No. US20020095031A1

GENERAL INFORMATION:

APPLICANT: Lambrowicz, Brian

APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. US20020095031A1e1 Human Polynucleotides and the

TITLE OF INVENTION: Polypeptides Encoded Thereby

FILE REFERENCE: LEX-0021-US-11

CURRENT FILING DATE: 2001-06-11

PRIOR APPLICATION NUMBER: US 60/132,343

PRIOR FILING DATE: 1999-05-04

NUMBER OF SEQ ID NOS: 1008

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 201

LEMGTH: 280
0 US-09-918-995-24284

US-09-880-107-1518

US-09-816-995-15177

US-09-816-995-15177

US-10-101-510-527

US-10-101-510-527

US-10-101-510-53

US-10-101-028-3

US-10-021-028-3

US-10-027-4878-385

US-10-027-482-102953

US-10-027-481-102953

US-10-027-481-102953

US-10-027-481-102953

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US-10-027-481-102953

US-10-027-481-106

US-10-121-469-13

US-10-121-2806-319

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US-10-122-206-381

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NAME/KEY: misc feature
LOCATION: (1)._. (280)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: homo sapiens
            46.6
46.6
45.8
45.6
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Sequence 2242, Ap
Sequence 2242, A
Sequence 8136, Ap
Sequence 22036, A
Sequence 948, App
Sequence 9696, App
                                                                                                                                                                                                 June 10, 2005, 14:23:14; Search time 724.339 Seconds (without alignments) 16311.995 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                         1 cattgggtcacgcggtggcg......tcattccttgaaaaaaaa 1906
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| Cgn2_6/ptodata/2/pubpna/US06_PUBW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*
                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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. US-10-029-386-82242

. US-10-029-386-8336

. US-10-029-386-22036

. US-10-029-386-22036

. US-10-276-774-948

. US-09-867-701-9696
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Gaps

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Length 280; Indels

Score 263.8; DB 9; Pred. No. 7.9e-71; 0; Mismatches 3;

Query Match
Best Local Similarity 98.6%;
Matches 276; Conservative

263.8 215.8 212.8 128 124 63.8

Score

Result

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Sequence 22242, Application US/10029386

Sequence 22242, Application US/1004A1

Sequence 22242, Application US/104A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G.
TITLE OF INVENTION: HUMAN GENOME-NET 1000

FILE REFERENCE: AEDONICA-K-2

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 22242
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Sequence 8336, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Fenn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: HAnzel, David R.
APPLICANT: LANGATION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PALLING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 8336
LENGTH: 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   677 AGTITGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGAACGTGACCTCCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          617 GICTGAACTCCATACTCTTTGCGATTAACATCGACAACAAGGATTTGAACGGGCAGAGTA
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                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO CHRIS.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: SMISSPROT HIT: 014197, EVALUE 2.10e-01
OTHER INFORMATION: W HIT: 9114779172, EVALUE 0.000e+00
OTHER INFORMATION: EST_HUMAN HIT: BF975008.1, EVALUE 0.00e+00
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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Matches 241; Conserv
RESULT 3
US-10-029-386-22242/c
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Publication No. US20030194704A1
Publication No. US20030194704A1
APPLICANT: Rank, David R.
APPLICANT: Hank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION UNMERR: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 8542
LENGTH: 542
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1464 GICCICIGAGCAGCCIGITA CITCIGCCICAGIGCCAGAGICCAIGACAAITAGIGAAC 1522
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                                                                                                                                                                             ACACCTTGAAAAGGAAGCTGGCTGAACAGGAGGAGCGGCAGGGCATGAAGGTCCAGGCGC
                      Gaps
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: IT HIT: G114779172, EVALUE 0.000+00
OTHER INFORMATION: SWISSPROT HIT: 0.14197, EVALUE 5.900-01
OTHER INFORMATION: EST_HUMAN HIT: BG340557.1, EVALUE 0.000+00
                                                                                                                                                                                                                                                                                                          TGGCCAGCTATCTTTGTGAGGAGATTCTAACC 1742
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Best Local Similarity 95.7
Matches 244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-10-029-386-8542/c
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Sequence 948, Application US/10276774

Sequence 948, Application US/10276774

Publication No. US20040053245A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TILLE OF INVENTION: NO. US20040053245A1e1 Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-030

CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT APPLICATION NUMBER: 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SEQ ID NO 948

LENGTH: 3931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3721 CTGGCTACTGGGTGCTCGTGGTGCATTTTACTCGGAGAGAGGCCATCAAGCAGATCGAGG 3662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 CCGTGTTCTGGTACTACGTGAAGGAGGTCCTCAACAAGCACGAGCTGCAGCGCTTCTACT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    548 CTTTTTATGAAGACTGGTCTTTTGTGATGGATGAAGAAAGGTCCAGTATGCTTCCTACCA 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 ACGAACACTCCCTGGAGCGCTACCTGCACATGCTCCTGGCCGACCGCTGCAGGCTGAGCA
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Fatent No. US2002013237A1

GRERAL INFORMATION:
APPLICANT: Adjate, Paul A.
APPLICANT: Jones, Robert
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER
FILE REFREENCE: 210121.497

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
3.3%; Score 63.8; DB 18;
Best Local Similarity 51.6%; Pred. No. 3.3e-08;
Matches 146; Conservative 0; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-948
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ORGANISM: Homo sapien
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                                                                                                                                            US-10-276-774-948/c
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Publication No. US20030194704A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: EXPERSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 22036
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OTHER INFORMATION: MAP TO CHRI6.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN HELACENTA, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3

OTHER INFORMATION: STISSROT HIT: 092883, EVALUE 1.200+00

OTHER INFORMATION: NT HIT: 9115315787, EVALUE 2.00e-65

OTHER INFORMATION: EST_HUMAN HIT: AL135642.1, EVALUE 2.00e-65

US-10-029-386-8336
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BUDLT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5
OTHER INFORMATION: BXPRESSED IN HELA, SIGNAL = 1.5
OTHER INFORMATION: BXT HUMAN HIT: AL135642.1, EVALUE 1.00e-63
OTHER INFORMATION: SWIŠSPROT HIT: Q9SXUI, EVALUE 6.00e+00
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Pred. No. 1.3e-27;
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Pred. No. 1.4e-28;
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100.0%; Pred. No. 1...
... 0; Mismatches
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100.0%; Pred. No. 1...
... 0; Mismatches
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CGAAACAG 468
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-029-386-22036
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US-10-029-386-22036
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US-09-854-867-118
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                                                                1793 GITCCTGAIAGICTCATITGAGCTCCTGGAICCAGTCTTTCCTGAAGCTGTGITTCCTCT 1852
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US-09-880-107-1518
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Sequence 1518, Application US/09880107

Patent No. US2002014298111

GENERAL INFORMATION:

APPLICANT: HORINE, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

APPLICANT: Gene Expression Profiles in Liver Cancer

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT APPLICATION NUMBER: US 60/211,379

PRIOR PILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 1518

LENGTH: 446
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APPLICANT: Hyesq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
FILE REFREENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOUTHWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24284
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  Pred. No. 1.8e-07;
0; Mismatches 34; Indels
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Pred. No. 7.4e-06;
0; Mismatches 29;
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Publication No. US20030073623A1
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Best Local Similarity 73.5%;
Matches 83; Conservative
ilarity 70.2%;
Conservative
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CORGANISM: Homo sapiens
US-09-918-995-24284
    Best Local Similarity
Matches 80; Conserv
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Sequence 118, Application US/09854867

Sequence 118, Application US/09854867

Publication No. US20030224356A1

GENERAL INFORMATION:

APPLICANT: NOGAN, KNOLL H

APPLICANT: ROGAN, ENTER K

TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING.

CURRENT APPLICATION NUMBER: US/09/854,867

CURRENT APPLICATION NUMBER: 2003-05-08

NUMBER OF SEQ ID NOS: 613

SOFTWARE: Patentin version 3.1
                                                                                            1795 recrearance entricas de la conserva en 1795 recreas de la 1853
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; Publication No. US20030073623A1
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
; TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
; TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 38054
; SEQ ID NOS: 38054
; SEQ ID NOS: 38054
; SEQ ID NO 15177
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57.8%; Pred. No. 1.3e-05;
iive 0; Mismatches 70; Indels
                                                 29; Indels
Score 54.6; DB 9;
Pred. No. 8.2e-06;
0; Mismatches 29;
         2.9%;
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Best Local Similarity 57.8
Matches 96; Conservative
            Query Match
Best Local Similarity 73.5°
Matches 83; Conservative
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LOCATION: (1)..(476)
OTHER INFORMATION:
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 476
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6443 TCCTGATGACAGCGTTTGTGCCCCTGGATCCAACCGTGCCTGAAGCTAGAATATCCCCTG 6502
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CURRENT FILING DATE: 2002-09-13
FRIOR PAPLICATION NUMBER: 09/764,897
FRIOR PAPLICATION NUMBER: 09/764,897
FRIOR PELING DATE: 2001-01-73
FRIOR PELING DATE: 2000-01-31
FRIOR PAPLICATION NUMBER: 60/180,628
FRIOR PELING DATE: 2000-02-04
FRIOR PELING DATE: 2000-02-04
FRIOR PELING DATE: 2000-05-28
FRIOR APPLICATION NUMBER: 60/217,487
FRIOR APPLICATION NUMBER: 60/217,487
FRIOR PELING DATE: 2000-06-18
FRIOR PELING DATE: 2000-07-11
FRIOR APPLICATION NUMBER: 60/225,758
FRIOR PELING DATE: 2000-08-14
FRIOR PELING DATE: 2000-07-16
FRIOR PELING DATE: 2000-08-14
FRIOR PELING DATE: 2000-08-14
FRIOR PELING DATE: 2000-08-14
FRIOR PELING DATE: 2000-07-12
FRIOR PELING DATE: 2000-07-14
FRIOR PELING DATE: 2000-07-14
FRIOR PELING DATE: 2000-07-14
FRIOR FILING DATE: 2000-08-14
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Sequence 527, Application US/10101510
| Publication No. US20030148295A1
| GENERAL INPORMATION:
| APPLICANT: WAN, JACKSON
| APPLICANT: WAN, JACKSON
| TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
| FILE REFERENCE: 15.17.0012
| CURRENT APPLICATION NUMBER: US/10/101,510
| CURRENT FILING DATE: 2002-03-20
| PRIOR PILING DATE: 2001-03-20
| WINDER OF FILING DATE: 2001-03-20
| NUMBER OF SEQ ID NOS: 805
| SOFTWARE: Patentin Ver. 2.1
| LENGTH: 7093
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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Pred. No. 0.00077;
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Publication No. US20030235831A1
GENERAL INFORMATION:
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Best Local Similarity 74.0%;
Matches 77; Conservative
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ORGANISM: Homo sapiens
US-10-101-510-527
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Best Local Similarity
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DATABASE ENTRY DATE:
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DATABASE ENTRY DATE: 1996-01-26
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                                     Query Match 2.8%; Score 53.2; DB 10; Length Best Local Similarity 69.5%; Pred. No. 2.3e-05; Matches 89; Conservative 0; Mismatches 33; Indels
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JOURNAL: Journal of Molecular Evolution
VOLUME: 35
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SOFTWARE: Patentin version 3.0
SEQ ID NO 118
LENGTH: 476
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LOCATION: (1)...(476)
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
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ORGANISM: Homo sapiens
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PAGES: 286-291
DATE: 1992-10-
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RESULT 15
US-10-437-963-63143
i Sequence 63143, Application US/10437963
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i Sequence 63143, Application US/20040123343A1
i GENERAL INCRMATION:
i APPLICANT: La Rosa, Thomas J.
APPLICANT: Exou, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Houkharov, Andrey A.
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 63143
TYDE: NUMBER OF SEQ.
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2.6%; Score 50.2; DB 19; Length 550;
Best Local Similarity 87.3%; Pred. No. 0.00021;
Matches 55; Conservative 0; Mismatches 8; Indels 0
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  0; Mismatches 26; Indels
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NAME/KEY: unsure
LOCATION: (1)..(550)
OTHER INFORMATION: unsure at all n locations
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    Matches 77; Conservative
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/clone="IMAGE:5088007"
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BM668241 UI-E-CKI-
BQ064251 AGENCOURT
BQ065026 AGENCOURT
BG055026 AGENCOURT
BG757448 602711092
BG758677 602712923
BG758425 602712623
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GenCore version 5.1.6 . Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                                         OM nucleic - nucleic search, using sw model
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		p mRNA linear 007, mRNA. Craniata; Vertebrata;	.mates; Catarrhini; Hominidae; Hom National Institutes of Health, M Cancer Genomics Office, National .ive, Room 11A03, Bethesda, MD 208	ci.nih.gov aboratory A.G.E. Consorti Canada Bosdet, Yaron Fjell, Erin Ga Fjell, Erin Ga ewson, Candice abbu, Parvaneh ith, Lorraine S tasja van den B	distribution information ium/LLNL at: http://imacColumn: 22
BF975008 BQ058038 BQ061749 BQ061744 AW974284 AW977633 BG757633 BG757633 BG757633 AX399019 AX39019 AX39019 AX39019 AX39315 AX39315 AX39333 AX39334 AX293334 AX63353 AX63353 AX63353 AX63353 AX63353 AX63353 AX63353 AX63353 AX63353 AX63353 BG759800	ALIGNMENTS	1981 b IMAGE:5088 130 Chordata;	a; Primates; Cata: 81) -2002) National II MGC), Cancer Genor ter Drive, Room I	h.gov n. Staudt n. Rubin L. ". The I.M. "e Sequenc uver, BC, Asano, Ian hiu, Chris Krzywinski arrisa Pr Michael Sm a-Liisa Pr Michael Sm a-Liisa Pr A-Liisa Pr A-Liis	tribution: MGC clone distribut he I.M.A.G.E. Consortium/LLNL RAL Plate: 42 Row: m Column: 2 has the following problem: 1 Location/Qualifiers 1. 1981 / organism="Homo sapiens" / mol type="mRNA" / db_xref="taxon:9606"
8.8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		clone :22028 human) azoa;	256	USA Contact: MGC help desk Contact: MGC help desk Email: cgapbs-rømail.nih.gov Tissue procurement: Lou Stau- CDNA Library Preparation: Ru- CDNA Library Arrayed by: The DNA Sequencing by: Genome Se BC Cancer Agency, Vancouver, infe@bcgsc.bc.ca Steven Jones, bennifer Asano Steven Jones, bennifer Asano Sen Lee, Victor Ling, Carrie Schich, Duane Smailus, Micha Michael Thorne, Miranada Tsa Michael Thorne, Miranada Tsa George Yang, Scott Zuyderduy	Clone distribution: MGC clone through the I.M.A.G.E. Consort Series: IRAL Plate: 42 Row: m This clone has the following F Location/Qualifiers 1. 1981 /organism="Homo sapie /Mol. type="mRNA" /db_xref="taxon:9606'
454.8 23. 445.2 23. 445.2 23. 431.2 22. 431.3 22. 431.4 22. 431.4 22. 382.4 22. 382.4 20. 382.4 20. 370.8 119. 370.8 119. 370.8 119. 371.6 118. 343.118.		BC024 HOMO BC024 BC024 HTC. HOMO	Mammalla 1 (base Strausbe Direct S Submitte Gene Col Institut	USA UNH-MGC Contact: Contact: Tissue P CDNA Lib DNA CAD DNA CAD DNA CAD DNA CAD DNA CAD DNA CAD DNA CAD DNA CAD DNA CAD DNA CAD CAD SUSANNA NESS, DESS, NESS, DESS, DESS, NESS, DESS, DESS, DESS, DESS, NESS, DESS, DESS	
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96; Conservative
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Homo sapiens
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855; Conservative 0; Mismatches
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/lab_host="DH10B"
/note="Vector: pOTB7"
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HRI human CDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
RRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTGGAGCGCTACCTGCACATGCTCCTGGCCGACCGCTGCAGGCTGAGCACTTTTTATG 556
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                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 730)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAGTTTGAAGCCGTCCTGCAGCATGGCTTGAAGAGAGGAGTCGAGGATTGGCACTCACAG
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AU122438 MAMMA1 Homo sapiens cDNA clone MAMMA1002380 5', mRNA
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97.9%; Pred. No. 8.5e-171
tive 0; Mismatches 13
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/organism="Homo sapiens"
/organism="Homo sapiens"
/mol type="mRNA"
/db xref="texon:9606"
/clone="MAMMA102380"
/clone lib="MAMMA1"
/note="Vector: pME18SFL3"
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                            Matches 681;
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Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seg prime: M13 Forward
POLYA=Yes.
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UI-E-CK1-afk-h-18-0-UI.82 UI-E-CK1 Homo sapiens cDNA clone
UI-E-CK1-afk-h-18-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                 AGTITGCTCCCACCGTITCAGACCTCTTAAAGGAGTCAACGCAGAACGTGACCTCCTIGC 736
AAGACTGGTCTTTGTGATGGATGAAGAAAGGTCCAGTATGCTTCCTACCATGGCAGCAG 616
                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 691)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                             GTCTGAACTCCATACTCTTTGCGATTAACATCGACAACAAGGATTTGAACGGGCAGAGTA
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Coordinated Laboratory for Computational Genomics
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sapiens
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site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Bye Institute (NEI).
TAG IISSUE-Poveal and Macular Retina TAG_LIB-UI-E-CK1
TAG_ESEQ=GTCC"
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5/, mRNA sequence.
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BQ064251.1 GI:19892719
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11; Conservative
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
1 (bases 1 to 990)
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BQ060776.1 GI:19884191
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ilarity 96.6%;
Conservative (
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Homo sapiens
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                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: egapbe-remail.nih.gov
Email: egapbe-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2098 row: column: 01
High quality sequence stop: 692.
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                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 998)
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Pred. No. 3e-159;
0; Mismatches 18;
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Best Local Similarity 96.7%;
Matches 675; Conservative
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G): Size-selected >500bp for average insert size
I.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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AGENCOURT_7049038 NIH_MGC_99 Homo sapiens CDNA clone IMAGE:5816452
5', mRNA sequence.
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NIH-MOC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt

cDNA Library Preparation: Rubin Laboratory

cDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/LLNL at:

http://image.llnl.gov

Right quality sequence stop: 686.
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Catarrhini, Hominidae, Homo.
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Pred. No. 1.2e-158;
); Mismatches 19;
                                                                                             1082 TCATGGAAATTGATTCCCTGTCTTTGAACGGGAGT
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EcoRI,coNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II.RT (Life Technologies). Note: this is a NIH_MGC
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Best Local Similarity 96.7%;
Matches 670; Conservative
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AGENCOURT 6856627 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929505
5', mRNA Sequence.
BQ065026
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            GTGA----CCTTGCTGAAGGAGTCCACGCAAGGAGTGAGCAGCGTGTTCAGGGAGATCACA
ACCATGGCAGCAGGTCCGAACTCCATACTCTTTGCGATTAACATTGACAACAAGGATTTG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
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                                                                                        544 AGCACTTTTATGAAGACTGGTCTTTTGTGATGGATGAAGAAAGGTCCAGTATGCTTCCT
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Score 624.2; DB 5;
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC_48"
/clone_lib="NHH MGC_48"
/note="Organ: B-cells, Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAhol sites using the
following 5' adaptor: GGGAGGAG(G). Size-selected 5:00bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 829)
 602711092F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851502 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCW1694 row: g column: 23
High quality sequence stop: 801.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                           Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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larity 95.9%; Pred. No. 6e-154;
Conservative 0; Mismatches 23; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4851502"
                                                      BG757448.1 GI:14068101
                                                                                              sapiens (human)
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602712923F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853188 5',
mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llhi.gov

Plate: LLCM1698 row: n column: 05

High quality sequence stop: 819.
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730 AAAAGCATCGATGATGAAGATGGGATGAAAACGAAGATGACGTGCTATGGAAAACTCATC
                                                                                                                                                      1023 ATCATGTCCGCCTTTGAAAGCCCCCTTCGGGCCTAACTCCAATGGAA-TCAGAGCAGCAAC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 835)
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/organism="Homo sapiens"
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov.bltp://image.llnl.gov.bltp://image.llnl.gov.cov.a column: 24 Plate: LLCMO165 row: a column: 24 High quality sequence stop: 641.
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Pred. No. 3.5e-152;
0; Mismatches 22;
                                                                                                                          organism="Homo sapiens"
                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 96.0%;
Matches 652; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1022)
                                                                                                                                                                                             GTGA---CCTTGCTGAAGGAGTCCACGCAAGGAGTGAGCAGCGTGTTCAGGGGGAGTCACACA
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
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17; Indels
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NH10B (cell line)"
/clone_lib="NH10B (cell line)"
/clone_lib="NH10B (cell line)"
/clone_lib="NH10B (cell line)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXXhoI sites using the following 5' adaptor: aGGACGAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                     BG756425 843 bp mRNA linear EST 15-MAY-2001
602712623F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853164 5',
mRNA sequence.
BG758428
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                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 843)
MNH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               544 AGCACTTTTTATGAAGACTGGTCTTTTGTGATGGATGAAGAAAGGTCCAGTATGCTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The T.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
High quality sequence stop: 835.
High quality sequence stop: 835.
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96.2%; Pred. No. 2.4e-151;
ive 0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .843
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9666"
/clone="IMAGE:4853164"
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
1202 GGAAGGAAGCACAGGGGCC 1220
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                                  727 ggacggaacacaggggc
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AUTHORS
TITLE
JOURNAL
COMMENT
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892 bp mRNA linear EST 29-MAR-2002
AGENCOURT 6769190 NIH_MGC_99 Homo saplens cDNA clone IMAGE:5812156
5', mRNA Sequence.
                                                                                                                                                                                                                                                                          963 AAAAAGACACCTGGGGCAGGGGAGAGCTCAGAGGACAACTCCGACCGCTCCTCTGTCAAT 1022
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NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                      559 AAAAAGACACCTGGGGGGGGGGGGGGGGTCAGGGGACAACTCCGACCACTCTGTGTATT
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Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2062 row: c column: 05
High quality sequence stop: 608.
439 GTGTCCAGGAATGTCAGTGCTGATGCCAAATGCAAAAAGCAGCGGAAGAAGAAAAAGCAA
                                                                                                                                                                                                499 GTGACCAACATTATCTCATTTGATGAGGAAGATGAGCAGAACTCTGGGGACATGTTT
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BM692924 609 bp mRNA linear EST 28-FEB-2002 UI-E-CK1-afk-h-18-0-UI.rl UI-E-CK1 Homo sapiens cDNA clone UI-E-CK1-afk-h-18-0-UI 5', mRNA sequence.
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of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                     GCCTCCTCTGCCGTCTCCATCAAACCTGAACAGGAGACCGA-CCCTTGCCTGTC
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                                                                                                                             7;
                                                                                                Length 892;
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                                                                                             Score 600.4; DB 5;
Pred. No. 2.8e-151;
0; Mismatches 51;
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                                                                                              Query Match 31.5%;
Best Local Similarity 92.1%;
Matches 678; Conservative
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BM692924.1 GI:19006182

EST

Homo sapiens (human) Homo sapiens

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/clone="UT-B-CK1-360"
/clone="UT-B-CK1-360"
/clone="UT-B-CK1-360"
/dev stage="Retina Foveal and Macular"
/dev stage="adult"
/lab_host="NbH00B (life Technologies) (T1 phage resistant)"
/clone lib="UT-B-CK1"
/clone lib="UT-B-CK1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UT-B-CK1 is a normalized cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonalo. Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library as sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1334
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                                                                                                                                                                                                                                                                                                                                                                                        Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (ases 1 to 609)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
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                                                                                                                                                                                                                                                              Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                        Contact: Soares, MB
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/lab_host="DH10B (phage-resistant)"
/clone_lib="MIH MGC_48"
/clone_lib="MIH MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: Xho1;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1Xho1 sites using the following 5' adaptor: GGGACGAGG): Size-selected >500pp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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E 1 (bases 1 to 813)

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602635896F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763783 5',
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/clone="IMAGE:4763783"
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Bonaldo, M.P., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                  <u> AGCACTTTTTATGAAGACTGGTCTTTTGTGATGGATGAAGAAAGGTCCAGTATGCTTCCT</u>
                                                                                                                                                                                            ACCATGGCAGCAGGTCTGAACTCCATACTCTTTGCGATTAACATCGACAACGATTTG
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     Length 813;
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Score 550.8; DB 4;
Pred. No. 7.9e-138;
0; Mismatches 17;
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BQ184171.1 GI:20359722
28.9%;
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                                               Conservative
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781

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/mol_type="maxna" saptems
/mol_type="maxna" saptems
/db xref="taxon:9606"
/clone="maxna" saptems
/tissue type="primary B-cells from tonsils (cell line)"
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/clone="by HMGC 48"
/note="organ: B-cells; vector: poTB7; Site_1: Xho1;
Site_2: EcoR1; cDNA made by oligo-dr priming.
Directionally cloned into EcoR1/XhoI sites using the
following 5: adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG759681 87 87 15-MAY-2001 802713374F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853346 5',
                                                                                                                                                                                  184 ACGTGACCTCCTTGCTGAAGAGTCCACGCAAGGAGTGAGCAGCCTGTTCAGGGAGATCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   544 AGCACTTTTTATGAAGACTGGTCTTTTGTGATGAAGAAAAGGTCCAGTATGCTTCCT 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Light Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1699 row: d column: 19
High quality sequence stop: 791.
High quality sequence stop: 791.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 819)
                                                                                                                                                                                                                                                                                                                      244 TGAACGGGCAGAGTAAGTTTGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGA
                                                                                                                                                                                                                                                        782 CAGCCTCCTCTGCCGTCTCCATCCTCATCAAACAGGAGACGA-CCCTTGCCTG
                        662 TGAACGGGCAGAGTAAGTTTGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGA
                                                                                                                                          722 ACGTGACCTCCTTGCTGAAGGAGTCCACGCAAGGAGTGAGCAGCCTGTTCAGGGAGATCA
                                                                                                                                                                                                                                                                                                                                                                             841 TCGTGTCCAGGAATGTCAGTGCTGATGCCAAATGCAAAAAGGAGCGGAAGAAGAAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Gaps
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Pred. No. 1.3e-127;
0; Mismatches 33;
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26.9%;
Best Local Similarity 93.3%;
Matches 603; Conservative
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/lab_nost="DH10B (Life Technologies) (T1 phage resistant)"
/lab_nost="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UI-B-ED1"
/note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-B-ED1 is a subtracted CDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand CDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded CDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT773-Pac
vector: The oligonodleocide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)! B tail. The
sequence tags for this library are: fetal eyes,
AGANTCAAGA; lens, CGATTAGCGA; eye anterior segment,
AATGCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI).
TAG_ENEB-Luman retina
TAG_ENEB-LI-E-ED1
TAG_ENEB-LI-E-ED1
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Lowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
7e1: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seg primer: M13 FORWARD
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCTCAACGAACACTCCCTGGAGCGCTACCTGCACATGCTCCTGGCCGACCGCTGCAGGC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTACTCCCTGCGCCACATCGCCTCAGACGTGGGCCGGGGTCGCGCCTGGCTGCGCTGTG 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTACCATGGCAGCAGGTCTGAACTCCATACTCTTTGCGATTAACATCGACAACAAGGATT 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGAGCCCGTGTTCTGGTACTACGTGAAGGAGGTCCTCAACAAGAGGACGAGGTGCAGCGCT
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                           AACGGGCAGAGTAAGTTTGGTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGAAC 723
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                         237 ACCATGGCAGCAGCAGCTCCCATACTCTTTGCGATTAACATTGACAACAACAACTTG
GTGAAAAGCATCGATGATGATGT--GGATGAAAACGAAGATGA 1182
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Sequence 16212, A
Sequence 12402, A
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Sequence 13770, A
Sequence 13770, A
Sequence 118, App
Sequence 12759, A
Sequence 15004, A
Sequence 15004, A
Sequence 15004, A
Sequence 15913, A
Sequence 15934, A
Sequence 15934, A
Sequence 15934, A
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2453, Ap
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12107, A
15878, A
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Compugen Ltd.
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US-09-513-999C-16212
US-09-270-767-12402
US-08-232-463-14
US-09-949-016-13770
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Sequence 8383, Ap Sequence 878, App Sequence 878, App Sequence 1119, App Sequence 1107, App Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 15, Appli
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                                                                                                                         94, Apr. 2882, Ap. 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16002, Application US/09513999C

| Patent No. 6783961
| Patent No. 6783961
| GENERAL INFORMATION:
| APPLICANT: Dumas Milne Edwards, J.B.
| APPLICANT: Duclert, A.
| APPLICANT: Giordano, J.Y.
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| PATENT FILE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| PATENT APPLICATION NUMBER: US/09/513,999C
| CURRENT FILING DATE: 1999-02-26
| CURRENT FILING DATE: 1999-02-26
| NUMBER: OF SEQ ID NOS: 36681
| SOFTWARE: PATENT: DOTE |
| SEQ ID NO 16002
| LENGTH: 190
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US-09-513-999C-16212
; Sequence 16212, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.; Patent No. 6783961
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                                                             US-09-902-540-2596
US-09-902-540-1119
US-09-902-540-1119
US-09-621-976-2882
US-09-621-976-2882
US-09-621-976-2882
US-09-621-976-2882
US-09-621-976-2882
US-09-130-114-1
US-08-910-647-1
US-08-910-647-1
US-07-884-811-15
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1304
13417
1774
1926
1926
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9600
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9600
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US-09-513-999C-16002
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   410 AGCTGCAGCGCTTCTACTCCCTGCGCCCACATCGCCTCAGACGTGGGCCGGGGTCGCGCCT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456 AACGTCAGAGGTATATGGACCTTAAGCAGATCTGGACGAATGTGGGGCAGAGACGTGCCT 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 GCAGGMMGGCGGCGCGCGCGCAGCCACCGGCCCCGGGAGAGGCACCATGAGCGGATCACAG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic 3126-094
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: 05/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12402
LENGTH: 811
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Matches 83; Conservative 2; Mismarth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 AACNATGACAAAAGACAATTTCTGCTGGAGCG 164
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               CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SSQ TD NO 16212
LENGTH: 100
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; ORGANISM: Drosophila melanogaster
US-09-270-767-12402
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US-09-513-999C-16212
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                                                                                                                                                                                                                                                                                   LOCATION: 13 OTHER INFORMATION: m=a or
FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 14
                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
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Matches 173; Conserv
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US-09-270-767-12402
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                                                                                                                                                                                                                                           FEATURE
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1000 ACTCCGACCGCTCCTCTGTCATATCATGTCCGCCTTTGAAAGCCCCTTCGGGCCTAACT 1059
940 AGCAGAACTCTGGGGACGTGTTTAAAAAGACACCTGGGGCAGGGGAGAGCTCAGAGGACA
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                                                                                                                Length 7218;
                                                                    650 ACAACAAGGATTTGAACGGGCAGAGTAAGTTTGCTCCCACCGTTTCAGAC
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
2.9%; Score 55.6; DB 1;
Best Local Similarity 4.7%; Pred. No. 0.00017;
Matches 19; Conservative 223; Mismatches 162;
                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
ITILE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT: Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                   Sequence 14, Application US/08232463; Patent No. 5670367; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
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IMMEDIATE SOURCE:
CLONE: pTZgpt-Fls
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ZIP: 22313-0299
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2.9%;
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Best Local Similarity 63.19
Matches 82, Conservative
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LOCATION: (1)..(476)
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
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                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-69138
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US-09-949-016-13770/c
; Sequence 13770, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR PLING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR SPLING DATE: 2000-10-03
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US-09-949-016-69138/C
US-09-949-016-69138/Application US/09949016
Facent No. 681239
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOJ1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                          6869 AAAAGTIGAACCAAGACGGAGAAAAGTITCCIGAIGACCTCATIAGAAIACCIGGAICCAG 6810
1060 CCAATGGAATCAGAGCAGCAACTCATGGAAAATTGATTCCCTGTCTTTGAACGGGGAGTT 1119
                                  TGGGTACCAGAAGCTTGATGTGAAAAGCATCGATGATGAAGATGTGGATGAAAACGAAGA 1179
                                                                                                                                                                                                                     1180 TGACGTGTATGGAAACTCATCAGGAAGGAAGCACAGGGGCCACTCGGAGTCGCCCGAGAA 1239
                                                                                                                                                                                                                                                    1768 AATGGAGGAGAGAAATCCAACAGTTCCTGATAGTCTCATTTGAGCTCCTGGATCCAG 1827
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                                                                                                                                                                                                                                                                                                                                  1240 GCCACTGGAAGGGAACACCTGCCTCTCCCAGATGCACAGCTGGG 1283
                                                                                                                                                                                                                                                                                                                                                                                   1076 RRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCCCAAGCTCGG 1033
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-13770
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APPLICANT: JOAN, KNOLL
APPLICANT: ROGAN, PETER
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATINFILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SOFTWARE: Patentin version 3.0
SEQ ID NO 118
LENGTH: 476
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PAGES: 286-291

DATABASE 286-290

DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)

DATABASE ENTRY DATE: 1996-01-26

US-09-573-0804-118
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                                                                                                                                                                                                                                                                                                                                       Score 54.4; DB 4; Length 601;
Pred. No. 0.0001;
1; Mismatches 47; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A TITLE: Prototypic sequences for human repetitive DNA JOURNAL: Journal of Molecular Evolution VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1768 AATGGAGGAGAGAGAAATCCAACAGTTCCTGATAGTCTC
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 69138
LENGTH: 601
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RESULT 10

US-09-949-016-15004/c

Sequence 15004, Application US/09949016

Sequence 15004, Application US/09949016

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOD.307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2007012

SOCTHARE: PSELSEQ for Windows Version 4.0

LENGTH: 60276
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Sequence 15694, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 00/0941,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
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3752 AAGAAAGAGAGTGAGTGACCATTTCTTTATTCCATCCTTTGAGGCCCTACACTAA 3811
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LOCATION: (60276)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-15004
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Sequence 221, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Purness, Mic
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Sequence 12759 Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,468
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-09
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Best Local Similarity 61.5%; Pred. No. 0.0067;
Matches 80; Conservative 0; Mismatches 50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 330927.1
US-09-976-594-221
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12759
LENGTH: 9811
                                        1890 TTCCTTGA 1897
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ORGANISM: Homo sapiens
                                                                                                                433 TTGCTTAA 440
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US-09-949-016-12759
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 6/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRAELSO for Windows Version 4.0
SEQ ID NO 12713
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Patent No. 6812339
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US-09-949-016-15935/C
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                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12713
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Fatent No. 6812339

GENERAL INFORMATION:
FOUNDAMINER, J. Craig et al.
APPLICART: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT FILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-02-16
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 11901
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOLAND

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
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                                                                                                                                                                                                                                      Score 46.8; DB 4; Length 60338;
Pred. No. 0.13;
0; Mismatches 22; Indels 0;
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67.3%; Pred. No. 0.16;
tive 0; Mismatches 32;
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                                                                                                                NAME/KEY: misc feature
LOCATION: (1)...(60338)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                      Query Match 2.5%;
Best Local Similarity 73.2%;
Matches 60; Conservative
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Matches 66; Conserv
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                                                   TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
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SEQ ID NO 15694
LENGTH: 60338
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE REPERBENCE: CL001307
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PLICATION NUMBER: 60/231,498
PRIOR PLILNG DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHARE: FEBSCE FOR WINDOWS VERSION 4.0
IERCHH: 94135
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Patent No. 6812339
GENERAL INFORMATION:
PAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
                                                                                                                                                                                    40227 AGAGCCTGAGAACACAGTTTAAGCATTTGAAGTCAGCTATGCCTGAAGCCATGCTCCCTC 40168
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Best Local Similarity 67.3%; Pred. No. 0.16;
Matches 66; Conservative 0; Mismatches 32;
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Best Local Similarity 67.3%; Pred. No. 0.16;
Matches 66; Conservative 0; Mismatches 32;
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                        45554873 segs, 20411521753 residues
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Maximum Match 100%
Listing first 45 summaries
                                       - nucleic search, using sw model
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1906
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Sequence 6, Appli
Sequence 5, Appli
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47 US-00-155-676-1

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128 US-09-629-469A-14016

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  Result
No.
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180 240 240 180 61 ATTCGAGGCCACGAAGGCCGGCGCGCGCGCANGCACCGGGCCCGGGGANAGGCNCCATG 120 9 9 121 AGCGGATCNCNGAACNATGACAAAAGAAATTTCTGCTGGAGCGACTGCTGGATGCAGTG AAACAGTGCCAGATCCGCTTTNGAGGGAGAAAGGAGATTGCCTCGGATTCCGACAGCAGG 1 CATTGGGTCACGCGGTGGCGCGCTCTAGAATAGTGGATCCCCCGGGCTGCAGGAATTCG RESULT 1
US-09-155-676-1
i Sequence 1, Application US/09155676
i GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: WALLACH, David
APPLICANT: WALLACH, Mark
APPLICANT: WOVILENKO, Andrei
APPLICANT: WOVILENKO, Andrei
APPLICANT: METT, IGOT
TITLE OF INVENTION: MODULATORS OF THE RECEPTOR ASSOCIATED
TITLE OF INVENTION: PACTOR (TRAF), THEIR PREPARATION AND USE
UNMBER OF SEQUENCES: 20
CORRESSONDRESSE: BROWDY AND NEIMAR, P.L.L.C.
STREET: 624 Ninth Street, N.W., Suite 300
CITT: WARBINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001 ö Query Match
99.6%; Score 1899; DB 17; Length 1906;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1906; Conservative 0; Mismatches 0; Indels 0; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER:
FILING DATE: 04-JAN-1999
CLASSIFICATION NUMBER: PCT/IL97/00117
APPLICATION NUMBER: PCT/IL97/00117
APPLICATION NUMBER: PCT/IL97/00117
FILING DATE: 01-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 11 117800
FILING DATE: 02-APR-1996
PRIOR APPLICATION NUMBER: 26-AUG-1996
ATTOMENTY RECOMMATION:
APPLICATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
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REGISTRATION NUMBER: 20-628-5197
TELEFRONE/POCKET NUMBER: 25,618
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TELEFRANCE 202-733-3528
INFORMATION FOR SEQ ID NO: 1:
COMPATION FOR SEQ ID NO: 1: LENGTH: 1906 base pairs TYPE: nucleic acid STRANDEDNESS: single ; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-09-155-676-1 181 181 g g ð g δ 엄 ò ò

ALIGNMENTS

	1501	1621 GCCGCGCTCCGCCAAGAGGTGGACACCTTGAAAAGAGGTGGCTGAACAGGGACGGGTBBD 1621 GCCGCGCTCCGGCAAGAGGCACCTTGAAAAGGGAGGGGCTGAACAGGAGGAGGAGGGGGGGG	QY 1801 TAGTCTCATTTGAGCTCCTGGATCCAGTCTTTCCTGAAGCTGTTTCCTCTGGACTTTT 1860 Db 1801 TAGTCTCATTTGAGCTCCTGGATCCAGTCTTTCCTGAAGTTTCCTCTGGACTTTT 1860 QY 1861 CATGTATGTGAGCCAATAAATTGCTTTCATTCCTTGAAAAAAAA	RESULT 2 US-09-155-676A-1 Sequence 1, Application US/09155676A GENERAL INFORMATION: APPLICANT: WALLACH, David APPLICANT: WALINN, Nikolai APPLICANT: ROUDIN, Mark APPLICANT: KOVALENKO, Andrei APPLICANT: METT, IGOT TITLE OF INVENTION: MODULATORS OF TWE RECEPTOR ASSOCIATED TITLE OF INVENTION: FACTOR (TARE), THEIR PREPARATION AND USE	·· 60 54 C C	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible CORRATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA: PILING DATE: 04-JAN-1999 PILOR APPLICATION NUMBER: US/09/155,676A PILING DATE: 04-JAN-1999 PILING DATE: 01-DATA: PILING DATE: 01-APR-1997 PILING DATE: 01-APR-1997 PRIOR APPLICATION NUMBER: IL 117800
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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             FILING DATE: 02-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 119133
FILING DATE: 26-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 26,618
REFERENCE/DOCKET NUMBER: WALLACH
TELECOMMUNICATION INFORMATION:
TELEPAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1906 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLGY: linear
MOLECTLE TYPE: CDNA
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Matches 1906; Conserv
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ç, B	1861 CATGTATGTGAGCCAATAAATTGCTTTCATTCCTTGAAAAAAA 1906 	cy Q	718 CAGAACGTGACCTCCTTGCTGAAGAGTCCACGCAAGAGTGAGCAGCCTGTTCAGGGAG 777
RESULT 3 US-10-070-255-4 ; Sequence 4, A ; GENERAL INFORM: APPLICANT: W	SULT 3 -10-070-255-4 Sequence 4, Application US/10070255 SEQUENCE INFORMATION: APPLICANT: WALLACH, David APPLICANT: MALININ, Nikolay	& & & & & & & & & & & & & & & & & & &	778 ATCACAGCCTCCTCTGCCGTCTCCATCCATAACCTGAACAGGAGACCGA-CCCTTG 836
HEFLICANT: HAPPLICANT: TITLE OF II: FILE REFER:	AFPLICANT: SIRHA, INDIANI.1 TITLE OF INVENTION: IREN PROTEIN, ITS PREPARATION AND USE FILE REFRENCE: WALLACH-2B.	ç d	897 AAGAAAGTGACCAACATAATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGAC 956
CURREN CURREN PRIOR PRIOR	CORRENT FILING DATE: 2002-12-16 PRIOR APPLICATION NUMBER: PCT/IL00/00517 PRIOR FILING DATE: 2000-08-31 PRIOR PLING DATE: 2000-08-31	cy Op	957 GTGTTTAAAAGACACCTGGGGCAGGGGAGGCTCAGAGGACAACTCCGACCGCTCCTCT 1016
PRIOR FIL. NUMBER OF SOFTWARE:	ING DATE: 1999-09 SEQ ID NOS: 14 Patentin version	oy G	1017 GTCAATATCATGTCCGCCTTTGAAAGCCCCTTCGGGCCTAACTCCAATGGAA-TCAGAGC 1075
	TYPE: DNA TYPE: DNA ONGANISM: Homo sapiens	oy G	1076 AGCAACTCATGGAAAATTGATTCCCTGTCTTTGAACGGGGAGTTTGGGTACCAGAAGCTT 1135
)	Query Match Best Local Similarity 99.6%; Proced No.0; Matches 1775; Conservative 0; Mismatches 4; Indels 3; Gaps 3;	ço Op	1136 GATGTGAAAAGCATCGATGAAGATGTGGATGAAACGAAACGAAGATGACGTGTATGGAAAC 1195
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GREERAL INFORMATION:
GREERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: SINHA, Indranil
APPLICANT: LEU, Stefan
ITILE OF INVENTION: IRRN PROTEIN, ITS PREPARATION AND USE:
FILE REFERENCE: WALLACH=28
CURRENT APPLICATION NUMBER: US/10/070,255
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/IL00/00517
PRIOR APPLICATION NUMBER: IL 131719
PRIOR APPLICATION NUMBER: IS 1809-09-02
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 6
LENGTH: 2873
                                                         ACTITICATGIAGGCCAAIAAAIIGCIIICAIICCIIG
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.6%;
Matches 1588; Conservative (
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; ORGANISM: Homo sapiens
US-10-070-255-6
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US-10-070-255-6
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US-09-629-469A-14016
; Sequence 14016, Application US/09629469A
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TRAAO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: HAYASHI, KOJI
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                                     Sequence 5, Application US/10070255
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: WALLIN, Nikolay
APPLICANT: SINHA, Indranil
APPLICANT: BLU, Stefan
APPLICANT: BLU, Stefan
TITLE OF INVENTION: IREN PROTEIN, ITS PREPARATION AND USE
FILE REFERENCE: WALLACH-28
CURRENT APPLICATION NUMBER: US/10/070,255
CURRENT PILING DATE: 2002-12-16
PRIOR PILING DATE: 2000-08-31
PRIOR FILING DATE: 1999-09-02
NUMBER: OF TILING DATE: 1999-09-02
NUMBER: OF TILING DATE: 1999-09-02
NUMBER: PALENTING DATE: 1999-09-02
SEQ ID NOS: 14
SEQ ID NOS: 14
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; Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.6
Matches 1588; Conservative
                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                      LENGTH: 3139
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US-10-070-255-5
                             10-070-255-5
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Sequence 14016, Application US/10917503

Sequence 14016, Application US/10917503

Sequence 14016, Application US/10917503

Sequence 14016, Application US/10917503

APPLICANT: ISSCAI, TAKAO

APPLICANT: SAITO, KAORU

APPLICANT: SAITO, KAORU

APPLICANT: SIGIYAMA, TOWOYASU

APPLICANT: SIGIYAMA, TOWOYASU

APPLICANT: NAGAL, KEILCHI

APPLICANT: NAGAL, KEILCHI

APPLICANT: NAGAL, KEILCHI

APPLICANT: NAGAL, KEILCHI

APPLICANT: OTSUKI, TETSUJI

TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE

FILE REFERENCE: 084335/0123
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TCTCCATCCTCATCAAACCTGAACAGGAGACCGA-CCCTTGCCTGTCGTGTCCAGGAATG
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      APPLICANT: SAITO, KAORU
APPLICANT: YAMANOTO, UUNICHI
APPLICANT: SHIJ, SHIZUKO
APPLICANT: SUGITAMA, TOMOYASU
APPLICANT: SUGITAMA, TOMOYASU
APPLICANT: WAKAMATUJ, AI
APPLICANT: WAKAMATUJ, AI
APPLICANT: OTSUKI, TETSUJI
APPLICANT: ONGONICA: DE 1009/629,469A
CURRENT APPLICATION NUMBER: US/09/629,469A
CURRENT APPLICATION NUMBER: US/09/07-29
PRIOR PILING DATE: 1999-00-729
PRIOR PILING DATE: 1999-00-139
PRIOR PILING DATE: 1999-00-118776
PRIOR PILING DATE: 2000-01-11876
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-03
PRIOR PILING DATE: 2000-05-03
PRIOR PILING DATE: 2000-05-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: CDS
; LOCATION: (63)..(1187)
US-09-629-469A-14016
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TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
TITLE REFERENCE: 782
CURRENT APPLICATION NUMBER: US/09/471,275
CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: US 09/234,611
EARLIER FILING DATE: 1999-01-20
EARLIER PILING DATE: 1999-01-20
EARLIER PELING DATE: 1999-01-25
EARLIER PELING DATE: 1999-01-29
EARLIER PELING DATE: 1999-01-8
EARLIER PELING DATE: 1999-01-18
EARLIER PELING DATE: 1999-01-18
EARLIER PELING DATE: 1999-01-18
EARLIER FILING DATE: 1999-01-18
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Pred. No. 3.8e-270;
0; Mismatches 65; I
   CURRENT AFFLICATION NUMBER: US/09/629,469
PRIOR APPLICATION NUMBER: US/09/629,469
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR PRIOR APPLICATION NUMBER: 60/183,322
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR PRIOR DATE: 2000-06-09
PRIOR PRIOR DATE: 2000-06-18
PRIOR FILING DATE: 2000-06-18
PRIOR PLING DATE: 2000-06-18
PRIOR FILING DATE: 2000-06-18
PRIOR FILING DATE: 2000-02-17
NUMBER: 0F SEQ ID NOS: 19025
SEQ ID NO 14016
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Best Local Similarity 94.7%;
Matches 1195; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: (63)..(1187)
US-10-917-503-14016
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GRUERAL INCORMATION:
GRUERAL INCORMATION:
APPLICANT: John Tillinghast
APPLICANT: And Tillinghast
APPLICANT: Are a sinku
APPLICANT: Radoje T. Drmanac
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REPERENCE: 784
CURRENT FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR APPLICATION NUMBER: US 09/034,341
PRIOR APPLICATION NUMBER: US 09/034,341
PRIOR PELING DATE: 1998-02-13
PRIOR PELING DATE: 1999-05-26
PRIOR PELING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: US 09/131,598
PRIOR APPLICATION NUMBER: US 09/131,598
PRIOR APPLICATION NUMBER: US 09/131,430
PRIOR APPLICATION NUMBER: US 09/131,430
PRIOR PELING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 09/131,430
PRIOR PELING DATE: 1999-10-28
PRIOR PELING DATE: 1999-10-28
PRIOR PELING DATE: 1999-10-28
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PRIOR PELING DATE: 1999-01-28
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US-09-488-725B-9141
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US-09-471-275-4362
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EARLIER APPLICATION NUMBER: US 60/125,453
EARLIER FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: US 60/126,605
EARLIER APPLICATION NUMBER: US 09/306,350
EARLIER FILING DATE: 1999-05-07
EARLIER FILING DATE: 1999-05-07
EARLIER FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/399,720
EARLIER FILING DATE: 1999-09-21
EARLIER FILING DATE: 1999-09-21
EARLIER FILING DATE: 1999-09-21
EARLIER FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 10451
SEQ ID NO 4362
EARLIER PLING DATE: 1999-12-16
SEQ ID NO 4362
EARLIER FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
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Matches 1137; Conserv
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NAME/KEY: misc feature
LOCATION: (1196)...(1516)
OTHER INFORMATION: similar to gil710216 in the genepept database release 114,
OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
                                                                                                                               TIGAAAGCCCCTTCGGGCCAAACTCCAATGGAAGTCAGAGCAGCAACTCGTGGAAAATTG 1043
                                                                                                                                                                      ATTCCCTGTCTTTGAACGGGGGTTTTGGGTACCAGAAGCTTGATGTGAAAAGCATCGATG 1154
                                                                                                          TTGAAAGCCCCTTCGGGCCTAACTCCAATGGAA-TCAGAGCAGCAACTCATGGAAATTG 1094
                                                                                                                                                                                                     1044 ATTCCCTGTCTTTGAACAGGGAGTTTGGGTACCAGAAGCTTGATGTGAAAAGCATCGATG 1103
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 GGGCAGGGGAGAGCTCAGAGGACAACTCCGACCGCTCCTCTGTCAATATCATGTCCGCCT
                                                                GGGCAGGGGAGAGCTCAGAGGACAACTCCGACCGCTCCTCTGTCAATATCATGTCGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tang, Y. Tom
APPLICANT: Tailinghast, John
APPLICANT: Tailinghast, John
APPLICANT: Sinku, Ankura
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids
TITLE OF INVENTION: Novel Nucleic Acids
FILE REFERRNCE: 784CIP
CURRENT APPLICATION NUMBER: US/09/552,317
CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 10289
SOFTWARE: PL CT genes Version 1.01
SEQ ID NO 9141
LENGTH: 1516
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                                                                       FEATURE:
NAME/KEY: misc feature
LOCATION: (1196)...(1516)
COTHER INFORMATION: Similar to gil710216 in the genepept database
OTHER INFORMATION: Run with FASTXY 3.3100, default parameters
US-09-488-725B-9141
                                                                                                                                                                                   57.3%; Score 1092.4; DB 22; Length 1516; ilarity 97.6%; Pred. No. 7e-259; Conservative 0; Mismatches 23; Indels 5;
                                                                                                                                                                                                                  23; Indels
SOFTWARE: pt_CT_genes Version 1.01
SEQ ID NO 9141
                                           TYPE: DNA
ORGANISM: Homo sapiens
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Matches 1137; Conserv
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Sequence 1043, Application US/09758472
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PH001
CURRENT APPLICATION NUMBER: US/09/758,472

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Best Local Similarity 98.4%; Pred. No. 2.9e-207
Matches 949; Conservative 3; Mismatches 6
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; OTHER INFORMATION: n equals a,t,g, or c
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CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR PILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR PILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9632
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1043
LENGTH: 1137
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                                                                                                   Score 883.6; DB 50
Pred. No. 2.9e-207
3; Mismatches 6
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   ; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1111)

; OTHER INFORMATION: n equals a,t,g,

US-10-235-926-1043
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98.4%;
                                                                                                                    Best Local Similarity 98.4
Matches 949; Conservative
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APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PHODICIN
CURRENT APPLICATION NUMBER: US/10/235,926
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/758,472
PRIOR APPLICATION NUMBER: 09/758,472
PRIOR APPLICATION NUMBER: 06/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9632
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 1043
LENGTH: 1137
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; GENERAL INFORMATION:
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LOCATION: (1100)
OTHER INFORMATION: n equals a,t,g,
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NAME/KEY: misc feature
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OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (1847)
OTHER INFORWATION: n equals
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NAME/KEY: misc feature
LOCATION: (540)
OTHER INFORMATION: n equals
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LOCATION: (8)
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APPLICANT: HAYASH, TETSUO
APPLICANT: HAYASH, TETSUO
APPLICANT: APLASH, KOJI
APPLICANT: SAITO, KAOUI
APPLICANT: SAITO, KAOUI
APPLICANT: SISHII, SHIZUKO
APPLICANT: WAKAMATSU, AI
APPLICANT: OTSUKI, TETSUJI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE
FILE REPREMENCE: 084335/012
CURRENT APPLICATION NUMBER: US/10/917,503
CURRENT FILING DATE: 2004-08-13
                                                                                                                                                                                                                                                                                                                                                                                            1469 AAGTGACCAACATTATCTCATTTGATGATGAGGAAGATGAGGCAGAACTCTGGGGACATGT 1528
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                                  841 TCGTGTCCAGGAATGTCAGTGCTGATGCCAAATGCAAAAAGGAGGGGAAGAAGAAAAAAA
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   662 TGAACGGGCAGAGTAAGTTTGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGA
                                                                                                                   722 ACGIGACCTCCTIGCTGAAGGAGTCCACGCAAGGAGTGAGCAGCCTGTTCAGGGAGATCA
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PRIOR PEDICATION NUMBER: US/05/629,469
PRIOR PELING DATE: 2000-07-28
PRIOR PELINGTON NUMBER: UP 1999-248036
PRIOR FILING DATE: 1999-07-29
PRIOR PELING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: UP 2000-118776
PRIOR APPLICATION NUMBER: UP 2000-118776
PRIOR PILING DATE: 2000-01-11
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-03
PRIOR PILING DATE: 2000-05-03
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GENERAL INFORMATION:
APPLICANT: OTA, TOSHOO,
APPLICANT: ISOGAL, TAKAO,
APPLICANT: NISHIKAWA, TETSUO
APPLICANT: HAYASHI, KOJI
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APPLICANT: 1SOGAI, TAKAO

APPLICANT: 1SOGAI, TAKAO

APPLICANT: 1SOGAI, TAKAO

APPLICANT: 1SOGAI, TAKAO

APPLICANT: HAYABHI, KOIT

APPLICANT: SAITO, KAORU

APPLICANT: YAMMANOTO, JUNICHI

APPLICANT: SUGINAMA, TOMOYASU

APPLICANT: TETSUJI

TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE

FILE REFERENCE: 084335/0128

FRICH REINIG DATE: 1999-00-07-28

FRICH REINIG DATE: 1999-00-27

FRICH REINIG DATE: 1999-00-27

FRICH REINIG DATE: 1999-100-23

FRICH FILING DATE: 2000-06-09

FRICH REINIG DATE: 2000-06-09

FRICH FILING DATE: 2000-06-09

FRICH FILING DATE: 2000-06-09

FRICH FILING DATE: 1999-10-18

FRICH FILING DATE: 1999-10-18

FRICH FILING DATE: 1999-10-18

FRICH FILING DATE: 1999-10-18

FRICH FILING DATE: 2000-06-09

FRICH FILING DATE: 2000-02-17

FRICH FILING DATE: 2000-06-09

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41.6%; Score 792.8; DB 28; Length 6045;
Best Local Similarity 96.8%; Pred. No. 1.5e-184;
Matches 852; Conservative 0; Mismatches 22; Indels 6;
                                                                                                                                                                                                             Sequence 18174, Application US/09629469A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (364)..(954)
US-09-629-469A-18174
                                                                 1132 TTCC 1135
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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: RECTEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: NUMBER: US/60/212,356
CURRENT APPLICATION NUMBER: 2000-06-19
CURRENT FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 411
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 340
LENGTH 1630
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 777.4; DB 90; Length 1630;
Pred. No. 6e-181;
0; Mismatches 36; Indels 6;
                                                          CAGGACGGAAGCACAGGGGCCACTCAGAGTCGCCCGAGAA 1808
                                        1200 CAGGAAGGAAGCACAGGGGCCACTCGGAGTCGCCCGAGAA
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Best Local Similarity 95.3%;
Matches 845; Conservative
                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: HUMAN
US-60-212-356-340
                                                                                                                                     US-60-212-356-340
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                                                                                                                                                                                                                                                                                                                                  AAAGCCCGTGTTCTGGTACTACGTGAAGGAGTCCTCAACAAGCACGCGGGTGCAGCGCT 991
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Pred. No. 1.5e-184;
0; Mismatches 22;
PRIOR APPLICATION NUMBER: 60/159,590
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PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 19025
SOFTWARE: PAECHLIN Ver. 2.1
LENGTH: 6045
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.8%;
Matches 852; Conservative 0
                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                ; LOCATION: (364)..(954)
US-10-917-503-18174
                                                                                                                                                                                 NAME/KEY: CDS
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1094 GATTCCTGTCTTTGAACGGGGAGTTTGGGTACCAGAACCTTGATGTGAAAAGCATCGAT 1153
1282 GATTCCTGTCTTTGAACAGGGAGTTTGGGTACCAGAAGCTTGATGTGAAAAGCATCGAT 1341
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Sequence 46181, A
Sequence 46181, A
Sequence 46660, A
Sequence 46660, A
Sequence 76, Appl
Sequence 71, Appl
Sequence 72, Appl
Sequence 72, Appl
Sequence 71, Appl
Sequence 72, Appl
Sequence 72, Appl
Sequence 214, Appl
Sequence 3234, Appl
Sequence 93804, Appl
                                                                                                                                                 June 10, 2005, 09:44:05; Search time 729.11 Seconds (without alignments) 11471.453 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                              1 cattgggtcacgcggtggcg......tcattccttgaaaaaaaaa 1906
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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5 US-60-680-473-46181
15 US-60-680-473-46660
15 US-60-680-473-46660
16 US-60-680-473-46660
17 US-60-680-473-49116
18 US-60-680-544-39116
18 US-60-680-574-39116
19 US-10-450-763-214
19 US-11-060-756-3234
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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APPLICANT: WALLACH, David
APPLICANT: WALLACH, David
APPLICANT: WALLACH, David
APPLICANT: WALLACH, Mark
APPLICANT: WALLACH, Mark
APPLICANT: WOULENKO, Andrei
APPLICANT: WOULENKO, Andrei
APPLICANT: WOULENKO, TO THE RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR
TITLE OF INVENTION: PREPARATION AND USE
FILE REFERENCE: WALLACH=21
CURRENT APPLICATION NUMBER: US/09/155,676B
CURRENT FILING DATE: 1999-01-04
PRIOR PAPLICATION NUMBER: DET/1L97/00117
PRIOR PAPLICATION NUMBER: 11 11900
PRIOR APPLICATION NUMBER: 11 119133
PRIOR FILING DATE: 1996-04-02
PRIOR APPLICATION NUMBER: 11 119133
PRIOR PLING DATE: 1996-04-02
PRIOR APPLICATION NUMBER: 11 119133
PRIOR PLING DATE: 1996-03-06
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 1
LENGTH: 1996 ö ö ö ģ Ď Ď ϋ ·υ TYPE: DIA ORGANISM: Homo sapiens ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature LOCATION: (94)...(94) OTHER INFORMATION: n is a, c, NAME/KEY: misc_feature LOCATION: (110)...(110) OTHER INFORMATION: n is a, c, ď NAME/KEY: misc feature LOCATION: (115)..(115) OTHER INFORMATION: n is

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APPLICANT: Rosenberg, Michael
APPLICANT: Subramaniam, S. Sai
APPLICANT: Subramaniam, S. Sai
APPLICANT: Stark, Suzanne
APPLICANT: Stark, Suzanne
APPLICANT: Li, Huo
APPLICANT: Li, Huo
APPLICANT: Derbel, Maher
TITLE OF INVENTION: Vucleotide Array Containing Polynucleotide Probes Complementary to INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
FILE REFERENCE: 21590290000
FILE REFERENCE: 21590290000
FILE REFERENCE: 21590290000
FILE REFERENCE: 21590290000
FILE REFERENCE: 2005-05-13
NUMBER OF SEQ ID NOS: 48714
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AGTITGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGAACGTGACCTCCTTGC 681
                                                                                                                                                                                                       ATTCCCTGTCTTTGAACGGGGAGTTTGGGTACCAGAAGCTTGATGTGAAAAGCATCGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 46181, Application US/60680473 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cooper, Matthew APPLICANT: Kinch, Deborah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo Sapiens
US-60-680-473-46181
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                                                                                                                                                                                                             APPLICANT: Rosenberg, Michael
APPLICANT: Stak, Suzanne
APPLICANT: Stak, Suzanne
APPLICANT: Stak, Suzanne
APPLICANT: Li, Huo
APPLICANT: Li, Huo
APPLICANT: Bandaru, Raj
APPLICANT: Bandaru, Raj
APPLICANT: Bandaru, Raj
TITLE OF INVENTION: Nuclectide Array Containing Polymuclectide Probes Complementary
TITLE OF INVENTION: Nuclectide Array Containing Polymuclectide Probes Complementary
TITLE OF INVENTION: Nuclectide Array Containing Polymuclectide Probes Complementary
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95.3%; Pred. No. 1.2e-259;
iive 0; Mismatches 57;
                                                                                                      ; Sequence 46181, Application US/60680544; GENERAL INFORMATION:
                                                                                                                                                           APPLICANT: Cooper, Matthew
APPLICANT: Kinch, Deborah
APPLICANT: Rosenberg, Michael
APPLICANT: Subramaniam, S. Sai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 95.3
Matches 1195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-60-680-544-46181
                                                       RESULT 2
US-60-680-544-46181
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APPLICANT: Cooper, Matthew
APPLICANT: Cooper, Michael
APPLICANT: Cooper, Michael
APPLICANT: Subramaniam, S. Sai
APPLICANT: Subramaniam, S. Sai
APPLICANT: Subramaniam, S. Sai
APPLICANT: Subramaniam, S. Sai
APPLICANT: Li, Huo
APPLICANT: Bardaru, Maher
TITLE OF INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
TITLE OF INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
TITLE OF SEQUENCE: 2159029000
CURRENT APPLICATION NUMBER: US/60/680,544
CURRENT FILING DATE: 2005-05-13
NUMBER OF SEQ ID NOS: 48014
SOFTWARE: Patent Sequence Analysis Tool Version 1.0
TEMBER OF SEQ ID NOS: 4814
SEQ ID NO 46660
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Pred. No. 1.3e-176;
0; Mismatches 20;
                                                                                                           ; Sequence 46660, Application US/60680544; GENERAL INFORMATION:
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ilarity 96.8%;
Conservative C
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CORGANISM: Homo Sapiens
US-60-680-544-46660
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Best Local Similarity
Matches 851; Conserv
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            ACCATGGCAGCAGGTCTGAACTCCATACTCTTTGCGATTAACATCGACAACAAGGATTTG
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Sequence B1, Application.

Sequence B1, Application.

APPLICANT: David W. Morris

APPLICANT: David W. Morris

APPLICANT: David W. Morris

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS IN CANCER

FILE REFERENCE: CHIRO062-500 (23356.0003)

CURRENT FILING DATE: 2004-10-21

PRIOR APPLICATION NUMBER: US 10/692,382

PRIOR APPLICATION NUMBER: US 10/691,209

PRIOR PILING DATE: 2003-10-21

PRIOR FILING DATE: 2003-10-21

PRIOR FILING DATE: 2003-10-21

NUMBER OF SEQ ID NOS: 3504

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 81

LENGTH: 1487
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ORGANISM: Homo sapiens
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APPLICANT: Cooper, Matthew
APPLICANT: Kinch, Deborah
APPLICANT: Rosenberg, Michael
APPLICANT: Rosenberg, Michael
APPLICANT: Sak, Suzanne
APPLICANT: Szak, Suzanne
APPLICANT: Li, Huo
TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary trithe OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary tribute 
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Best Local Similarity 96.8
Matches 851; Conservative
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; ORGANISM: Homo Sapiens
US-60-680-473-46660
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                                                                                                                                                      1221 ACTOGGAGTOGCCCGAGAGGCCACTGGAAGGGAACACCTGCCTCTCCCAGATGCACAGCT 1280
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                                                                   TGTCTTTGAACGGGGAGTTTGGGTACCAGAAGCTTGATGAAAAGCATCGATGATGAAG
                                                                                                                                                                                                           1281 GGGCTCCGCTGAAGGTGCTGCACATGACTCCGACATCCTCTTCCCTG 1328
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Pred. No. 1e-68;
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                                                                                                                                                                                                                                                                                                     ; Sequence 39116, Application US/60680544; GENERAL INFORMATION:
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Best Local Similarity 94.7%;
Matches 356; Conservative (
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cooper, Matthew
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US-60-680-544-39116
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LENGTH: 376
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                                                                                                                                       TGGACTTCGGTACAGTGGGAAGCCAGCTCTCCAGGCCACGGAAGTCCTCTGAGCAGCCT
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        GCCACTGGAAGGGAACACCTGCCTCTCCCAGATGCACAGCTGGGCTCCGCTGAAGGTGCT
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APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Mater S. Malandro
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS IN CANCER
FILE REPERENCE: CHIROG62-500 (23356.0003)
CURRENT APPLICATION NUMBER: PCT/US04/37982
CURRENT FILING DATE: 2004-10-21
PRIOR FILING DATE: 2003-10-22
PRIOR FILING DATE: 2003-10-22
PRIOR FILING DATE: 2003-10-21
NUMBER OF SEQ ID NOS: 3504
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 76
LENGTH: 527690
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LOCATION: (1)...(527690)

COTHEN INFORMATION: n = A, C, G or T/U

PCT-US04-37982-76
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Best Local Similarity 89.1:
Matches 417; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: David W. Morris
APPLICANT: David W. Morris
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS IN CANCER
FILE REFERENCE: CHIROG62-500 (23366.0003)
CURRENT APPLICATION NUMBER: PCT/US04/37982
CURRENT FILING DATE: 2004-10-21
PRIOR APPLICATION NUMBER: US 10/692,382
PRIOR APPLICATION NUMBER: US 10/691,209
                                                                                                                                                                                                                                                                                                                                                                                            Length 1725;
                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                     16.0%; Score 304.2; DB 1
80.1%; Pred. No. 1.2e-61;
cive 0; Mismatches 82
CURRENT FILING DATE: 2004-10-21
PRIOR APPLICATION NUMBER: US 10/692,382
PRIOR FILING DATE: 2003-10-22
PRIOR PRILING DATE: 2003-10-21
NUMBER OF SEQ ID NOS: 3504
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74
LENGTH: 1725
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                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 80.1
Matches 387; Conservative
                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mus musculus
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APPLICANT: Cooper, Matthew
APPLICANT: Kinch, Deborah
APPLICANT: Storenbergy, Michael
APPLICANT: Storenbergy, Michael
APPLICANT: Stak, Suzanne
APPLICANT: Szak, Suzanne
APPLICANT: Li, Huo
APPLICANT: Derbel, Maher
TITLE OF INVENTION: Nuclectide Array Containing Polynuclectide Probes Complementary
TITLE OF INVENTION: Nuclectide Array Containing Polynuclectide Probes Complementary
TITLE OF INVENTION: Numbers: US/60/680,473
CURRENT APPLICATION NUMBER: US/60/680,473
CURRENT APPLICATION NUMBER: 2005-05-13
NUMBER OF SEQ ID NOS: 48114
SOFTWARE: Patent Sequence Analysis Tool Version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGAGCTCAGAGGACAACTCCGACCGCTCCTCTGTCAATATCATGTCCGCCTTTGAAAGC 1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GATGATGAGGAGGATGAGGCAGAACTCTGGGGACATTTTTAAAAAGACACCTGGGGCAGGG 120
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APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS IN CANCER
FILE REFERENCE: CHIRON62-500 (23356.0003)
CURRENT APPLICATION NUMBER: PCT/US04/37982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 333.6; DB 15; Length
Pred. No. 1e-68;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                          , Application US/60680473
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PCT-USO4-37982-74
; Sequence 74, Application PC/TUS0437982
; GENERAL INFORMATION:
                                    1223 TCGGAGTCGCCCGAGA 1238
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Matches 356; Conservative
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; ORGANISM: Macaca Mulatta
US-60-680-473-39116
                                                                                                                                                                                                                                       ; Sequence 39116, Appli
; GENERAL INFORMATION:
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LENGTH: 376
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Best Local Similarity
Matches 277; Conserv
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PCT-US04-37982-71
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OTHER INFORMATION: 58% homologous to Homo sapiens Partial segeunce of the clone OTHER INFORMATION: 9 protein, accession number W42400, Smith-Waterman Score=142.
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                                                                               16;
                                                Length 1622;
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
                                                                               Indels
                                                                                                                                                                           CCCAGATGCACAGCTGGGCTCCGCTGAAGGTGCTGCACAA-----
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                                               Score 293.4; DB 1;
Pred. No. 4.3e-59;
0; Mismatches 101;
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                                               Query Match
Best Local Similarity 77.4%;
Matches 400; Conservative
 ; ORGANISM: Mus musculus
PCT-US04-37982-72
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ORGANISM: Homo sapiens
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NAME/KEY: SIMILAR
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US-10-450-763-214
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LENGTH: 454
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                                                                                                                        27 gecedecececerecagecaceerrocesesaacacecareareaceareacaaaca
                                                                                                                                                                          ATGACAAAAGACAATTTCTGCTGGAGCGACTGCTGGATGCAGTGAAACAGTGCCAGATCC
                                                                                                                                                                                                                                                                              7870 ITGATGATGATGAGGAGGAGCAGGGTACTGGGGACACTTTAAAAAAGATGCCTGGGACTG
                     Gaps
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APPLICANT: Marc S. Malandro
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS IN CANCER
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS IN CANCER
FILE REFERENCE: CHINGO62-500 (23356.0033)
CURRENT APPLICATION NUMBER: PCT/US04/37982
CURRENT APPLICATION NUMBER: US 10/692,382
PRIOR FILING DATE: 2003-10-21
PRIOR FILING DATE: 2003-10-22
PRIOR FILING DATE: 2003-10-22
PRIOR FILING DATE: 2003-10-21
NUMBER OF SEQ ID NOS: 3504
SOFTWARE: FRSESEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.6%; Score 221; DB 1; Length 369941; 76.9%; Pred. No. 1.7e-41;
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Pred. No. 8.8e-55;
0; Mismatches 11;
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    CTHER INFORMATION: n = A, C, G or T/U
PCT-US04-37982-71
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ilarity 96.2%;
Conservative
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Best Local Similarity 76.9
Matches 296; Conservative
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LENGTH: 369941
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### TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
### TITLE OF INVENTION: Target Genes
### FILE REFERENCE: AM101083 (031896-042000)
### CURRENT APPLICATION NUMBER: US/11/060,756
### CURRENT FILING DATE: 2005-02-18
### SOFTWARE: Patentin version 3.2
### SOFTWARE: Patentin version 3.2
### SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                          APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PATENTIN VERSION 3.2
                       449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 206.8; DB 13;
Pred. No. 9e-39;
0; Mismatches 12;
                                                                             1221 ACTCGGAGTCGCCCGAGAGCCACT 1245
                                                                                                      8167 ACGCGGAGTCGCCAGACAGGTGAGT 8191
                                                                                                                                                                                                                     ; Sequence 3234, Application US/11060756; GENERAL INFORMATION:
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Best Local Similarity 94.5
Matches 225; Conservative
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        450 GGTGGGCGGGGCTGGCGTGTGCCCTCCACGAACACTCCCTGGAGCGCTA 509

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        570 TGTGATGGATGAAGAAAGGTCCAGTATGCTTCCTACCATGGCAGCTGAACTCC 627

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(c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

Human tumour necrosis factor receptor-associated factor 2; TRAF2; TRAF-2 binding protein; NF-kappaB activity; NF-kappaB induction; intracellular signalling activity; acute hepatitis; autoimmune-induced cell death. Partial segeunce of the clone 9 protein "not specified" specified" /note= "not specified" "not specified" "not specified" note= "not specified" specified" "not specified" note= "not specified" "not specified" specified" "not specified" Location/Qualifiers AAW42400 standard; protein; 604 AA "not "not "not "not "not

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                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the sequence encoded by the 5' end of clone 9, and is a TRAF2 binding protein. Clone 9 is a partial clone, which lacks most of its 5' end of the coding DNA sequence. A CDNA library prepared from B-cells was screened for proteins that associate with TRAF2, and clone 9 DNA isolated. The clone 9 protein is capable of TRAF2, and clone 9 DNA isolated. The clone 9 protein is capable of pinding to at least amino acids 222-501 of TRAF2. The TRAF2 binding protein or mediation in cells of the activity proteins can be used for modulation or mediation in cells of the activity of NF-kappaB or any other intracellular signalling activity modulated or mediated by TRAF2. TRAF-binding proteins are sepecially used for concept of pathological conditions associated with NF-KB induction, e.g. acute hepatitis, autoimmune-induced cell death, e.g. catable of the beta langerhans cells or the pancreas that results in capable of the beta langerhans cells or the pancreas that results in coligodendrocytes in the brain in multiple sclerosis, and AIDS-inhibited Toligodendrocytes in the brain in multiple sclerosis, and AIDS-inhibited Toligodenotrocytes in the brain in multiple sclerosis, and AIDS-inhibited Toligodenotrocytes in the brain in multiple sclerosis, and AIDS-inhibited Toligodenotrocytes in the brain in whith a creating of ligands capable of binding to a protein, which are useful for modulating cellular activity modulated/mediated by TRAF2
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Human; Tumour Necrosis Factor; TNF; TNF Receptor Associated Factor; TRAF2; TRAF2 binding protein; IREN; IkappaB Regulator; immunosuppressive; nuclear factor-kappaB; NF-KappaB; Cyfostafit; tumour, AlDS; acquired immune deficiency syndrome; rheumatic disease; apoptosis; autoimmune disease; septic shock; graft-vs-host reaction; inflammation; anorexia; anti-HIV; therapy.
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                         TTPTAPLSISCPPLKAPSGLTPMESEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKR
                                                                                                              VAMMNRKDELLEBENRSLRNLLDGEMEHSAALRQEVDTLKRKVAEQEERQGMKVQALASYL
                                                                                                                                                                                                                                                                          542 CYFVRREXPHVRTMWWRNGGREKSNSSXXSHLSSWIQSFLKLCFLWTFHVCEPINCFHSL
                                                                                  RXRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEGAAQXLRHPLPCQWRGLLQPS
                                                                                                                                                                  RCPPRKPGERDRTRGPRSPGSWTSVQCGSQLSRPRKSSEQPVTSASVPESMTISELRQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TNF receptor-associated factor (TRAF2) binding protein, IREN
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/note= "TRAF2 binding region"
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AAE00685 standard; protein; 784

AAE00685

(first entry)

04-JUL-2001

AAE00685;

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The present sequence is human tumour necrosis factor (TNF) receptorassociated factor (TRAF2) binding protein, IREN. A fragment of this IREN molecule is capable of binding to TRAF2 protein at position 255-501. The invention relates to human tumour necrosis factor (TNF) receptoral invention relates to human tumour necrosis factor (TNF) receptoral results of the sequence of the sequ
6; 118pp; English.
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Sequence 541 AA;

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CALNEHSLERYLHMLLADRCKLSTFYEDWSFVMDEERSSMLPTWAAGLNSILFAINIDNK 180
                                                                                                                                                                                                                                                                                                                                                        181 DLNGQSKFAPTVSDLLKESTQNVTSLLKESTQCVSSLFREITASSAVSILIKPEQETDP- 239
                                                                                                                                                                   RGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLR 128
                                                                                                                                                                                                                                                CALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSILFAINIDNK 188
                                                                                                                                                                                                                                                                                                                                DLNGQSKFAPTVSDLLKESTQNVTSLLKESTQGVSSLFREITASSAVSILIKPEQETDPC 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 DDVY-----GNSSGRKHRGHSESPEKPLEGNTC-----LSOMHSWAPLKVLHND 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ATGREHLPLPDAQLGSAEGAAQXLRHPLPCQWRGLLQPSRCPPRKPGERDRTRG 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 ----LPVVSRNVSADAKCKKERKKKKVTNIISFDDEEDEQNSGDVFKKTPGAGESSED 294
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                                                                                                        1 MSGSQNNDKRQFLLERLLDAVKQCQIRFGGRKEIASDSDSRVTCLCAQFEAVLQHGLKRS 60
                                                                                9 MSGSXNXDKRQFLLERLLDAVKQCQIRFXGRKEIASDSDSRVTCLCAQFEAVLQHGLKRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRSPGSWTSVQCGSQLSRPRKSSEQPVTSASVPESMTISELRQATVAMMNRKDELEEENR
                                              Gaps
51.6%; Score 1594.5; DB 4; Length 541; 61.8%; Pred. No. 2.5e-137; ive 22; Mismatches 101; Indels 103;
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                                      Matches 366; Conservative
                     Similarity
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Claim 14; Fig 8; 118pp; English.

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Human; Tumour Necrosis Factor; TNF; TNF Receptor Associated Factor; TRAF2; TRAF2 binding protein; IREN; IkappaB Regulator; IREN-E; immunosuppressive; nuclear factor-kappaB; NF-kappaB; cytostatic; tumour; AIDS; acquired immune deficiency syndrome; rheumatic disease; apoptosis; autoimmune disease; septic shock; graft-vs-host reaction; inflammation; anorexia; anti-HIV; therapy.
                                                                                                                                                                                                                                             domain spanning amino acids 769-820 of NIK (Nuclear factor (NF)-kappaB Inducing Kinase) which is essential for IKK-1 (KappaB Kinase) binding to NIK in a 2-hybrid assay and NF-kappaB activation by NIK over expression.
                                                                                                                                                                                                                                  /note= "This motif is also present within 51 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA sequence encoding Tumor Necrosis Factor receptor associated factor (TRAF) binding proteins (IREN) for treatment or prevention of pathological conditions associated with NF-kappaB induction.
                                                               Human TNF receptor-associated factor binding protein, IREN-E
                                                                                                                                                                                                    198. .388
/note= "TRAF2 binding region"
326. .331
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                                                                                                                                                                                                                         Region
                                                                                                                                                                  Homo
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The present sequence is human tumour necrosis factor (TNF) receptorassociated factor (TRAF2) binding protein isoform, IREN-E. A fragment of this IREN-E molecule is capable of binding to TRAF2 protein at position 225-501. The invention relates to human tumour necrosis factor (TNF) receptor-associated factor (TRAF2) binding protein designated as IREN (KappaB REGHISTOR). Its isoforms IREN-18, IREN-E and their corresponding CDNA molecules. IREN is useful for modulating/mediating the activity of transcription factor NF (Nuclear Factor)-kappaB or any other intracellular signalling activity mediated by TRAF2. IREN is useful in the prevention and treatment of a pathological condition associated with NF-kappaB induction (abnormal) e.g. AIDS (acquired immune deficiency of the prevention and graft-vs-host reactions. IREN also plays an important cole in the control of inflammation and other non-apoptotic effects of method for screening, identifying and producing a molecule capable of modulating activities mediated by IREN. IREN antibodies are useful for the purification of new proteins from different sources, including cell extracts or transformed cell lines, in addition IREN can be used in diagnostic purposes for identifying disorders related to abnormal diagnostic purposes for identifying disorders related to abnormal functioning of cellular effects mediated directly by TRAF proteins

Sequence 784 AA;

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443
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                                                                                                                                                   61 RGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLR 120
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//note= "TRAF2 binding region"
326. 331
/note= "This motif is also present within 51 amino acid domain spanning amino acids 769-820 of NIK (Nuclear Eactor (NF)-kappaB Inducing Kinase) which is essential for IKK-1 (KrappaB Kinase) binding to NIK in a 2-hybrid assay and NF-kappaB activation by NIK over expression"
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                                                               9 MSGSXNXDKRQFLLERLLDAVKQCQIRFXGRKEIASDSDSRVTCLCAQFEAVLQHGLKRS
                                                                                               1 MSGSQNNDKRQFLLERLLDAVKQCQIRFGGRKEIASDSDSRVTCLCAQFEAVLQHGLKRS
                                   Gaps
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                               101; Indels 103;
   Length
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/ Match 49.7%; Score 1537.5; DB 4. Local Similarity 61.2%; Pred. No. 7.6e-132; nes 356; Conservative 22; Mismatches 101;
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The present sequence is human turmour necrosis factor (TNF) receptorassociated factor (TRAF2) binding protein isoform, IREN-10B. A fragment of this IREN-10B molecule is capable of binding to TRAF2 protein at content at the invention relates to human turmour necrosis factor (TNF) receptorassociated factor (TRAF2) binding protein designated as (TNF) receptorassociated factor (TRAF2) binding protein designated as IREN-10B. IR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSGSXNXDKRQFLLERLLDAVKQCQIRFXGRKEIASDSDSRVTCLCAQFEAVLQHGLKRS
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                                                                                                                                                                                                                                                                                                                                     New DNA sequence encoding Tumor Necrosis Factor receptor associated factor (TRAF) binding proteins (IREN) for treatment or prevention of pathological conditions associated with NF-kappaB induction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.7%; Score 1537.5; DB 4;
61.2%; Pred. No. 8e-132;
ive 22; Mismatches 101;
                                                                                                                                                                                                                                   Leu S;
                                                                                                                                                                                                                                   Sinha I,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Fig 7; 118pp; English
                                                                                                                                                                                         CO LTD
                                                                                                                                             99IL-00131719.
                                                                                                   31-AUG-2000; 2000WO-IL000517
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Best Local Similarity 61.2%
Matches 356; Conservative
                                                                                                                                                                                         (YEDA ) YEDA RES & DEV
                                                                                                                                                                                                                                   Malinin N,
                                                                                                                                                                                                                                                                                  WPI; 2001-281387/29.
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                  WO200116314-A1
                                                                                                                                                  02-SEP-1999;
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The present invention describes primer sets for synthesising 5602 full-length cDMAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence. Where the oligonucleotide comprises a 1'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the oligonucleotide comprises a 1-end sequence; where the oligonucleotide comprises a 1-end sequence; where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence 3'-end sequence; selected from those defined in the specification. The primers are used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the
                                     DDVY-----GNSSGRKHRGHSESPEKPLEGNTC------LSQMHSWAPLKVLHND 398
                                                                               ----ATGREHLPLPDAQLGSAEGAAQXLRHPLPCQWRGLLQPSRCPPRKPGERDRTRG 436
                                                                                                                                                                                   -SSPGH-----SLLPSASVPESMTISELRQATVAMMRKDELEEERR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
FPVFERGVWVPEAXCEKHR-------XXRCGXKRRXRVWKLIRKEAQGPLGVARE-
                                                                                                                       -----DPGLRYSVEA
                                                                                                                                                          PRSPGSWISVQCGSQLSRPRKSSEQPVISASVPESMIISELRQAIVAMMNRKDELEEENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primer; detection; diagnosis; antisense therapy; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 14017; 2537pp + Sequence Listing; English.
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                                                                                                                                                                                                                                            SLRNLLDGEMEHSAALRQEVDTLKRKVAEQEERQGMKVQALA 538
                                                                                                                                                                                                                                                                     Saito K,
, Otsuki '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                   SDILFPVSGVGSYSPADAPLGSLENGTGPEDHVLP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein sequence SEQ ID NO:14017
                                                                                                                                                                                                                                                                                                                                                                                    AAB93962 standard; protein; 375 AA
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Sugiyama T, Wakamatsu
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11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences, and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                          128
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                                                                                                                                                                                                                                                                          RGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLR
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                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                 12;
                                                                                                                                                   Length 375;
                                                                                                                                                                                 Indels
                                                                                                                                                 Query Match 38.7%; Score 1196; DB 4;
Best Local Similarity 82.2%; Pred. No. 6.8e-101;
Matches 244; Conservative 11; Mismatches 30;
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                           present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS64410.
                                                                                                                       Sequence 375 AA;
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The internation relates to isolated polymiciscide (ii) and polypeptide (iii) regequences. (i) is useful as hybridisation probes, polymiciscide (iii) regequences. (i) is useful as hybridisation probes, polymiciscidenties are also used in diagnostics as expressed sequence tags for identifying expressed sequence tags and involving expressed sequence tags for identifying expressed sequence to the internation and into into an antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food suspended in tissue, as molecular weight markers and as a food suspended in the binding partners are useful for reacting disorders involving aberrant protein expression or biological activity. The involving aberrant protein expression or biological activity. The collapseptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this amino acid sequences of the invention. Note: The sequence data for this electronic format directly from MNPO at the vipo.int/pub/published_pot_sequences
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   and polypeptide (II)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 388; DB 4; Length 2. Pred. No. 1.96-27; 3; Indels
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96.3%;
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11-JUL-2000; 2000US-00614150
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Best Local Similarity 96.3
Matches 79; Conservative
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N-PSDB; ABL05602.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABH30511), expressed DNA aequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 302; DB 4; Length 520;
; Pred. No. 1.9e-18;
59; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #28004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            9.8%;
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23-AUG-2000; 2000US-00649167.
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Best Local Similarity
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Matches
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                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II).

sequences. (I) is useful as hybridisation probes, polymerase chain
reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
and in recombinant production of (II). The polynucleotides are also used
in diagnostics as expressed sequence tags for identifying expressed
genes. (I) is useful in gene therapy techniques to restore normal
activity of (II) or to treat disease states involving (II). (II) is
useful for generating antibodies against it, detecting or quantitating a
cuseful for generating antibodies against it, detecting or quantitating a
cuseful for generating antibodies against it, detecting or quantitating
consupplement. (II) and its binding partners are useful in medical imaging
of sites expressing (II). (I) and (II) are useful for treating disorders
involving abberrant protein expression or biological activity. The
polypeptide and polynucleotide sequences have applications in
collapsostics, forensics, gene mapping, identification of mutations
condition acid sequences. ABG00010-ABG30377 represent novel human diagnostic
amino acid sequences of the invention. Note: The sequence data for this
patent did not appear in the printed specification, but was obtained in
electronic format directly from MIPO at
the propertion of the printed specification, but was obtained in
electronic format directly from MIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 PDAQLGSA-----EGAAQXLRHPLPCQWRGLLQPSRCPPRKPGERDRTRGPRSPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.6%; Score 236; DB 4; Length 131; 57.6%; Pred. No. 3.1e-13;
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                                            Claim 20; SEQ ID NO 58372; 103pp; English.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 131 AA;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 LSATFNVIAGDVER-RPEPSFWAPCMVFWHKQVIEQVQGLSQITSETGQCRAWVRQSLNE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 TAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLRCALNE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 HSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNS----ILFAINIDNKD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 PFGRNSNFGVPELSQRENLDLLIQKFDEMD-----VINEEQTGGDKAETNETAE 296
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genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 NENAREIBFE-----VKÓKSLEVLGVCB-----QTSALCTTLEALFLHGLKDS----F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 NXDKRQFLLERLLDAVKQCQIRFXGRKEIASDSDSRVTCLCAQFEAVLQHGLKRSRGLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 125; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 TQGVSSLF--REITASSAVSILIKPEQETDPCLSCPGMSVLMPNAKRSGRRK-
                                                                                                                       Disclosure; SEQ ID NO 14316; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.9%; Score 183.5; DB 4;
21.8%; Pred. No. 2.4e-07;
tive 61; Mismatches 162;
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les 97; Conservative
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention. The polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention differentiation activities, including cytokine, cell proliferation or cell differentiation activities, including cytokine, cell proliferation or cell differentiation activities, receptor or ligand activities, or may be involved in oncogenesis receptor or ligand activities, or may be involved in oncogenesis, receptor or ligand activities, or may be conditions or the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions include conditions include conditions e.g., by protein or gene therapy. Such conditions include conditions and ulcers), while those with including repeats of the invention are encoding them) may be used to promote enlisted and society and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, because the used to an activity may be used in the invention of an author or an activity may be used in cell culture to an activity may be used in cell culture to an activity may be used in the used to an activity of a such activities a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiathmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 278; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, Drmanac RT;
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                                                                                                                                       Homo sapiens.
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can be used to augment or replace cells damaged by illness, immune disease or accidental damage. The polypeptides and nucleotides also be used in the diagnosis of the above conditions, and in drug aning techniques. The present sequence represents a novel human peptide of the invention
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                                                                                                                                                                                                                                                      5.9%; Score 183; DB 4; Length 1019;
22.2%; Pred. No. 4.4e-07;
ive 75; Mismatches 196; Indels 132;
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Matches 115, Conservative
                                                                                                                                                                                                 Sequence 1019 AA;
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                                                                                                                                                                                                                                                                                                                               267 -- ORONP----FNEEPAETVSSSDTTPVHTTSQEKE-----EAQALDPPDACTELEVI 313
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i K, Irie R, Tamechika I;
Masuho Y;
LIERLIDDAVKOCOIRFXG-RKEIAS--DSDSRVTCLCAQFEAVLQHGLKRSRGLALTAAA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.
                                                                                                                                     78 IKQAAGFASKTETEPVFWYVKEVLNKHELQRFYSLRHIASDVGRGRAWLRCALNEHSLE
                                                                         138 RYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLNGQSKFA
                                                                                                                                                                             PTVSDLLK-ESTQNVTSLLKESTQGVSSL----FREITASSAV--SILIKPEQET----D
                                                                                                                                                                                                                                         PCLSCPGMSVLMPNA------KRSGRRKRKXPTXSHLMMRKMSRTLGTCLKRHLGQG
                                                                                                                                                                                                                                                                                                                                                             356 RCGXKRRXRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEGAAQXLRHPLPCQWR
                                                                                                                                                                                                                                                                                                                                                                                                                       416 GLLQPSRCPPRKPGERDRTRGPRSPGSWTSVQCGSQLSRPRKSSEQPVTSASVPESMTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----KKC--AKQGDGDSRNGSPSLGRDSP---DTMLASPQEEGEGP---SSTTES---S
                                                                                                                                                                                                                                                                   224 VFPAVPS----VPSTDWEDGDLTDTVSGPRS----TASDLTSSKASTRSPT-----
                          ILENISLSVKKLÓSYFAACEDEIPAIRNHDKVLORLCEHLDHALLYGLO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476 ELROATVAMMNRKD-ELEEENRSLRNLLD---GEMEHS 509
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Hio Y, Otsuka K, Nagai K,
Otsuka M, Nagahari K, Masul
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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24-JAN-2002; 2002US-0350435P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein, SEQ ID 1936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ., Sugiyama T,
J, Isono Y, H
Yoshikawa T, O
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N-PSDB; ADA52729.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYSLRHIASDVGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSML 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 PTMAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLLK--ESTQGVSSLFR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 AGMLLGLNAIDFSFCLKGEGLDGS---FPAVID-----YTPYLKYIQSSDSISSDEE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 GXGXMSGSXNXDKRQFLLERLLDAVKQCQIRFXGRK-----EIASDSDSRVTCLCAQF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GGGGGGKKSLSARNAAVER-RNLITVC--RFSVKTLIDRSCFETIDDSSPEFNNFAAIL 70
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Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                         The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human heat mitochondrial protein as a therapeutic target SeqID2491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 473;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibson BW, Taylor SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.7%; Score 175.5; DB 6; Best Local Similarity 28.5%; Pred. No. 7.2e-07; Matches 75; Conservative 35; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteopathic; ophthalmological; cytostatic.
                                                                                                                                            SEQ ID NO 1936; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EI-TASSAVSILIKPEQETDPCL 249
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17-JUN-2002; 2002US-0389987P.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003087768-A2.
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                                                                                                                                            Claim 14;
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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRR) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 GGGGGGGKKSLSARNAAVER-RNLITVC--RFSVKTLIDRSCFETIDDSSPEFNNFAAIL
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Local Similarity 28.5%; Pred. No. 7.2e-07;
les 75; Conservative 35; Mismatches 118;
                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 2491; 180pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SCPGMSVLMPNAKRSGRRKRKXPTXSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----REITASS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 ASSSQLSCSLNSDSCLLQENGSKSPDHCEEPMSCDS-DLGTANAEDSDRSLQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55; Mismatches 157; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.5%; Score 171; DB 4; Length 1006; 22.7%; Pred. No. 5.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 FAPTVSDLLKESTQNVTSLLKESTQGVSSLF-----
                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 51537; 103pp; English.
  30-MAR-2001; 2001WO-US008631.
                                          2000US-00540217
2000US-00649167
                                                                                                                                               Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 22.79
Matches 103, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 AVSILIKPEQETDPCL
                                                                                                                                                                                   WPI; 2001-639362/73.
N-PSDB; AAS85365.
                                                                                                                                               Liu C,
                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1006 AA;
                                        31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                               biodiversity.
                                                                                                                                               Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                     Claim 20;
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The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the cell to the agent of the gene in an expression of the gene of the agent and identifying fat cell number or size in the subject with the agent comprises an antisense of oligonucleotide. The subject comprises an ammal, preferably a human. The oligonucleotide to the agent, detecting binding of the agent to the agent, detecting binding of the agent to the oppypeptide or a change in an activity of the polypeptide, treating a comprises an antibody. A method of regulating fat cell subject with the agent comprises an antibody. A method of regulating fat cell number or size comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the subject is altered. The method is useful for identifying a composition for influence fat cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents a composition for treating or preventing obesity or diabetes. This sequence represents a composition in the constant of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                   Mouse; fat cell number; fat cell size; obesity; diabetes; anorectic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.2%; Score 160; DB 8; Length 2845;
20.2%; Pred. No. 0.00025;
Live 80; Mismatches 224; Indels 178;
467
                                     401
                                     PTSPKNKSWIS---EDDFYRP--SREQPLESAS
  PRSP--GSWTSVQCGSQLSRPRKSSEQPVTSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; SEQ ID NO 372; 275pp; English.
                                                                                                                                          Ą.
                                                                                                                                          AD008046 standard; protein; 2845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-OCT-2002; 2002US-00267502.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 20.2'
Matches 122; Conservative
                                                                                                                                                                                                                                                                Mouse polypeptide #42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LIFE-) LIFE SCI DEV
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N-PSDB; ADO07829.
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                                                                                                                                                                                                                                                                                                                                                                                                    US2004071700-A1.
                                                                                                                                                                                                                                                                                                                          antidiabetic.
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                                                                                                                                                                                 AD008046;
  437
                                                                                                                                                                                                                                                                                                                                                               Mus sp.
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                                                                                             |:| :: | :: | :: | 2089 HAFSPGSENFDWKAIQEGANSIVSSLHQAAAAAAACLSRQASSDSDSILSLKSGISLGSPF 2148
                    2002 QASGYAPKSFHVEDTPVCF-----SRNSSLSSLSID-----SEDDLL 2038
                                                         2039 QECISSAMPKKKRPSR-----IKSESEKQSPRKVGGI--LAEDLTLDLKDLQRPDSE 2088
                                                                                                                                           2149 HLTPDOEEKPFTSNKGPRILKPGEKSTLEAKKIESENKGIKGGKKVYKSLITGKIRSNSE 2208
                                                                                                                                                                            2354 ASTKSSGSGKMSYTSP--GRQLSQQNLTKQASLSKNASSIPRSESASKGLNQMSNGNGSN 2411
                                                                                                                                                                                                                                                                                                                                              GS-RDSTPSRPTQ-----QPLSRPMQSPGRNSISPGRNGISPPNKLSQLPRTSSPST 2353
                                                                                                                                                                                                                                                                                                                                                                                            2472 DSPTRSQAQTPVLSPSLPDMSLSTHPSVQAGGWRKLPPNLSPTIEYNDGRPTKRHDIARS 2531
 QAAGFASKT---ETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLRCALNEHSL 136
                                                                                                                         -----NAK 262
                                                                                                                                                               263 RSGRRKRKKPTXSHLMMRKMSRTLGTCLKRHLGQGRAQRTTPTAPLSISCPPLKAPSGLT 322
                                                                                                                                                                                                        PMESEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKRRXRVWKLIRKEAQGPLGVARE 382
                                                                                                                                                                                                                                                  383 ATGREHLPLPDAQLGSAEGAAQXLRHPLPCQWRGLLQPSR---CPPRKPGERDRTRGP-- 437
                                                                                                                                                                                                                                                                                         438 ---RSPG----SWTSVQCGSQLSRPR--KSSEQPVTSASVPESMTISE-LRQATVAM-MN 486
                                      ERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDL----NGQ
                                                                                194 SKFAPTVSDL----LKESTQNVTSLLKESTQGVSSLFREITASSAVSILIK-----
                                                                                                                                                                                                                                                                                                                                 RKDELEEENRSLRNLLDGE-MEHSAALRQEV-----DTLKRKVAEQEE------
                                                                                                                                                                                                                                                                                                                                                                         ----RQGMKVQALASYLCYFVRRFXPHVRTMWWR--------NGGR-EKSNSSXXS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                       241 ---PEQETDPCLSCPGMSVLMP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #21165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG21174 standard; protein; 388 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-00540217
2000US-00649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                  HLSS 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
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                                       137
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80
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding pattners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this electronic format directly from MPO at the printed specification, but was obtained in electronic format directly from MPO at the printed specification, but was obtained in electronic format directly from MPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 TFYEDWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLN------GQSKFAPTVSDLL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SSLFREITASSAVSIL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLSTSGAELQRKESLDSISHSSGSEDIEVHHSGHKIRRNQKPTASSLSLDTASSSQLSCS 231
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                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.0%; Score 154; DB 4; Length 388; 25.7%; Pred. No. 5.1e-05; Live 29; Mismatches 76; Indels '
                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 51533; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 IKPEQETDPCLSCPGMSVLMPNAKRS 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7, 2005, 11:57:19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 25.7% tes 53; Conservative
WPI; 2001-639362/73.
N-PSDB; AAS85361.
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Matches
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 7, 2005, 11:43:10; Search time 20.8699 Seconds (without alignments) 2784.626 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-155-676B-2 3093 1 XTGPGXGXMSGSXNXDKRQF......FLWTFHVCEPINCFHSLKKK 604

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote	pheromone response	hypothetical prote	hypothetical prote	neurofilament trip	hypothetical prote	neurofilament prot	KIAA0637 protein -	ankyrin 2, neurona	hypothetical prote	CREB-binding prote	homeotic protein C	giantin - human	translation elonga	gene APXL protein	myosin heavy chain
101029	369204	10037	15624	S15762	AE2304	A46194	T00380	837431	T17245	539161	I48314	A56539	S47630	I37183	B43402
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699 2 T	-	7	~	7	1008 2	1200 2	1171 2	3924 2	~	~	-	3259 1	237 1	1616 2	2007 1
699 2	840 1 8	1323 2	651 2	858 2	3.4 1008 2	•	•		878 2	2441 2	1332 1	•		•	••
699 2	3.4 840 1 8	3.4 1323 2	3.4 651 2	3.4 858 2	3.4	3.4	3,3	3.3	3.3 878 2	3.3 2441 2	3.3 1332 1	3.3	3.3	3.3	3.3

ALIGNMENTS

· · · · · · · · · · · · · · · · · · ·	RESULT 1 T2709 Ty2709 Ty2709 C; Species: Caenorhabdit C; Date: 15-Oct-1999 #se C; Accession: T27096 R; Smye, R. Bubmitted to the EMBL D A; Reference number: Z20 A; Accession: T27096 A; Catus: preliminary; A; Molecule type: DNA A; Reference number: C20 A; Accession: T27096 A; Cross-reference: UNI A; Experimental source: C; Genetics: C; Genetics: C; Genetics: A; Map position: Z A; Introns: 6/3; 57/2; 9 C; Superfamily: Caenorha	RESULT 1 Tyough the companies of the co
	Query Match Best Local Matches 7	<pre>Query Match 5.8%; Score 178.5; DB 2; Length 624; Best Local Similarity 26.6%; Pred. No. 2.1e-05; Matches 71; Conservative 44; Mismatches 117; Indels 35; Gaps 9;</pre>
	Oy 29	29 VKQCQIRFXGRKEIASDSDSRVTCLCAQFEAVLQHGLKRSRGLAL 73
	Oy 74 Db 84	74 TAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLRCALNE 133
	Oy 134 Db 134	134 HSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDL 190
	Qy 191 Db 194	191 NGGSKFAPTVSDLLKESTQNVTSLLKESTQGVSSLFREITASSAVSILIKPEGETDPCLS 250 :- :- :- :- :- :- :-
	Qy 251 Db 250	251 CPGMSVLMPNAKRS-GRRKRKKPTXSH 276

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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Status: gridues: "G'. 143-171, 'P', 173-179 <SPI>
A, Cross-references: GB:S67787; NID:g461061; PIDN:AAD13997.1; PID:g4261697
A, Cross-references: GS: Ballhausen, W.G.
Hun. Genet. 90, 650-652, 1993
A, Title: Identification of an alternative 5' untranslated region of the adenomatous poly A, Reference number: 154271; MUID:93186137; PMID:8383094
                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
B; Miki, Y.; Nishisho, I.; Horii, A.; Miyoshi, Y.; Utsunomiya, J.; Kinzler, K.W.; Vogelst
B; Miki, Y.; Nishisho, I.; Horii, A.; Miyoshi, Y.; Utsunomiya, J.; Kinzler, K.W.; Vogelst
A; Miki, Y.; Nishisho, I.; Horii, A.; Miyoshi, Y.; Utsunomiya, J.; Kinzler, K.W.; Vogelst
A; Mile: Disruption of the APC gene by a retrotransposal insertion of L1 sequence in a C
A; Reference number: A44928; MUID:92119623; PMID:1310068
A;Accession: A37261
A;Molecule type: mRNA
A;Residues: 1-2843 «KIN»
A;Residues: 1-2843 «KIN»
A;Residues: 1-2843 «KIN»
A;Cross-references: UNIPROT:P25054; GB:M74088; NID:g182396; PIDN:AAA03586.1; PID:g182397,
A;Cross-references: UNIPROT:P25054; GB:M74088; NID:g182396; PIDN:AAA03586.1; PID:g182397,
B;Josslyn, G.; Carlson, M.; Thliveris, A.; Albertsen, H.; Gelbert, L.; Samowitz, W.; Grod
arrington, J; McPherson, J.; Wasmuth, J.; Le Paslier, D.; Abderrahim, H.; Cohen, D.; Le
arrington, J; McPherson, J; Wasmuth, J.; Le Paslier, D.; Abderrahim, H.; Cohen, D.; Le
A;Title: Identification of deletion mutations and three new genes at the familial polypol
A;Reference number: A39658; MUID:91330307; PMID:1678319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: GDB:APC
A; Gene: GDB:APC
A; Gross-references: GDB:119682; OMIM:175100
A; Cross-references: GDB:119682; OMIM:175100
A; Map position: 5q21-5q22
A; Note: mutations of this gene can result in familial adenomatous polyposis on grotein
C; Superfamily: adenomatous polyposis coli protein
C; Reyworfamily: daminial adenomatous polyposis; tumor suppressor
E;1-730/Domain: leucine-rich <NTD>
F;7-22/Region: coli #stetus predicted
F;185-227/Region: coli #stetus predicted
F;185-227/Region: coli #stetus predicted
F;185-227/Region: coli #stetus predicted
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A;Molecule type: DNA
A;Residues: 1506-1525 «MIK>
A;Residues: 1506-1525 «MIK>
A;Cross-references: GB:S78214; NID:g243541; PIDN:AAB21145.1; PID:g243542
A;Cross-references: GB:S78214; NID:g243541; PIDN:AB2114; NCBIP:78218)
A;Note: sequence extracted from NCBI backbone (NCBIN:78214, NCBIP:78218)
B;Spirio, L; Olschwang, S.; Groden, J.; Robertson, M.; Samowitz, W.; Joslyn, Cell 75, 951-957, 1993
A;Title: Alleles of the APC gene: an attenuated form of familial polyposis.
A;Title: Alleles of the A9319; MUID:94073973; PMID:8252630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2139 -KSGISLGSPFH------LTPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 DWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLL
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A;Rotule: preliminary; translated from GB/EMBL/DDBJ
A;Rotules: 1-4 <LAM>A;Residues: 1-4 <LAM>A;Cross-references: GB:S56365; NID:g266243; PIDN:AAD14918.1; PID:g4262770
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21.9%; Pred. No. 0.21;
tive 60; Mismatches 140;
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F,1558-1577/Region: acidic
F,1866-1893/Region: highly charged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 21.99
Matches 95; Conservative
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                                      C;Accession: 149505
R;Su, L.
Science.256, 668-670, 1992
A;Title: Multiple intestinal neoplasia caused by a mutation in the murine homolog of the A;Reference number: 149505; MUID:92263101; PMID:1350108
A;Accession: 149505, MUID:92263101; PMID:1350108
A;Accession: 149505
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-2484 <RES>
A;Cross-references: UNIPROT:061315; GB:M88127; NID:g191991; PIDN:AABS9632.1; PID:g191992
C;Superfamily: adenomatous polyposis coli protein
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R, Kinzler: A. 10cc.1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C, Accession: A37261, B39658; A44928; A49319; I54271
R, Kinzler: K.W.; Nilbert, M.C.; Su, L.K.; Vogelstein, B.; Bryan, T.M.; Levy, D.B.; Stinnl, S.F.; Horii, A.; Ando, H.; Miyoshi, Y.; Miki, Y.; Nishisho, I.; Nakamura, Y. Science 253, 661-665, 1991
A; Title: Identification of FAP locus genes from chromosome 5q21.
A; Reference number: A37261; MUID:91335210; PMID:1651562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2354 ASTKSSGGCKMSYTSP--GRQLSQQNLTKQASLSKNASSIPRSESASKGLNQMSNGSN 2411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2261 PSEG-------PGATTSPRGTKPAGKSELSPITRQTSQISGSNKGSSRS 2302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2303 GS-RDSTPSRPTQ-----QPLSRPMQSPGRNSISPGRNGISPPNKLSQLPRTSSPST 2353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2209 ISSQMKQPLPTNMPSISR--CRTM----IHI-PGLRNSSSTSPVSKKGPPLKTPASKS 2260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002 QASGYAPKSFHVEDTPVCF-----SRNSSLSSLSID-----SEDDIL 2038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 QAAGFASKT---ETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLRCALNEHSL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 ERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLFTWAAGLNSILFAINIDNKDL---NGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 SKRAPTVSDL----LKESTONVTSLLKESTOGVSSLFREITASSAVSILIK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2845;
                                                                                                                                                                                                                                                                                                                                                                                                                                  5.2%; Score 160; DB 2; Length 28.
20.2%; Pred. No. 0.0037;
tive 80; Mismatches 224; Indels
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Best Local Similarity 20.2%
Matches 122; Conservative
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2138

262

G.; Gelber

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A;Cross-references: UNIPROT:Q61290; GB:L29346; NID:9522330; PIDN:AAA59206.1; PID:9522331
A;Note: authors translated the codon AGG for residue 788 as Lys, and CCT for residue 886
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riscong, T.W.; Stea, A.; Hodson, C.D.; Dubel, S.J.; Vincent, S.R.; Snutch, T.P.
Science 260, 1133-1136, 1993
A;Title: Structure and functional expression of a member of the low voltage-activated ca
A;Reference number: A37490; MUID:93262464; PMID:8388125
A;Accession: A37490
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
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A;Experimental source: Larain
A;Note: sequence extracted from NCBI backbone (NCBIP:132101)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 AMMNRKDE--LEEENRS-------LANLLDGEMEHSAALRQEVDTLKRKVA 524
                                                                                                                                                                                                                                                                                                                                                                                                                         761 EPRSSHLRERRRRHHMSVWEQRTSQLRRHMQMSSQEALNKEEAPPMNPLN----PLNPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 GLTPMESEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKRRXRVWKLIRKEAQGPLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 CPPRKPGERDRIRGPRSPGSWTSVQCGSQLSRPRKSSEQPVTSASVPESWTISELRQATV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            864 LTSALDNQRSPL---SLGK-----REPPWLPRSCHGNCDP1QQEAGGGETVVTFEDR
                                                                                                                                                                                                                                                             155 EDWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSL
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                                                                                                                              Query Match
4.0%; Score 123; DB 2; Length 2272;
Best Local Similarity 20.8%; Pred. No. 1.6;
Matches 90; Conservative 58; Mismatches 181; Indels 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             voltage-dependent calcium channel alpha IE - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1024 TEQEAEGSSEQAL 1036
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A;Residues: 1-2272 <WIL>
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voltage-dependent calcium channel alpha IE - mouse

(;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Accession: C54972

R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L. J. Biol. Chem. 269, 22347-22357, 1994

A;Title: Structure and functional characterization of neuronal alpha-IE calcium A;Reference number: A54972; MUID:9435092; PMID:8071363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143467.

hypothetical protein DKF2p434A1727.1 - human
hypothetical protein DKF2p434A1727.1 - human
C;Speciaes: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43467
C;Accession: T43467
Bandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, December 1999
A;Reference number: Z22513
                                                                                                363 XRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEG-----AAQXLRHPLPCQWRGL 417
                                                                                                                                                                                                                                                                                                                     SASVPESMTISE-LRQATVAM-MNRKDEL-----EEENRSLRNLLDGEMEHSAAL, 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 VLNK---HELQRFYSLRHIASDVGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDW 157
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                                                                                                                                                                                                                               2329 ISPGRNGISPPNKLSQLPRISSP-STASIKSSGSGKMSYTSPGRQMSQNLTKQTGLSKN
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                                                                                                                                                                                       418 LOPSR----CPPRKPGERDRTRGPRSPGSWTSVQCG--SQLSRPRKSSEQPVT----
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2241 SSTSPVSKKGPPLKTPASKSPSEGQTATTS-----PRGA-KPSVKSE-
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Genetics:

A, Note: DKFZp434A1727.1

C, Superfamily: human hypothetical protein DKFZp434A1727.1
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A,Status: preliminary
A,Moidecule type: manA
A,Residues: 1-364 <AAA>
A,Residues: 1-364 <AAA>
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Pred. No. 0.04;
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53; Conservative
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OY 351 KHRXKRCGXKRRKRVWKLIRKEAOGPLGVAREATGREH 388	ULT 8 715 715 715 715 716 717 717 718 718 718 718 718 718 718 718	
	Db 914 QSSHSKRPTIH EERTOLRRINSLAWPRGSGLVGALDBAETPLVOPOPELEVGKDAAL 973 Qy 525 EQRERGARKVQAL 537 Db 974 TEQEABCSSEQAL 986 RESULT 7 G84708 PSCD4108 PSCD4108 PSCD4108 C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: Arabidopsis thaliana C.Species: Arabidopsis thaliana C.Species: Arabidopsis thaliana M.; Accession: G84708 A; Reference number: Ask420; Multe, O.; Eisen, J.A.; Salaberg, S.E.; Praser, C.M.; Venter, J. A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: Ask420; Multi-20083487; PMID:10617197 A; Molecule type: DNA A; Recension: G84708 A; Reterances: UNIPROT:004346; GB:AE002093; NID:G1946371; PIDN:AAB63089.1; GSPDB:GR C; Generics: Arg30470 A; Map position: 2 Guery Match Best Local Similarity 21.8*; Fred. No. 0.61; Matches 122; Conservative 75; Mismatches 243; Indels 119; Gaps 30; Matches 122; Conservative 75; Mismatches 243; Indels 119; Gaps 30; Matches 122; Conservative 75; Mismatches 243; Indels 119; Gaps 30; A; Best Local Similarity 21.8*; Pred. No. 0.61; Db 202 GMKHISPSGNWHCSANILQKPSRPAISTPPVASKSAPARIGRAPPERGRG 255 Qy 92PUFWYYVKEVLINGHELQRPYSILARASHARACARAPPEPT 314 C) 135 SLERYLHWILAD-RCRISTPYEDWSFWMDERRSMLPTWARGLNSILF	369 FSRVDPGGKLIMGSRKAANAGDMQGCGLTNG†STEDTSSGGVTENPPSINGSSCISLIPK 241PEQETDPCLSCPGMSVLMPNAKRSGRRKRKXFTXSHLMMRKMSRTLGTCLKR

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A,Map position: 5
A,Introns: 10/3; 33/3; -67/3; 139/2; 183/3; 451/3; 487/3; 535/3; 631/1; 825/2; 914/3; 992
C,Forwords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific pro
F,1-1192/Product: probable serine/threonine-specific protein kinase, long splice form #s
F,1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short splic
                                                                                 A;Cross-references: UNIPROT:Q9TW45; EMBL:Z81027; PIDN:CAB54179.1; GSPDB:GN00023; CESP:H3
                                                                                                                                                                                                                                                                                                                                                               A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: 11192 (WILI3>
A;Residues: 1-1192 (WILI3>
A;Cross-references: EWBL:Z96102; PIDN:CAB54263.1; GSPDB:GN00023; CESP:H39E23.1a
A;Experimental source: clone H39E23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA
A,Rebidues: 1-487,536-1192. <WLL4>
A;Cross-references: EMBL:296102; PIDN:CAB54262.1; GSPDB:GN00023; CESP:H39E23.1b
A;Experimental source: clone H39E23
                                                                                                                                                                                                                            GSPDB:GN00023; CESP:H39E23.1b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :(: :|:::: | | :::: | :::: | RSSLDNIMKDRWMNVGYEDD-ELKPFIEPPKDQIDEQRIEKLIQIFQLGFNKAAILESVE 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.7%; Score 113.5; DB 2;
19.9%; Pred. No. 3.5;
ative 70; Mismatches 201;
                                                                                                                                                                                                                         PIDN: CAB54178.1;
                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, June 1997
A;Reference number: Z19696
                                                                                                     A;Experimental source: clone AH10
A;Accession: T18610
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: T23143
A; Status: translated from GB/EMBL/DDBJ
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A,Gene: CESP:H39E23.1a; CESP:H39E23.1b
              translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                               A; Experimental source: clone AH10 R; McMurray, A.
                                                                                                                                                                             A,Molecule type: DNA
A,Residues: 1-487,536-1192 <WIL2>
A,Cross-references: EMBL:281027; 1
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Best Local Similarity 19.9%
Matches 91; Conservative
                                     A;Molecule type: DNA
A;Residues: 1-1192 <WIL1>
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RESULT 9

G89287

protein H39E23.1 [imported] - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C; Accession: G89287
R; anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A; Rote: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A; Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A; Accession: G89287
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1246 <STO>
A; Residues: 1-1246 <STO>
A; Connetice
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C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T18611; T18610; T23144; T23143
B; McMurray, A.

submitted to the EMBL Data Library, October 1996
A; Reference number: Z18997
A; Accession: T18611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%; Score 118; DB 2; Length 1246;
19.9%; Pred. No. 1.7;
ative 75; Mismatches 211; Indels 116;
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A,Gene: H39E23.1
A,Map position: (
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Best Local S:
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Conservative
                     3.6%
Best Local Similarity 18.7%
Matches 80; Conservative
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Best Local Similarity
Matches 96; Conserv
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centromere protein C - mouse
N.Alternate names: cenpc protein
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Aug-1995
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Aug-1995
C;Accession: A54654
R;McKay, S.; Thomson, E.; Cooke, H.
Genomics 22, 36-40, 1994
A;Title: Sequence homologies and linkage group conservation of the human and mouse (A;Title: Sequence number: A54654
A;Reference number: A54654
A;Reternce number: A54654
A;Reternce number: Brain ary
A;Relatus: preliminary
A;Relatus: Preliminary
A;Relatus: 1-905 kmCK>
A;Cross-references: GB:U03113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microtubule-associated protein homolog - fruit fly (Drosophila melanogaster)
Milternate names: hypothetical protein EG:49E4.1
C;Species: Drosophila melanogaster
C;Spanos, L; Papagiannakis, G; Siden-Kiamos, I; Louis, C.
R;Spanos, L; Papagiannakis, G; Siden-Kiamos, I; Louis, C.
A;Reference number: 217689
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: 217689
A;Accession: T1356
A;Accession: T1356
A;Accession: T1356
A;Kesidues: 1-527 <SSPA>
A;Kesidues: 1-527 <SSPA>
A;Cross-references: UNIPROT:076891; EMBL:AL031128; PIDN:CAA20006.1
C;Genetics:
A;Cross-references: PlyBase:FBGn0025392
A;Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1
A;Note: EG:49E4.1
C;Superfamily: Drosophila 576K microtubule-associated protein homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 PCQWRGLLQPSRCPPRKPGERDRTRGPRSPGSW--TSVQCGSQLSRPRKSSEQPVTSASV 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 AVPFSPPP-----PSDWKLLEDBFIIDRSDRSFSSRLWVMIPSKDRHLSAHKPSP 303
                                                                                                                                                                                                                                                                                                                                                                                             188 KDLNGQSKFAPTVSDLLKESTQNVTSLLKESTQGVSSLFREITASSAVSILIKPEQETDP 247
                                                                                                                                                                                                                                                                                                                                                                                                                         248 CLSCPGMSVLMPNAKRSGRRKRKRYTXSHLMMRKMSR-TLGTCLKRHLGQGRAQRTTPTA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 RKTNSTQTNKEKSGKKFFSGGS-----KNKFVPKKVTLTSRRSRRISQRPSEWHVKSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 PLSISCPPLKAPSGLTPMESEQQLMENXPPV----FERGVWVPEAXCEKHRXXR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 L-----SBVQSRSKKNFSELFLETVKRKSKSSSVVRH------TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CGXKRRXRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEGAAQXLRHPL
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                Query Match
3.7%; Score 113; DB 2; Length 905;
Best Local Similarity 20.4%; Pred. No. 2.7;
Matches 86; Conservative 55; Mismatches 147; Indels 134;
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A;Gene: CESP:C55C3.3
A;Map position: 4
A;Introns: 17/1; 46/3; 139/2; 173/1; 204/3; 250/3; 266/3; 286/2; 327/1; 362/3; 393/3; 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3162 EKSKEESRRESVAEKSPLPSKEASRPASVAESV-------KDEADKSK 3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EESRRESGAEKSPLASKEASRPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEASRPT 3262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           482 VAMMURKDELEE-ENRSLRN-----LLDGEMEHSAALRQEVDTLKRKVAEQEERQGMK 533
                                                                                              17;
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A;Experimental source: strain Bristol N2; clone C55C3
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29187
S;Noessne, J.; Stellyes, L.
Submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid C55C3.
A;Reference number: Z2058.
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                                                                                                                                                                                                                                                                                                                                                                                           233 SAV----SILI-----KPEQETDPC--LSCPGMSVLMPNAKRSGRRKRKXPTXSHLMMRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQLMENXPPVFERGVWVPEAXCEKHRXXRCGXKRRXRVWKLIRKEAQGPLGVA-----
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                                                                                              Indels 107;
Length 5327;
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18.0%; Pred. No. 2.9;
tive 73; Mismatches 188;
          DB 2;
                                                                                                         176;
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     3.6%; Score 112.5;
18.7%; Pred. No. 29;
tive 64; Mismatches
                                                                                                                                                                                                             188 KDINGOSKFAPTVSDLLKESTQNVTSL--
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Search completed: June 7, 2005, 12:03:26 Job time: 24.2033 secs
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LRCDDEKEOFL 935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F4P12.20 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress) (Species: Arabidopsis thaliana (Mouse-ear cress) (Spate: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 (S.Accession: T45872 (S.Accession: T45872 (S.Accession: T45872 (S.Accession: T45872 (Squence Database, January 2000 A.Reference number: 223016 A.Reference number: 223016 A.Reference number: 223016 A.Reference number: 223016 A.Residues: Preliminary A.Rolocule type: DNA A.Residues: 1-553 & Latus: DNA A.Residues: 1-553 & Latus: DNA A.Residues: UNIPROT:Q9LFI5; EMBL:AL132966 A.Experimental source: cultivar Columbia; BAC clone F4P12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                            | : ::| ||: || SKINLVRNGGRIVNTTDLKDCSEARAIPKCDKLTDFQTSTNSEQSPADAISAVAPTKLTG 440
                                                                                                                                                                                                 SQSQSERQEIEKMPNSFRELQDSKFKPAEAPIPKPEEERKGSTEQSTTEPTKLAGSQSPS 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 FYEDWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 MESEQQLME-----NXFPVFERGVWVP-EAXCEKHRXXRCGXKRRXRV--WKLI----- 369
                                                                                                                                                                                                                                                 370 -RKEAQGPLGVAREATGREHLPLPD--AQLGSAEGAAQXLRHPLPCQWRGLLQPSRCPPR 426
                                                                                                                                                                                                                                                                                                                      427 KPGERDRTRGPRSPGSWTSVQCGSQLSRPRKSSEQPVTSASVPESMTISELRQATVAMMN 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLLKESTQGVSS---LFREITA----SSAVSILIKPEQE-----TDPCLSCPGMSVLMPN 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKRSGRRKRKXPTXSHLMMRKMSRTLGTCLKRHLGQGRAQRTTPTAPLSISCPPLKAPSG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIPMESEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKRRXRVWKLIRKEAQGP-LGV 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 AREATGREHLPLPDAQLGSAEGAAQXLRHPLPCQWRGL---LQPSRCPPRKP----- 428
264 WYDFLKKLVYRYHHCGNMRPLLKIALTAVFGISIIVAYRLYIVKTRRRGGNQIKKKKPAK 323
                                    ---KPEQETDPCLSCP---GMSVLMPNAKRSGRRKRKXPTX 274
                                                                                                        SHL-MMRKMSRTLGTCLKRHLGQGRA------QRTTPTAPLSISCPPLKAPSGLTP 323
                                                                                                                                                                                                                                                                                                                                                       ------PGN-----RRRNSETSONDTISPVPTKLVGTQ-----SPS 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 LSKVRPLSTTSTN-----RSSLDISKTQQEKNSKLPAG------KEPLGPRISM 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GERDRIRG----PRSPGSWTSVQCGSQLSRPRKSSEQPVTSASVPESM 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                          487 RKDELEEENRSLRNLLDGEMEHSAALRQEVDTLKRKVAEQEERQGMKVQALA 538
                                                                                                                                                                                                                                                                                                                                                                                                              3.6%; Score 111; DB 2; Length 553;
20.1%; Pred. No. 2;
.ive 66; Mismatches 177; Indels 126;
                                                                                                                                                                                                                                                                                  501 ERQÉIQOMPNSFRELQDSKFKPAPSPKSEKGPÁE---ÓSLSEPSPV-----
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A;Introns: 35/1; 108/1; 197/1; 209/3; 231/3; 281/1; 491/3
A;Note: F4P12.20
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93; Conservative
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Best Local S:
Matches 93
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350 NDSSSRLSSQPLANRSTSRGIMGQPRIPPQQT----NKTSKPKLSSSVP-TAGSISDYS 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKRSRGLA------PVFWYYVK 99
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                                                                              TISELRQATVAMMNRKDELEEENRSLRNLLDGEMEHSAALRQEVDTLKRKVAEQEERQGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cidate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 0
Cidate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 0
Cidate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 0
Rixcehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, September 1999
A;Reference number: 218722
A;Reference number: 218722
A;Reference protein RNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1291 kNOE>
A;Experimental source: adult uterus; clone DKPZp586B1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1291;
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Best Local Similarity 20.4%; Pred. No. 6;
Matches 39; Conservative 41; Mismatches 71; Indels
                                                                                                                                                                                                                                                  533 K-VQALASYLCYFVRRFXPHVRTMWWRNGGREKSNSSXXSHL 573
                                                                                                                                                                                                                                                                                                                                     lypothetical protein DKFZp586B1417.1 - human (fragment)
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OM protein - protein search, using sw model

June 7, 2005, 11:40:40; Search time 88.3902 Seconds (without alignments) 3499.208 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-155-676B-2 3093 1 XTGPGXGXMSGSXNXDKRQF......FLWTFHVCEPINCFHSLKKK 604

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q9ha26 homo sapien	Q8iui4 homo sapien	рошо	Q9d3s3 mus musculu	Q8k050 mus musculu	Q9vk31 drosophila	Q6p2r5 homo sapien		_	Q80tg5 mus musculu		-	094928 homo.sapien	Q9xwj7 caenorhabdi	Q96nl0 homo sapien	Qépdco mus musculu		anop	Q71s93 homo sapien			Q61315 mus musculu	Q92622 homo sapien	Q6pd22 mus musculu	homo	homo	Q96p51 homo sapien	homo	homo	mus n	Q8bmp7 mus musculu
SOUTHERES	ID	О9НА26	Q8IUI4	Q8TEQ0	Q9D3S3	Q8K050	Q9VK31	Q6P2R5	Q9Y4G2	Q7TSI1	Q80TQ5	QBIWES	Q9W293	094928	Q9XWJ7	O96NL0	Q6PDC0	Q8TBG7	Q7QE57	_			APC_MOUSE	Y226_HUMAN	Q6PD22	OBIWWS	RUF1 HUMAN	Q96P51	Q8WXA3	Q9P1Z1	Q9EPM6	Q8BMP7
	ength DB	375 2	249 2				520 2		1058 2		1087 2				604 2	473 2	408 2	387 2	496 2	708 2			2845 1		961 2	329 2		590 2	606 2	619 2	600 2	941 2
مد	Query Match Length	38.7	12.9	11.6	10.6	10.0	9.8	8.3	8.3	8.1	6.2	6.1	ري و.	5.9	5.8	5.7	5.6	5.5	5.4	5.4	5.5	5.2	5.2	5.2	5.1	5.0	4.9	4.8	4.8	4.8	4.8	4.8
	Score	1196	400.5	358.5	329	308.5	302	257	257	251	190.5	189	183.5	183	178.5	175.5	172	171	167	166	160	160	160	159.5	157.5	155	151	149	149	149	148	147.5
	Result No.		8	e	4	S	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22		24	25	56	27	28	53	30	31

32 147.5 4.8 941 2 QBBY22 34 145.5 4.7 606 2 QBR4C2 35 144.5 4.7 628 2 Q6SZH1 36 143.5 4.6 941 2 Q6SZH3 37 142.5 4.6 941 2 Q6NWW8 37 142.5 4.6 556 2 QBBL21 38 141 4.6 469 2 Q6BFK7 39 140.5 4.5 503 2 QBBKQ4 41 139.5 4.5 503 2 QBBKQ4 42 139.5 4.5 446 2 QBNY95 44 137.5 4.4 375 2 QBN4U6 45 137.5 4.4 469 2 Q9D394	Q8by22 mus musculu Q8r4c2 mus musculu Q8cy21 mus musculu Q9csv9 mus musculu Q8h121 mus musculu Q8Bk7 xenopus lae Q8vd10 mus musculu Q8bkq4 mus musculu Q80y95 mus musculu Q8cy25 mus musculu Q8cy25 homo gazti.	Q9d394 mus musculu
a 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Q8BY22 Q8R4C2 Q6CSV1 Q9CSV1 Q8NWW Q8BFZ1 Q8BFX7 Q8VD10 Q8VD10 Q8VD5 Q8CS76 Q8CS76	Q9D394
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ALIGNMENTS

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Query Match
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KX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

KX Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

KA Riausner R.D.; Collins F.S.; Warger L.; Shenmen C.M.; Schuler G.D.;

KA Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

KA Altschul S.F.; Joedan H.; Moore T.; Max S.I.; Wang J.; Haishe F.;

KA Diatchenko L.; Marusina K., Farmer A.A.; Rubin G.M.; Hong L.;

KA Diatchenko L.; Marusina K., Farmer A.A.; Rubin G.M.; Hong L.;

KA Scapleton M.J.; Uodin T.B.; Toshiyuki S., Carninof P., Frange C.;

KA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

Rosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Ganzatne P.H.;

Rosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gab L.J.; Hulyk S.W.;

KILlalon D.K.; Muzry K.C.; Hale S.; Garcia A.M.; Gab L.J.; Hulyk S.W.;

Willialon D.K.; Muzry D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

KRAYMINGH M.I.; Skalska U.; Smailus D.E.; Schnerch A.; Schein J.E.;

Kraywinski M.I.; Skalska U.; Smailus D.E.; Schnerch A.; Schein J.E.;
                                                                                                                                                                                                                                                                                                                                                                                61 RGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSILFAINIDNK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DINGQSKFAPTVSDLLKESTQNVTSLLKESTQGVSSLFREITASSAVSILIKPEQETDPC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLR 128
                                                                                                                                                                                                                            9 MSGSXNXDKRQFILLERLLDAVKQCQIRFXGRKEIASDSDSRVTCLCAQFEAVLQHGLKRS 68
                                                                                                                                                                                                                                                                   Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 LSCPGMSVLMPN-----AKRSGRRKRKXPTXSHLMMRKMSRTLGTCLKRHLGQGRA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 -----EPVVSRNVSADAKCKKERKKKKKVTNIISFDDEEDEGNSGDVFKKTFGAGES 291
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
PLJ12363 protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                      12;
                                                                                                            38.7%; Score 1196; DB 2; Length 375; 82.2%; Pred. No. 1e-73; tive 11; Mismatches 30; Indels 1.
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC041583; AAH41583.1; -.
SEQUENCE 249 AA; 27224 MW; 5F665B3F6BCE7FEB CRC64;
                              350826; RUN; 1.
375 AA; 41861 MW; F7DFBCBB4297CD95 CRC64;
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proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                          Best Local Similarity 82.2
Matches 244; Conservative
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SMART; SM00593; RUN; 1. PROSITE; PS50826; RUN; 1 SEQUENCE 375 AA; 4186
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                                                                                                                                                                                         60 GVSSVFREITASSAISILIKPEQETDP-----LPVVSRNVSADAKCKKERKKKKQVTNI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 SPGH-----GSPLS-----SLLPSASVPESMTISELRQATVAMMNRKDELEBENRSL 51
                                                                                                                       59
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                                                                                                      161 MDEERSSWLPTWAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLLKESTQ
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus adult male testis CDNA, RIKEN full-length enriched
library, clone:4933437K13 product:hypothetical PX (Beml/NCF1/PI3K)
Name-4933437K13Rik; Synonyms=Snx29;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AKO74072; BAB84898.1; GO. GO:0007242; P:intracellular signaling cascade; IEA. InterPro; IPR001683; PX.
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                                         13;
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Length 249;
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                                           Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             499 RNLLDGEMEHSAALRQEVDTLKRKVAEQEERQGMKVQALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.6%; Score 358.5; DB 2;
81.0%; Pred. No. 2.2e-16;
tive 1; Mismatches 5;
    12.9%; Score 400.5; DB 2;
64.8%; Pred. No. 1.7e-19;
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                                           11; Mismatches
                                                                                                                                                                                                                                                                              : : | | : | | : | 138
                                                                                                                                                                                                                                                        277 LMM--RKMSRTLGTCLKRHLGQGRA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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01-JUN-2002 (TrEMBLrel. 21, Li
01-JUN-2003 (TrEMBLrel. 24, Li
FLJ00143 protein (Fragment).
Name-FLJ00143;
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00787; PX; 1.
SMART; SM00312; PX; 1.
PROSITE; PS50195; PX; 1.
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                                               94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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  Query Match
Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE=Spleen;
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53184 MW; 34017FF86269D81A CRC64;

476 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                           The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
hanlysis of the mouse transcriptome based on functional annotation of
60,770 full-length oDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS'BL/6J; TISSUE=Testis; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Itoh M., Hayashizaki Y.; Pubraction of cap-trapper-selected cDNAB to prepare full-length CDNA lbraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                STRAIN=CS7BL/6J; TISSUE=Testis; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/64; TISSUE=Testis; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                     RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Testis;
MEDLINE-21085660; PubMed-11217851; DOI-10.1038/35055500;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
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EMBL; AF399755; AAK94018.1; -.
MGD; MGI:1921728; 4933437K13Rik.
GQ; GO:0007242; P:intracellular signaling cascade; IEA.
InterPro; IPR001683; PX.
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STRAIN-C57BL/6J; TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
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SMART; SM00312; PX; 1.
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PS50195; PX; 1.

PROSITE; PS50195; PX; Hypothetical protein.

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Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altaubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altaubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

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Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casrainci P., Prange C.,

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Raha S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Annes S.J., Marra M.A.,

Jones S.J., Marra M.A.,

""Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                    113 S-----SLLPSASVPESMTVHELRQAIVAMMRKXDELEEENGSLRNLLDGEMEHSAAL 165
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                                                                                                                                                                               DAPVGSLENGTCTENHIIP-----GSPL
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                                                                                                                                          393 DAQLGSAEGAAQXLRHPLPCQWRGLLQPSRCPPRKPGERDRTRGPRSPGSWTSVQCGSQL
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                                                                                      Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                           Length 476;
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Straubberg R.;
Straubberg R.;
Straubberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034114; AAH34114.1; -.
MGD; MGI:1921728; 4933437K13Rik.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
4933437K13Rik protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                        10.6%; Score 329; DB 2;
55.5%; Pred. No. 3.1e-14;
tive 7; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 AA.
                                                                                                                                                                                                                                                                                                                                                                                     513 ROEVDTLKRKVAEQEERQGMKVQALA 538
                                                                                                                                                                                                                                                                                                                                                                                                                      166 RQEVDALRRKVTEQQERHATKVQALA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
Query Match
Best Local Similarity 55.5.
These 81; Conservative
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Best Local Similarity
Matches 70; Conserv
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REQUENCE FROM N.A.

RADILINES-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RADILINES-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

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Button G.G., Worthman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RADILINES. C., Bagera Y.H., Blazei R.G., Champen M., Pfelffer B.D.,

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RADILINE, R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RADILINE, R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RADILINE, R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RADICKOWA D. Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RADIORNE, Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22456065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Glbbs R.A., Rubin G.M.; Finishing a Whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                  RNLIDGEMEHSAALRQEVDTLKRKVAEQEERQGMKVQALA 538
                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                       RNLLDGEMEHSAALRQEVDALRRKVTEQQERHATKVQALA
                                                                                                                                   520 AA
                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                   PRELIMINARY;
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                      499
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VGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSI 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 MSGSXNXDKRQFLLERLLDAVKQCQIRFXGRKEIASDSDSRVTCLCAQFEAVLQHGLKRS
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SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22426069; PubMed=12537572;
Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapheton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
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REMBL; AX095047; AAM11375.1; --
REMBL; AX095047; PRINTACellular signaling cascade; IEA.
REMBL; REMO01683; PX.
InterPro; IPR001683; PX.
InterPro; IPR00187; PX; 1.
REMBL; SM00187; PX; 1.
REMBL; SM00187; PX; 1.
REMBL; SM00187; PX; 1.
REMBL; PS50195;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99; Indels
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
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19.4%; Pred. No. 2.4e-12;
.ve 59; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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--HQKPLPQPVFWPLLKAVTHKHIISELEHLTFVNTDVGRCRAWLRLALNDGLMECYLKL 137
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257 ASSQLSCSINSDSCLLQENGSKSPDHCEEPMSCDS-DLGTANAEDSDRSLQE----- 308
                                                                                                                                                                                                                                                                                                                                                                                                                               309 VLLEFSKAQVNSVPTW---GLSQETEIPTPQASLSLHGLNTSTYLHC---EAFAEPLPAQ 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 AASGTQD-------GVHVQEP-------RAGGTQD-VES 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGREHLPLPDA-----QLGSAEGAAQXLRHPLPCQWRGLLQPSRCPPRKPGERDRTRG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GAGLKLVVSS 432
                                                                                                                                                                 LLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLN-----GQSK 195
                                                                                                                                                                                                                                           198 LCP-LSELDPLSTSGAELQRKESLDSISHSSGSEDIEVHHSGHKIRRNQKLTASSLSLDT 256
                                                                                                                                                                                                                                                                                                                          234 AVSILIKPEQETDPCL------SCPGMSVLMPNAKRSGRRKRKRYFTXSHL 277
                                                                                                                                                                                                                                                                                                                                                                                                      278 MMRKMSRTLGTCLKRHLGQGRAQRT---TPTAPLS-----ISCPPLKAPSGLTPME 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKRRXRVWKLIRKEAQGPLGVAR--EA 383
                                                                                  GFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLRCALNEHSLERYLHM
      ERLIDAVKQCQIRFXGRKEIASDSDSRVTCLCAQFEAVLQHGLKRSRGLALTAAAIKQAA
                            20 KKLVGSVKALQKQYVSLDTVVTSEDGDANTMCSALEAVFIHGLHAKHIRAEAGGKRKKSA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460
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Pfam; PF02759; RUN; 1.
SWART; SW002109; C1; 1.
SWART; SW00231; PH; 2.
SWART; SW00593; RUN; 1.
PROSITE; PS00190; CYTOCRCOME C; UNKNOWN 1.
PROSITE; PS500091; DAG PE BIND DOM 2; 1.
PROSITE; PS50003; PH DOWAIN; 1.
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Name=KIAA0356;
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TISSUE=Brain;
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SEQUENCE
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Gaps
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Pleckstrin homology domain containing, family M (With RUN domain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.3%; Score 257; DB 2; Length 1056;
23.8%; Pred. No. 7.3e-09;
tive 68; Mismatches 183; Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Straubberger R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2003) to the EMBL; BC064361; AAH64361.1; --
GO, GO:0007242; P:intracellular signaling cascade; IEA.
R InterPro; IPR00145; Pintracellular signaling cascade; IEA.
R InterPro; IPR00149; Ph.
R InterPro; IPR004012; Run.
R Pfam; PF02759; Ruy; 1.
R Pfam; PF02759; Ruy; 1.
R SMART; SM00169; Ph; 1.
R SMART; SM00199; Cl; 1.
SMART; SM00199; Cl; 1.
SMART; SM00199; Cl; 1.
SMART; SM00199; Cl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117442 MW; 24004093CFA89079 CRC64;
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                                                                                                                                                                                                    PRT; 1056 AA
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                                                                                                                                                                                                                                           Created)
                                                         235 VSIL---IKPEQETD 246
                                                                                      257 TEDLIGALKPIESVE 271
                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27,
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Matches 122; Conservative
                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                        Name=PLEKHM1;
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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C STRAIN-C57BL/6; TISSUE-Brain;

MEDLINE-25388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MELAGORER R.D., Coolling F.S., Wargner L., Shemmen C.M., Schuler G.D., Marshen R.F., Jorden H., Moorer T., Max S.I., Wang J., Hong L., Brownstein M.J., Uddin T.B., Toshlywki S., Carninci P., Scheetz T.E., Raplecon M.J., Uddin T.B., Toshlywki S., Carninci P., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Michards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A., Hellon E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                               PAPTVSDLLKESTQNVTSLLKESTQGVSSLF--------REITASS---- 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364
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                                                                                                                                                                                                                                                                               GFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLRCALNEHSLERYLHM 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SCPGMSVLMPNAKRSGRRKRKXPTXSHL 277
                                                                                                                                                                                                                                                                                                                                                                                                                           LLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLN------GQSK 195
                                                                                                                                                                                                             81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 LCP-LSELDPLSTSGAELQRKESLDSISHSSGSEDIEVHHSGHKIRRNQKLTASSLSLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | : | | : | | 3.59 ASSSQLSCSLNSDSCLLQENGSKSPDHCEEPMSCDS-DLGTANAEDSDRSLQE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 SEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKRRXRVWKLIRKEAQGPLGVAR--EA
                                                                                                                                                                                                          KKLVGSVKALQKQYVSLDTVVTSEDGDANTMCSALEAVFIHGLHAKHIRAEAGGKRKKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RPQAPSPLDLQQPVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGREHLPLPDA-----QLGSAEGAAQXLRHPLPCQWRGLLQPSRCPPRKPGERDRTRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GAGLKLVVSS
                                                                                                                                           ERLILDAVKQCQIRFXGRKEIASDSDSRVTCLCAQFEAVLQHGLKRSRGLALTAAAIKQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musimus; Musimus]
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Pleckstrin homology domain containing, family M (With RUN domain)
8.3%; Score 257; DB 2; Length 1058; 23.8%; Pred. No. 7.3e-09; arive 68; Mismatches 183; Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSGQQ----PSSTVSETAREVGQGNGLQKAQAHD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTSPKNKSWIS---EDDFYRP--SREQPLESAS 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRSP--GSWTSVQCGSQLSRPRKSSEQPVTSAS 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 AASGTQD-----GVHVQEP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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01-0CT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Plekhml;
Mus musculus (Mouse)
                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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              Query Match
Best Local
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Q7TSI1;
                                                                                    Matches
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392 284 RILGICLKRHLGQGRAQRITPTAPL-SISCPPLKAPSGLIPMESEQQLMENXFPVFERGV 342 SLHSLATSTH-------LHFGGSEELFPAHKSSGTSSGGHKHQLLPQETPD 382 383 EKQLGTAQAGPAQSTSDQQPSSPVGGAAGQGSGPWKALEYGRVGPKLVVSSPTSPKGKSW 442 21; 132 283 -----RE 228 291 191 429 -GERDRIRGPRSP-----GSWISVQCGSQLSR------PRKS-SEQPVISASVP 469 501 78 99 WVPEAXCEKHRXXRCGXKRRXRVWKLIRKEAQGPLGVAREAT-----GREHLPLP----Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human 229 ITASS-----AVSILIKPEQETDPCLSCPGMSVLMPNAKRSGRRKKKXPTXSHLMMRKMS LTASSLSLDTASSSQLSCSLNSDSCL-----LOENGPKS-----PDHSEEPMSYDS -----DLGMANTDDPDRSLQEVLSEFSKAQVNSAPSSGPNQ--EPDTPMFQTPL KQAAGFASKTET-----EPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLRCALN EHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTWAAGLNSILFAINIDNKDLN-19 OFLLERLLDAVKOCQIRFXGRKEIASDSDSRVTCLCAQFEAVLOHGLKRSRGLALTAAAI Gaps ---WRGLLQPSRCP-----PRKP-8.1%; Score 251; DB 2; Length 1074; llarity 24.5%; Pred. No. 1.9e-08; Conservative 58; Mismatches 209; Indels 140; -----GOSKFAPTVSDLLKESTQNVTSLLKESTQGVSSLF-----118533 MW; 56EDA05514E4B9F9 CRC64; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002) DAQLGSAE-GAAQXLRHPLPCQ------DOM_2; 1. Pfam; PF00169; PH; 1.
Pfam; PF00169; RUN; 1.
SMART; SM00109; C1; 1.
SMART; SM0053; PH; 2.
SMART; SM0053; PH; 2.
SMART; SM0053; PH; 2.
PROSITE; PS00190; CYTOCHROWE C; UN PROSITE; PS50003; PH DOWAIN; 2.
PROSITE; PS50003; PH DOMAIN; 2.
PROSITE; PS50003; PH DOMAIN; 2.
SEQUENCE 1074 AA; 118533 MW; 5 SEQUENCE FROM N.A. STRAIN=C57BL/6; TISSUE=Brain; sequences." Local Similarity nes 132; Conserv and mouse cDNA 127 246 339 292 343 133 192 79 Query Match Best Loca Matches g 셤 g ò g ò 셤 δ 셤 ò g qq à ŏ ð

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408 LARDPSDTVLASPQEQGEGLSSTAG---SSELSELSQMGLLIPEMKDTSMECLGQPLSKV 464
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                    LSRPRKSSEQPVTSASVPESMTISELRQATVAMMNRKD-ELEEENRSLRNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.1%; Score 189; DB 2; Length 1095;
22.3%; Pred. No. 0.00034;
tive 77; Mismatches 207; Indels 134; Gaps
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 PH domain.
EMBL; BCO40441; AAH40441.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1095 AA; 120171 MW; 757F5B7D142B089C CRC64;
                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEHYDR_CYS; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002086; Aldehyd_dehydrog.
InterPro; IPR0101849; PH.
InterPro; IPR0101036; PH_related.
InterPro; IPR004012; Run.
Pfam; PF002159; PH; 1.
SMART; SM00233; PH; 1.
SMART; SM00593; RUN; 1.
                                                                                                                                                                                                                                                   Created)
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PROSITE; PS50003; PH DOMAIN; 1.
PROSITE; PS50826; RUN; 1.
                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                    PLEKHM2 protein (Fragment).
Name=PLEKHM2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 22.3%
Matches 120; Conservative
                                                                                                            : | | ::: |
465 IDKLHGQLDPS 475
                                                                                                                                                                                                                PRELIMINARY;
                                                                                        LD---GEMEHS
                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissum=Ovary;
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                                                                                        502
                    452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 VLQHGLKRSRGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 VGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFAINIDNKDLNGQSKFAPTVSDLLK-ESTQNVTSLLKESTQGVSSL----FREITASSA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCLKRHLGQGRAQRTTPTAPLSISCPPLKAPSGLTPMESEQQLMENXFPVFERGVWVPEA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----CTELEVIRVTK--KKKIGKKKKTKLDEDASPLHPTS-SQQKCGQQGEGDGLVGTPG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 VSILIKPEQETDPCLSCPGMSVLMPNAKR-----SGRRKRKXPTXSHLMMRKMSRTLG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----EWDD-----SAIAPSSEDGDLTDTISGPRS----TASDLTSSKTSTKSP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 XCEKHRXXRCGXKRRXRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEGAAQXLR 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPLPCQWRGLLQPSRCPPRKPGERDRTR----GPRSPGSWTSVQCGSQ------ 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GPGXGXMSGSXNXDKRQFLLERLLDAVKQCQIRFXGRKE---IASDSDSRVTCLCAQFEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | | : | : : | : : | : : | : : | CGGGSAMEPREVKDR---ILENISLSVKKLQSYFAACEDETPAIRNHDKVLQRLCEHLDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 LGRSRAWLYLALNENSLESYLRLFQENLGLLQKYYVRNALVCSHDHLTLFLTLVSGLEFI
                                                                                                                                                                                                                                                                Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S., Nakajima D., Nagase T., Ohara O., Koga H.;
"Prediction of the coding sequences of mouse homologues of KIAA gene: II. The complete nucleotide sequences of 400 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EEAQAP-----DOPDA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%; Score 190.5; DB 2; Length 1087;
20.7%; Pred. No. 0.00027;
tive 79; Mismatches 175; Indels 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T--ORHNPFNEEQAET------ASSDTTPVHTTSQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1087 AA; 120057 MW; F1FAD62EFF9A0F3 CRC64;
                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
PROSITE; PS50003; PH DOMAIN; 1.
PROSITE; PS50826; RUN; 1.
PRT; 1087 AA
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002086; Aldehyd_dehydrog.
InterPro; IPR001849; PH.
InterPro; IPR011036; PH_related.
InterPro; IPR004012; Run.
                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 10:35-48(2003).
-!- SIMILARITY: Contains 1 PH domain.
EMBL; AK122386; BAC6568.1; -.
                                   Created)
                                                                                                                                                                                                                             TISSUE=Brain;
MEDLINE=22579291; PubMed=12693553;
                                                 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26, MKIAA0842 protein (Fragment)
                                   01-JUN-2003 (TrEMBLrel. 24,
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00169; PH; 1.
Pfam; PF02759; RUN; 1.
SMART; SM00233; PH; 1.
SMART; SMO0593; RUN; 1
                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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RN SEQUENCE FROW N.A.

RN SECURINE FROW N.A.

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., In P.W., Hoskins R.A., Galle R.F.,

RA Gocayne R.A., Lewiss S.E., Richards S., Ashburner M., Henderson S.N.,

Ratton G.G., Wortman J.R., Yandall M.D., Zhang Q., Chen L.X.,

RA Bardon R.C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Bellew R.W., Baran B.P., Bhandari D., Bolshakov S.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,

RA Foaler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heinan T.J., Hernandez J.R., Harris M.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,
"Prediction of the coding sequences of unidentified human genes. XII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 5:355-364 (1998).
-I- SIMILARITY: Contains 1 PH domain.
EMBL, AB020649; BAA74865.1;
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                               61; Mismatches 162; Indels 125;
                                                                                                                                                                                                                                       Score 183.5; DB 2; Length 720; Similarity 21.8%; Pred. No. 0.00048;
SMART; SM00593; RUN; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS50089; ZF_RUN; 1.
PROSITE; PS50089; ZF_RING_2; 1.
SEQUENCE 720 AA; 81068 WW; 2E7CFB469FBDE720 CRC64;
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InterPro; IPR002086; Aldehyd_dehydrog.
InterPro; IPR01849; PH.
InterPro; IPR011036; PH_related.
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Mammalia, Eutheria, Primates;
NCBI_TaxID=9606;
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01-MAY-1999 (TrEMBLrel. 10, L
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KIAAO842 protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 RCGXKRRXRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEGAAQXLRHPLPCQWR 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 RYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTWAAGLNSILFAINIDNKDLNGQSKFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 VPPAVPS----VPSTDWEDGDLTDTVSGPRS----TASDLTSSKASTRSPT-----
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                                                                                                                                                                                                                                                                                                                                                                                            21 LLERLLDAVKQCQIRFXG-RKEIAS--DSDSRVTCLCAQFEAVLQHGLKRSRGLALTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                            78 IKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLRCALNEHSLE
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                            Query Match 5.9%; Score 183; DB 2; Length 1020; Best Local Similarity 22.2%; Pred. No. 0.00081; Matches 115; Conservative 75; Mismatches 196; Indels 132;
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Science 282:2012-2018(1998).
Pfam; PF00169; PH; 1.

SMART; SM00231; PH; 1.

SMART; SM00231; PH; 1.

PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.

PROSITE; PS50003; PH DOMAIN; 1.

PROSITE; PS5006; NUN; 1.

NON TER

SEQÜENCE 1020 AA; 112850 MW; FFD857F1851BD49A CRC64;
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, La
01-OCT-2003 (TrEMBLrel. 25, La
Hypothetical protein Y51H1A.2.
ORFNames=Y51H1A.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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X PubMed-14702039, DOI=10.1038/ng1285;

X PubMed-14702039;

A Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

Makamatsu A., Hayashi K., Sato H., Najahara T., Tanaka T., Ishii S.,

Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

A mamanco J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

Murakami K., Yasuda T., Iwayanagi T., Nagatsuma M., Shiratori A.,

Sudo H., Hosoiri T., Kaku Y., Kodira H., Kondo H., Sugawara M.,

A Tahahashi M., Kanda K., Yokoi T., Puruya T., Kikkawa E., Omura Y.,

A Pakahashi M., Kanda M., Yamashita H., Murakawa K., Fujimori K.,

Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

Ninomiya K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,

Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,

Masashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

Moshikawa Y., Matsunawa H., Satoh N., Takami S., Terashima Y., Suzuki O.,

A poshikawa Y., Matsunawa H., Satoh N., Takami S., Terashima Y., Suzuki O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 HSLERYLHMLLADRCRLSTFYEDWSF---VMDEERSSMLPTWAAGLNSILFAINIDNKDL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGQSKFAPTVSDLLKESTQNVTSLLKESTQGVSSLFREITASSAVSILIKPEQETDPCLS 250
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                                                                                                                                                                                                                                                                                                                                                                                                      TRYA------KYPEPNFWPFVSKFSHRSITSQIACLGQIRSEIGKSRAWIRIVLNE
                                                                                                                                                                                                                                                                                                                       29 VKOCQIRFXGRKE-----IASDSDSRVTC-----LCAQFEAVLQHGLKRSRGLAL
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                           DB 2; Length 604;
                                                                                                                                                                                                                                                                                          Indels
                                                                Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                             EMBL; ALO12644; CAA21666.2; -
PIR; T27096; T27096.
Wormbase; WBGene00013093; Y51H1A.2.
Wormbep; Y51H1A.2; CE32758.
InterPro; IPR004012; Run.
Pfam; PF02759; RUN; 1.
SMART; SM00593; RUN; 1.
PROSITE; P550806; RUN; 1.
PROSITE; P550806; RUN; 1.
SROCHELL POCCE; RUN; 1.
SROCHELL PCCE 604 AA; 66549 MW; AB317F77F2B63201 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ30671.
                                                                                                                                                                                                                                                          Query Match 5.8%; Score 178.5; DB 2; Best Local Similarity 26.6%; Pred. No. 0.00085; Matches 71; Conservative 44; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 CPGMSVLMPNAKRS-GRRKRKXPTXSH 276
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SP--SYLEKRRRALSRPIRKSENDDH 274
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                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
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RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Yujimori Y., Komyayama M., Tashiro H., Tanigami A., Fukuzumi Y.,
RA Cho T., Yamada K., Fuji Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Saaki M.,
A Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Saroh T., Shirai Y., Takahashi Y., Nakagawa K.,
A Mizushima-Sugano J., Saroh T., Shirai Y., Takahashi Y., Yamashita R.,
A Nakai K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
R. "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 IENMENVSSSRAKGRAWIRVALMEKHLSEYISTALRDFKTTRRFYEDGAIVLGEE-ANML 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 PTWAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLLK--ESTQGVSSLFR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GXGXMSGSXNXDKRQFLLERLLDAVKQCQIRFXGRK-----BIASDSBVTCLCAQF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 GGGGGGKKSLSARNAAVER-RNLITVC--RFSVKTLIDRSCFETIDDSSPEFNNFAAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 EAVLOHGLKR----SRGLALTAAAIK-QAAGFASKTETEPVFWYYVKEVLNK---HELOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 FYSLRHIASDVGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVWDEERSSML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mat. Genet. 36:40-45(2004).

EMBL, AKO5523; BAB70882.1; -.

Interpro; IPR004012; Run.

Pfam; PF02759; RUN; 1.

SMART; SMO0593; RUN; 1.

PROSITE; PS50826; RUN; 1.

SROUSITE; PS50826; RUN; 1.
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5.7%; Score 175.5; DB 2;
Best Local Similarity 28.5%; Pred. No. 0.00099;
Matches 75; Conservative 35; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              completed: June 7, 2005, 12:02:13
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Sequence 191, Application US/09370838;
Patent No. 644425
BEBERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohmmath, Roadoh
APPLICANT: Mohmmath, Roadoh
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1: /cgn2_6/ptodatea1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodatea1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodatea1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodatea1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodatea1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodatea1/iaa/Packfiles1.pep:*
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US-09-854-133-191

US-07-741-940-7

US-08-289-548A-7

US-08-452-654-7

US-08-452-654-7

US-08-452-658-7

US-08-452-658-7

US-08-452-658-7

US-08-452-658-7

US-08-452-658-7

US-08-450-582-7

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US-09-949-116-6556

US-09-949-016-6556

US-09-949-016-7774

US-09-949-016-778-1

US-09-949-016-778-1

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US-09-949-016-778-1

US-09-949-016-7567-1

US-09-949-016-7567-1

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Sequence 9, Appli
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Sequence 3308, A
Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
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Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 270
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Sequence 11433, P
Sequence 17206, P
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9.6%; Score 295.5; DB 4; Length 270;
Best Local Similarity 31.7%; Pred. No. 2.7e-21;
Matches 64; Conservative 46; Mismatches 81; Indels 11
             US-09-352-166-9

US-09-771-045B-9

US-09-770-564A-9

US-09-252-991A-30848

US-09-252-991A-30848

US-09-695-795A-2

US-08-875-891A-30438

US-08-252-991A-30438

US-08-456-390-4

US-08-466-390-4

US-08-467-781-4

US-08-457-781-4

US-08-457-294-1

US-08-452-294-1

US-09-949-016-11433

US-09-252-991A-17206
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LFALNVDTTELNAPRRSTPSVA 247
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ORGANISM: Drosophila melanogaster
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RESULT 4
US-07-741-940-7
SEQ ID NO 191
LENGTH: 704
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                                                                                                                                                                                                                                                                                                                                                      116 IASDVGRGRAWIRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTWAAG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 LUSILFAINIDNKDLNGQ-----SKFAPTVSDL--LKESTQNVTSLLKESTQGVSSLFR
                                                                                                                                                                                                                                                                 Query Match
4.9%; Score 151; DB 4; Length 704;
Best Local Similarity 21.3%; Pred. No. 5.3e-06;
Matches 111; Conservative 71; Mismatches 190; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHODS FOR
DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210.121.475C1 CURRENT APPLICATION NUMBER: US/09/370,838 CURRENT APPLICATION NUMBER: US 09/285,323 EARLIER PRILING DATE: 1999-04-02 NUMBER OF SEQ ID NOS: 289 SOFTWARE FALSE FALSE PASSEC FOR Windows Version 3.0 SEQ ID NO 191
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Sequence 191, Application US/09854133
Sequence 191, Application US/09854133
Sequence 191, Application US/09854133
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Menderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: THE THERAPY AND DIAGNOSI;
FILE REPERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILLING DATE: 2001-05-11
CURRENT FILLING DATE: 2001-05-11
CURRENT FILLING DATE: 2001-05-11
SOFTWARE: FastSEQ for Windows Version 3.0
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CORGANISM: Homo sapien
US-09-370-838-191
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457 KSSEQPVTSASVPESM----TISELRQATVAMMNRKDELEEENRSLRNLLDGEMEHSA 510
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                                                                                                                                                                                                                                                                                                                                           56 OFBAVLOHGLKRSRGLALTAAAIKQAAGFASKTETEPVFWYVVKEVLNKHELQRFYSLRH 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 IASDVGRGRAWIRCAINEHSLERYLHMILADRCRISTFYEDWSFVMDEERSSMLPTWAAG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INSILFAINIDNKDLNGO-----SKFAPTVSDL--LKESTQNVTSLLKESTQGVSSLFR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306
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                                                                                                                                                                                                                                                                                                                                                                                                                                  143 ÖFFVVWEHCLK--HGLKVKKSFIGONKSFRGPLELVEKLCPEASDIATS----VRNLPE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 -SAEGAAQXLRHPLPCQWRGLLQPSRCPPRKPGERDRTRGPRSPGSWTSVQCGSQLSRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BITASSAVSILIKPEQETDPCLSCPGMSVLMPNAKRSGRRKRKXPTXSHLMMRKMSRTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 TCLKRHLGQGRAQRTTPTAPLSISCPPLKAPSGLTPWESEQQLMENXFPVFERGVWVPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...----SLQEEQQQLREQNELIRERSEKSVEI
                                                                                                                                                              Query Match
4.9%; Score 151; DB 4; Length 704;
Best Local Similarity 21.3%; Pred. No. 5.3e-06;
Matches 111; Conservative 71; Mismatches 190; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILLP J.
APPLICANT: JOSLYN, GROFF
APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER P.
APPLICANT: NARKHAM, ALEXANDER P.
APPLICANT: NARMIRA, YUSUKE
APPLICANT: THILVERIS, ANDREW
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----DILKRKV-AEQEEROGMK 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1001 G Street, NW STATE: D.C. STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/07741940 Patent No. 5352775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALBERTSEN, HANS
ANAND, RAKESH
CARLSON, MARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         511 ALRQEV------
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ZIP: 20001-4598
COMPUTER READABLE FORM:
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ADDRESSEE: Banner, F
TYPE: PRT
ORGANISM: Homo sapien
US-09-854-133-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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2328 ISPGRNGISPPNKLSQLPRTSSP-STASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKN 2386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2138 -KŚGISLGSPFH-----LTPDQEEKPFTŚNKGPRILKPGEKSTLETKKIESESK 2185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2281 --LSPVARQTSQ--IGGSSKAPSRS-----GSRDSTPSRPAQQPLSRPIQSPGRNS 2327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 DWSFVMDEERSSMLPTWAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----KRKXPTXSHLMMRKMSRTLGTCLKRHLGQGRAQRT 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 LQPSR----CPPRKFGERDRTRGPRSPGSWTSVQCG--SQLSRPRKSSEQPVT------ 464
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21.9%; Pred. No. 0.0014;
Live 60; Mismatches 140; Indels 139; Gaps
                                                                                                                                                                              APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF I
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION WHER: US/08/289,548A
FILING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Banner & Allegretti, LTD STREET: 1001 G Street, NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-508-9100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                KINZLER, KENNETH
MARKHAM, ALEXANDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY. 2001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2842 amino acids
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Best Local Similarity 21.94
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---RSGRR---
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                                                                                                                APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2138 -KSGISLGSPFH------LTPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESK 2185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2186 GIKGGKKVYKSLITGKVRSNSEISGQMKQPLQANMPSISRGRTM----IHI-PGVRNSS 2239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2240 SSTSPVSKKGPPLKTPASKSPSEGQTATTS-----PRGA-KPSVKSE------ 2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2328 ISPGRNGISPPNKLSQLPRTSSP-STASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKN 2386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 DWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --RSGRR-----KRKXPTXSHLMMRKMSRTLGTCLKRHLGQGRAQRT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 TPTAPLSISCPPLKAPSGLTPMESEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKRR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 XRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEG----AAQXLRHPLPCQWRGL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 SASVPESMTISE-IRQATVAM-MNRKDEL------EEENRSLRNLLDGEMEHSAAL 512
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CDERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,940
FILING DATE: 19920109
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.035574
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-929
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Patent No. 5648312
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
APPLICANT: CARLSON, MARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-508-9299
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2842 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: ||:||:|
2444 KEAPSPTLRRKLEE 2457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; IMMEDIATE SOURCE:
; CLONE: APC
US-07-741-940-7
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US-08-289-548A-7
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                                                                                                                                                                                                                                                                                                                                                                                                               363 XRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEG----AAQXLRHPLPCQWRGL 417
                                                                                                                                                                          -----KRKXPTXSHLMMRKMSRTLGTCLKRHLGQGRAQRT 302
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CARLSON, WARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
MARKATAM, ALEXANDER F.
NAKAMURA, YUSUKE
THIVURIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
GENE IN COLORECTAL CANCER IN HUMANS
                                                             216 KESTQGVSSLFREITASSAVSILIKPEQETDPCLSCPGMSVLMPNAK-
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449, 731
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REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.46943
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Banner & Allegretti, LTD
STREET: 1001 G Street, NW
CITY: Washington
   -----GANSIVSSLH--
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    APPLICATION WUNBER: 08/289,548
    FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: <Unknown>
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COUNTRY: USA
ZIP: 2001-458
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08449731
Patent No. 6413727
GENERAL INFORMATION:
GENERAL ALBERTSEN, HANS
ANAND, RAKESH
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                                                                                                                        2138 -KSGISLGSPFH---
            2099 DWKAIQE--
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US-08-449-731-7
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                                                                             --- EEENRSLRNLLDGEMEHSAAL 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INHERITED AND SOMATIC MUTATIONS OF APC
GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
4.4%; Score 136.5; DB 1;
Best Local Similarity 21.9%; Pred. No. 0.0014;
Matches 95; Conservative 60; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OFERALING SIGLEM: 1-25-203/M3 203
OSOTWARRE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,654
FILING DATE: 25-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.035574
TELECOMMINICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                 465 SASVPESMTISE-LROATVAM-MNRKDEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND TITLE OF INVENTION: GRANT CORPORTION: GRANT CORPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08452654 Patent No. 5691454 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALBERTSEN, HANS
ANAND, RAKESH
CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
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2444 KEAPSPTLRRKLEE 2457
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2842 amino acids
                                                                                                                                                                   RQEVD-TLKRKVAE 525
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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STRANDEDNESS: si
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IMMEDIATE SOURCE:
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APPLICANT:
                                                                                                                                                                   513
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Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                  216 KESTQGVSSLFREITASSAVSILIKPEQETDPCLSCPGMSVLMPNAK------ 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KRKXPTXSHLMMRKMSRTLGTCLKRHLGQGRAQRT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 TPTAPLSISCPPLKAPSGLTPMESEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKRR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 XRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEG-----AAQXLRHPLPCQWRGL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----EEENRSLRNLLDGEMEHSAAL 512
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                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                            Query Match
4.4%; Score 136.5; DB 4; Length 2842;
Best Local Similarity 21.9%; Pred. No. 0.0014;
Matches 95; Conservative 60; Mismatches 140; Indels 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Banner, Birch, McKie & Beckett
                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 SASVPESMTISE-LRQATVAM-MNRKDEL
TELEPHONE: 202-508-9100
TELEFAX: 202-508-929
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2842 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
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                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALBERTSEN, HANS
ANAND, RAKESH
CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
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2444 KEAPSPTLRRKLEE 2457
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APPLICANT:
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2100 DWKAIQE-------GANSIVSSLH------QAAAAACLSRQASSDSDSILSL- 2138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2282 --LSPVARQTSQ--IGGSSKAPSRS-----GSRDSTPSRPAQQPLSRPIQSPGRNS 2328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2241 SSTSPVSKKGPPLKTPASKSPSEGQTATTS-----PRGA-KPSVKSE------ 2281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 DWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLL
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4.4%; Score 136.5; DB 1; Length 2843;
Best Local Similarity 21.9%; Pred. No. 0.0014;
Matches 95; Conservative 60; Mismatches 140; Indels 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 KESTOGVSSLFREITASSAVSILIKPEQETDPCLSCPGMSVLMPNAK-----
                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,940
FILING DATE: 19920109
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/POCKET UNBER: 1107.035574
TELECOMMULCATION:
TELEPHONE: 202-508-9100
                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5648212
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2445 KEAPSPTLRRKLEE 2458
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INFORMATION FOR SEQ ID NO: 2:
ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           513 RQEVD-TLKRKVAE 525
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MARKHAM, ALEXANDER F.
                                                                                                                                              Sequence 2, Application US/08452654 Patent No. 5691454
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                       ALBERTSEN, HANS
ANAND, RAKESH
CARLSON, MARY
                                       :: ||:||: |
2445 KEAPSPTLRRKLEE 2458
                                                                                                                                                                                                                                                             GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
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                   513 RQEVD-TLKRKVAE 525
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 DWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 --RSGRR------KRKXPTXSHLMMRKMSRTLGTCLKRHLGQGRAQRT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 IPTAPLSISCPPLKAPSGLIPMESEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKRR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            465 SASVPESMTISE-LRQATVAM-MNRKDEL-----EEENRSLRNLLDGEMEHSAAL 512
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                                                                APPLICANT: KINZLER, NEWNALL...
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVENES, ANDREW
APPLICANT: THLIVENES, ANDREW
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 KESTQGVSSLFREITASSAVSILIKPEQETDPCLSCPGMSVLMPNAK-
                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Comparible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/289,548A
FILING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60; Mismatches 140;
                                                                                                                                                                                 STREET: 1001 G Street, NW CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 12-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kegan, Sarah A.
REGISTRATION NUMBER: 32,141
REFRENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-508-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
CARLSON, MARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 21.9
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                  ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner &
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2139 -KSGISLGSPFH-----LTPDQEBKPFTSNKGPRILKPGEKSTLETKKIESESK 2186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 DWSFVMDEERSSMLPTWAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLL 215
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APPLICANT: NAKAMURA, YUSUKE
PEPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INTERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,654
FILING DATE: 25-MAY-1995
CLASSIFICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATPONNEY/AGENT INPOWAMTION:
NAME: KAGAIN, SAZAH A.
NAME: REGISTRATION NUMBER: 32,141
                                                                                                                                                                                            ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1107.035574
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2100 DWKAIQE-------GANSIVSSLH------QAAAACLSRQASSDSDSILSL- 2138
                                                                                                                                                                                                                                                                                       2139 -KSGISLGSPFH-----LIPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESK 2186
                                                                                                                                                                                                                                                                                                                                                                      1187 GIKGGKKVYKSLITGKVRSNSEISGQMKQPLQANMPSISRGRTM----IHI-PGVRNSS 2240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 --RSGRR------KRKXPTXSHLMMRKMSRTLGTCLKRHLGQGRAQRT 302
                                                                                                                                                                                                                                                                                                                                                                                                                303 TPTAPLSISCPPLKAPSGLTPMESEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKRR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 LQPSR----CPPRKPGERDRTRGPRSPGSWTSVQCG--SQLSRPRKSSEQPVT------ 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 XRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEG-----AAQXLRHPLPCQWRGL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 SASVPESMTISE-LRQATVAM-MNRKDEL------EEENRSLRNLLDGEMEHSAAL 512
                                                                                                                                                                 156 DWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLL
                                                                                                                                                                                                                                                216 KESTQGVSSLFREITASSAVSILIKPEQETDPCLSCPGMSVLMPNAK------
                                                                                                                           Gaps
                                                                                Query Match
4.4%; Score 136.5; DB 1; Length 2843;
Best Local Similarity 21.9%; Pred. No. 0.0014;
Matches 95; Conservative 60; Mismatches 140; Indels 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THILIVERIS, ANDREM
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                          : |:|:|
2241 SSTSPVSKKGPPLKTPASKSPSEGQTATTS-----PRGA-KPSVKSE-
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,655B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Banner & Witcoff, Ltd.
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KINZLER, KENNETH
MARKHAM, ALEXANDER F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANAND, RAKESH
CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
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2445 KEAPSPTLRRKLEE 2458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOSLYN, GEOFF
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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APPLICANT:
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APPLICANT:
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APPLICANT:
                                        US-08-452-655B-2
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APPLICANT:
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                                                                                                  363 XRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEG-----AAQXLRHPLPCQWRGL 417
                                                                                                                                                                                                                                                                      --- EEENRSLRNLLDGEMEHSAAL 512
                   303 TPTAPLSISCPPLKAPSGLTPMESEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKRR 362
                                                                                                                                                                                418 LQPSR---CPPRKPGERDRTRGPRSPGSWTSVQCG--SQLSRPRKSSEQPVT-----
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APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
WUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,655B
FILING DATE: 25-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/289,548
FILING DATE: US 08/289,548
FILING DATE: US 08/289,548
FILING DATE: US 08/289,749
FILING DATE: US 08/289,548
FILING DATE: US 07/741,940
FILING DATE: US 07/741,940
FILING DATE: US 07/741,940
FILING DATE: US 07/741,940
                                                                                                                                                                                                                                                                 SASVPESMTISE-LROATVAM-MNRKDEL
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1001 G Street, NW
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Patent No. 5783666
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ANAND, RAKESH
APPLICANT: CARLSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: KINYY, GEOFF
APPLICANT: KINYY
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REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                       2445 KEAPSPTLRRKLEE 2458
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4.4%; Score 136.5; DB 1; Length 2843;
Best Local Similarity 21.9%; Pred. No. 0.0014;
Matches 95; Conservative 60; Mismatches 140; Indels 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2. Application US/08370235A
Patent No. 5910418
GENERAL INFORMATION:
APPLICANT: KINZLER, KENNETH W.
APPLICANT: HILL, DAVID E.
APPLICANT: GONSON, KAREN A.
TITLE OF INVENTION: ANTIBODIES AND ASSAYS FOR DERMINING
           CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 320-508-9100
TELECAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
TYPE: amino acid
STRANDENRESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HAPPOTHETICAL: YES
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25-MAY-1995
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US-08-370-235A-2
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2329 ISPGRNGISPPNKLSQLPRİSSP-STASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKN 2387
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Best Local Similarity 21.9%; Pred. No. 0.0014;
Matches 95; Conservative 60; Mismatches 140; Indels 139;
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                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,235A
FILING DATE: 01-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A:
REGISTRATION NUMBER: 32,141
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.48688
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 202 508 9199
MUTATIONS IN THE APC GENE
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                               STATE: DC
STATE: DC
STATE: DC
STATE: DC
STATE: DC
STATE: DC
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2445 KEAPSPTLRRKLEE 2458
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    TITLE OF INVENTION: MUUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                          COUNTRY: U
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US-08-450-582-2
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2329 ISPGRNGISPPNKLSQLPRTSSP-STASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKN 2387
                                                                                    418 LQPSR----CPPRKPGERDRTRGPRSPGSWTSVQCG--SQLSRPRKSSEQPVT------ 464
                                                                                                                                                                         465 SASVPESMTISE-LRQATVAM-MNRKDEL: -----EEENRSLRNLLDGEMEHSAAL 512
363 XRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEG----AAQXLRHPLPCQWRGL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSERICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/452,655
PILING DATE: 2-MAY-1995
APPLICATION NUMBER: US 08/289,548
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,548
PRIOR PAPLICATION NUMBER: US 08/289,548
PRIOR DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERNICE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION: TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08450582; Patent No. 6114124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINZLER, KENNETH
MARKHAM, ALEXANDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
                                                                                                                                                                                                                                                                                          :: ||:||: |
2445 KEAPSPTLRRKLEE 2458
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1001 G Street, NW
                                                                                                                                                                                                                                                                 513 RQEVD-TLKRKVAE 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALBERTSEN, HANS
ANAND, RAKESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
STATE: D.C.
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-450-582-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2100 DWKAIQE------GANSIVSSLH-----QAAAACLSRQASSDSDSILSL- 2138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2139 -KSGISLGSPFH------LTPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESK 2186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 DWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 KESTQGVSSLFREITASSAVSILIKPEQETDPCLSCPGMSVLMPNAK------ 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 TPTAPLSISCPPLKAPSGLTPMESEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKRR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/452,655
FILING DATE: 25-MAY-1995
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTONNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                          Banner & Witcoff, Ltd
                                                                                                                                                                     MARKHAM, ALEXANDER F. NAKAMURA, YUSUKE THLIVERIS, ANDREW
             ALBERTSEN, HANS
MANDI, RAKESH
CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
                                                                                                                                                                                                                                                                                                                                               : 1001 G Street, NW
Washington
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INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 21.9'
Matches 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-450-582-2
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                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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APPLICANT:
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APPLICANT:
APPLICANT:
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2388 ASSIPRSESASKGLNQMNNGMANKKVELSRMSSTKSSGSESBRSERPVL---VRQSTFI 2444
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                                                                                                                                                                                                                                                                2139 -KSGISLGSPFH------LTPDQEEKPFTSNKGPRILKFGEKSTLETKKIESESK 2186
                                                                                                                                                                                                                                                                                                        303 TPTAPLSISCPPLKAPSGLTPMESEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKRR 362
                                                                                                                                                                                                                                                                                                                                                                  363 XRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEG----AAQXLRHPLPCQWRGL 417
                                                                                                                                                                                                                                                                                                                                                                                                                            418 LQPSR----CPPRKPGERDRTRGPRSPGSWTSVQCG--SQLSRPRKSSEQPVT----- 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 SASVPESMTISE-LROATVAM-MNRKDEL-----EEENRSLRNLLDGEMEHSAAL 512
                                                                                                                                                                                     216 KESTQGVSSLFREITASSAVSILIKPEQETDPCLSCPGMSVLMPNAK------ 262
                                                                                                                                                                                                                                               263 --RSGRR-----KRKXPTXSHLMMRKMSRTLGTCLKRHLGQGRAQRT 302
                                                                                                                          156 DWSFVMDEERSSMLPTWAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLL 215
                                                                                                  Gaps
                                                                   Query Match
Best Local Similarity 21.9%; Pred. No. 0.0014;
Matches 95; Conservative 60; Mismatches 140; Indels 139;
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2445 KEAPSPTLRRKLEE 2458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      513 RQEVD-TLKRKVAE 525
, MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
US-08-450-582-7
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Search completed: June 7, 2005, 12:04:48 Job time : 25.6321 secs Sequence 30, Appl Sequence 30, Appl Sequence 21, Appl Sequence 1970, Ap

Sequence 3 Sequence 1

3547, Ap 3340, Ap 2, Appli 126375,

Sequence Seq

Perfect score:

Sequence:

protein

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Run on:

Scoring table:

Searched:

Database

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Sequence 2298, Application US/10276774
; Sequence 2298, Application US/10276774
; Publication No. US20040053245A1
; GENERAL. INFORMATION:
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVERTION:
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-04-3
; NUMBER OF SEQ ID NOS: 2700
; COSTWARE: CUSCOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLRCALNEHSLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.9%; Score 183; DB 15; Length 1019; Best Local Similarity 22.2%; Pred. No. 1.3e-06; Matches 115; Conservative 75; Mismatches 196; Indels 132; Gaps
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US-10-302-131-21
US-10-408-765A-1970
US-10-408-765A-1970
US-10-408-765A-1970
US-10-202-330
US-10-202-330
US-10-31-32-330
US-10-33-343-4
US-10-108-260A-3547
US-10-108-260A-3340
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US-10-325-635-18369
US-10-325-18369
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US-10-325-18369
US-10-428-275-232
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11253
11253
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2641
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1246
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                                                                                 SEQ ID NO 2298
LENGTH: 1019
136.5
136.5
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Sequence 372, App
Sequence 131, App
Sequence 191, App
Sequence 191, App
Sequence 191, App
Sequence 2780, Ap
Sequence 1412, Ap
Sequence 1465, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2298, Ap
Sequence 1936, Ap
                                                                                                           7, 2005, 12:02:31 ; Search time 76.4207 Seconds (without alignments) 2846.907 Million cell updates/sec
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1: \cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*

3: \cgn2_6/ptodata/1/pubpaa/NCT_MEW_PUB.pep:*

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13: \cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-094-749-1936

US-10-408-765A-2491

US-10-267-502-372

US-09-738-973-191

US-09-854-133-191
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US-10-264-237-2780
US-10-276-74-1412
US-10-296-115-1340
US-10-296-115-1465
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Maximum Match 100%
Listing first 45 summaries
                                                                               - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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27, Appl 25, Appl 45308, A 183619,

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61, Appl 60, Appl 63, Appl

App]

Sequence Sequence Sequence Sequence Sequence Sequence

1425, Ap

25;

28 77

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183 175.5 175.5 160 161 151 151 151 151 137 137

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Score

Result

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                                                                                                                                                                                                                       EAVLOHGLKR----SRGLALTAAAIK-QAAGFASKTETEPVFWYYVKEVLNK---HELQR 109
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14 GGGGGGKKSLSARNAAVER-RNLITVC--RFSVKTLIDRSCFETIDDSSPEFNNFAAIL
                                                                                                                                                                                        110 FYSLRHIASDVGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSML
                                                                              EAVLOHGLKR----SRGLALTAAAIK-QAAGFASKTETEPVFWYYVKEVLNK---HELQR
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| Sequence 2491, Application US/10408765A
| Publication No. US20040101874A1
| GENERAL INFORMATION:
| APPLICANT: Glosh, Soumitra S.
| APPLICANT: Glosh, Bing
| APPLICANT: Glosh, Bradford W.
| APPLICANT: Taylor, Stewen W.
| APPLICANT: Taylor, Stewen W.
| APPLICANT: Warnock, Dale E.
| TITLE OF INVENTION: TDENTIFIED IN THE MITOCHONDRIAL PROTEOME
| FILE REFERENCE: 660088 465
| CURRENT APPLICATION NUMBER: US/10/408,765A
| CURRENT FLING DATE: 2003-04-04
| NUMBER OF SEQ ID NOS: 3077
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; Pred. No. 2e-06;
35; Mismatches 118;
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US-10-267-502-372
; Sequence 372, Application US/10267502
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US-10-408-765A-2491
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                                                                                                                                              RYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTWAAGLNSILFAINIDNKDLNGQSKFA
                                                                                                                PTVSDLLK-ESTQNVTSLLKESTQGVSSL----FREITASSAV--SILIKPEQET----D
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Publication No. US20030219741A1
GENERAL INFORMATION:
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YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
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SEKI, NACHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
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Best Local Similarity 28.5%
The Conservative 75; Conservative
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NAGAI, KEIICHI
IRIE, RYOTARO
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US-10-094-749-1936
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TITLE OF INVENTION: Proteins, Polymucleotides Encoding Them and Methods of TITLE OF INVENTION: Using the Same TITLE OF INVENTION: Using the Same TITLE OF INVENTION: Using the Same CURRENT APPLICATION NUMBER: 06/248,153 PRIOR APPLICATION NUMBER: 06/248,153 PRIOR PELLOR TILING DATE: 2000-11-13 PRIOR PELLOR TILING DATE: 2000-11-17 PRIOR PELLOR DATE: 2000-11-17 PRIOR PELLOR TILING DATE: 2001-11-17 PRIOR PELLOR TILING DATE: 2001-01-26 PRIOR FILING DATE: 2001-02-26 PRIOR PELLOR NUMBER: 60/269,262 PRIOR APPLICATION NUMBER: 60/269,562 PRIOR APPLICATION NUMBER: 60/269,562 PRIOR PELLOR DATE: 2001-02-16 PRIOR FILING DATE: 2001-07-10 PRIOR FILING DATE: 2001-07-10 PRIOR FILING DATE: 2001-07-11 PRIOR FILING DATE: 2001-07-11 PRIOR FILING DATE: 2001-07-11 PRIOR FILING DATE: 2001-07-11 PRIOR FILING DATE: 2001-08-17 NUMBER OF SEQ ID NOS: 205

NUMBER OF SEQ ID NOS: 205

NUMBER PARCENTIN NUMBER: 60/313,283

PRIOR FILING DATE: 2001-08-17 SEC ID NOS: 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.9%; Score 151; DB 15;
Best Local Similarity 21.3%; Pred. No. 0.00042;
Matches 111; Conservative 71; Mismatches 190;
                                                                                                                                                           Li, Li
Padigaru, Muralidhara
                                                                                        Gangolli, Esha A
Shimkets, Richard A
Taupier, Raymond J
                                              Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 ERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTWAAGLNSILFAINIDNKDL---NGO 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ---PEQETDPCLSCPGMSVLMP-----NAK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSGRRKRKKPTXSHLMMRKMSRTLGTCLKRHLGQGRAQRTTPTAPLSISCPPLKAPSGLT 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 ATGREHLPLPDAQLGSAEGAAQXLRHPLPCQWRGLLQPSR---CPPRKPGERDRTRGP-- 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----RQGMKVQALASYLCYFVRRFXPHVRTMWWR------NGGR-EKSNSSXXS 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QASGYAPKSFHVEDTPVCF-----SRNSSLSSLSID-----SEDDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 SKFAPTVSDL----LKESTQNVTSLLKESTQGVSSLFREITASSAVSILIK-----
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                                                                                                                                                                                                                                                                                                                                                         Query Match 5.2%; Score 160; DB 15; Length 2845; Best Local Similarity 20.2%; Pred. No. 0.00063; Matches 122; Conservative 80; Mismatches 224; Indels 178;
                                     APPLICANT: Kim, Jaeseob
APPLICANT: Kim, Jaeseob
APPLICANT: Galant, Ron
TITLE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SOFTWARE: PatentIn version 3.2
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US-10-015-115-73
Sequence 73, Application US/10015115
Publication No. US20030207800A1
GENERAL INFORMATION
APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spency, Suresh G
  US20040071700A1
                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus musculus
US-10-267-502-372
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Publication No. US20
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.9%; Score 151; DB 9; Length 704; Best Local Similarity 21.3%; Pred. No. 0.00053; Matches 111; Conservative 71; Mismatches 190; Indels 150;
                                                                                                                                                                                                                                                                                                           APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
APPLICANT: Ralos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-112-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 191
LENGTH: 704
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                   --- DTLKRKV-AEQEERQGMK 533
                                                                                                       Sequence 191, Application US/09738973
Patent No. US20020110563A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                      Reed, Steven G.
Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
Algate, Paul A.
Secrist, Heather
Indirias, Carol Yoseph
Benson, Darin R.
Elliot, Mark
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CORGANISM: Homo sapien
US-09-738-973-191
   511 ALRQEV---
                                                                                             US-09-738-973-191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IASDVGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAG 175
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4.9%; Score 151; DB 9; Length 704;
Best Local Similarity 21.3%; Pred. No. 0.00053;
Matches 111; Conservative 71; Mismatches 190; Indels 150;
                                                                                                                                                                                                           APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FREESEQ FOR WINDOWS Version 3.0
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                           558
|:||: | XLQQELGGRIGALQLQLSQLHEQCSSLEKELKSEKEQRQALQ
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                                                                                                                                          Sequence 191, Application US/09854133; Publication No. US20020183499A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     511 ALRQEV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien
US-09-854-133-191
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US-10-144-649A-191
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LENGTH: 704
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NUMBER OF SEQ ID NOS: 2876
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                                                                                                                                                                                                                                                                                                                                                                                                                                      457 KSSEQPVTSASVPESM-----TISELRQATVAMMNRKDELEEENRSLRNLLDGEMEHSA 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 TCLKRHLGQGRAQRTTPTAPLSISCPPLKAPSGLTPMESEQQLMENXFPVFERGVWVPE-
                  APPLICANT: Fan, Liqun
APPLICANT: Algate, Paul A.
APPLICANT: McMeill, Particia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C11
CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE PARISEQ for Windows Version 3.0
SEQ ID NO 191
LENGTH: 704
                                                                                                                                                                                                                                                                                     Query Match
4.9%; Score 151; DB 14; Length 704;
Best Local Similarity 21.3%; Pred. No. 0.00053;
Matches 111; Conservative 71; Mismatches 190; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2780, Application US/10264237

Publication No. US20040009491A1

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PAL31P1

CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR FILING DATE: 2001-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-19
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Lodes, Michael J.
                Tongtong
              Wang, Tongto
Fan, Liqun
                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapien
US-10-144-649A-191
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US-10-264-237-2780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 TQGVSSLFREITASSAVSILIKPEQETDPCLSCPGMSVLMPNAKRSGRRKRKXPTXSHLM 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 LPDAQLG---SAEGAAQXLRHPLPCQWRGLLQPSRCPPRKPGERDRTRGPRSPGSWTSVQ 447
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APPLICANT: Hyseq, inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT EMPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2000-11-18
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-02-03
NUMBER: OF SEQ ID NOS: 2700
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NAME/KEY: MISC FEATURE
LOCATION: (537)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring
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4.7%; Score 145; DB 15; Length 546;
Best Local Similarity 20.5%; Pred. No. 0.0012;
Matches 109; Conservative 69; Mismatches 177; Indele 176;
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                                                                                                                                                                               NAME/KEY: MISC FEATURE
LOCATION: (534)
OTHER INFORMATION: Xaa equals any
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            Patentin Ver. 3.1
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 2780
LENGTH: 546
TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20040053248A1
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TITLE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
TITLE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
THER REPERRNCE: 784PCT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11.18
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR PILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
SEQ ID NOS: 1478
SEQ ID NO 1340
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                                                                                                                                                                       18;
                                                                                                                                4.4%; Score 137; DB 15; Length 286; 28.1%; Pred. No. 0.0025;
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4.4%; Score 137; DB 15; Length 286;
Best Local Similarity 28.1%; Pred. No. 0.0025;
Matches 52; Conservative 33; Mismatches 82; Indels 10
                                                                                                                                                                      Indels
                                                                                                                                                                  82;
                                                                                                                                                                    33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1340, Application US/10296115
Publication No. US20040053248A1
GENERAL INFORMATION:
                                                                                                                          Query Match
Best Local Similarity 28.11
Matches 52; Conservative
                                                                       ; ORGANISM: Homo sapiens
US-10-276-774-1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1340
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SOFTWARE: Custom
SEQ ID NO 1412
LENGTH: 286
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                                                        TYPE: PRT
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RESULT 12 US-10-296-115-1465 ; Sequence 1465, Application US/10296115

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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 OFEAVLOHGLKRSRGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRH 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 IASDVGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 LNSILFAINIDNKDLNGQ----SKFAPTVSDL--LKESTQNVTSLLKESTQGVSSLFR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OF INVENTION: NO. US20040053248Alel Nucleic Acids and Polypeptides
TITLE OF INVENTION: NO. US20040053248Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 784PCT
CURRENT APPLICATION NUMBER: US09/488,725
PRIOR PILING DATE: 2002-11-18
PRIOR PILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 1465
LENGTH: 286
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Sequence 2045, Application US/10264237

Sequence 2045, Application US/10264237

Publication No. US20040009491A1

GENERAL INFORMATION:

APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1

CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT PILING DATE: 2002-10-04

PRIOR FILING DATE: 2001-05-18

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: PATCHTIN VET. 3.1

SEQ ID NO 2045

LENGTH: 369
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4.4%; Score 136.5; DB 15; Length 369;
Best Local Similarity 23.3%; Pred. No. 0.004;
Matches 77; Conservative 41; Mismatches 124; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.4%; Score 137; DB 15; Length 286;
Best Local Similarity 28.1%; Pred. No. 0.0025;
Matches 52; Conservative 33; Mismatches 82; Indels 10
                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1465
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NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Db 2100 DWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDILSL- 2138 Ov 216 KESTOGYSSLFREITASSAVSILIKPEOETDPCLSCPGMSVLMPNAK 262	2139 -KSGISLGSPFHLTPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESK 2 263RSGRRKRKKPTXSHLMMRKMSRTLGTCLKRHLGQGRAQRT 3	: :: :: :: :: :: 303 TPTAPLSISCOPIKAPSGITPMESCOLMENYEPVPERGYWYPEAXCEKHRXXRCGXKRR		OY 363 KKVWKLIRKEAQGPLGYAREATGREHLPLPDAQLGSAEGAAQXLRHPLPCQWRGL 417	Qy 418 LQPSR	2329 ISPGRNGISPPNKISOLPRTISSP-STASTKSSGSGRWSYTSPGRQMSQQNLTKQTGLSKN 465 SASVPESMTISE-LRQATVAM-MNRKDELEEENRSLRNLLDGEMEHSAAL ::	2388	Qy	RESILT. 15	US-09-987-1 ; Sequence 1, Application US/09987482 ; Publication No. US20020184656A1		; TITLE OF INVENTION: IN VIVO ASSAY SYSTEM FOR SCREENING AND VALIDATION OF ; TITLE OF INVENTION: DRUGS AND OTHER SUBSTANCES : FITLE OF INVENTION: DRUGS AND OTHER SUBSTANCES : FITLE DREEPENDED. DRUGS AND OTHER SUBSTANCES	CURRENT APPLICATION UNMER: US/09/987,482	·· a)	ENGTH: 2843 FPE: PRT	. ORGANISM: Homo sapiens US-09-987-482-1	Query Match 4.4%; Score 136.5; DB 9; Length 2843; Best Local Similarity 21.9%; Pred. No. 0.076; Matches 95; Conservative 60; Mismatches 140; Indels 139; Gaps 23;	156 DWSFVMDEERSSMLPTWAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLL	ZIOO DWKAIQEGANSIVSSKIHQAAAAACLSKQASSUUDSILSE-	OY 216 KESIQOVSSLEKEIIASSAVSLIIKFEQFIDFULSCFGMSVLMFAKK 262 	QY 263RSGRRKRKKPTXSHIMMRKWSRTLGTCLKRHLGQGRAQRT 302	Db 2187 GIKGGKKVYKSLITGKVRSNSEISGQMKQPLQANMPSISRGRTMIHI-PGVRNSS 2240	OY 303 TPTAPLSISCPPLKAPSGLTPMESEQQLMENXFPVFERGWWPEAXCEKHRXXRCGXKRR 362	OY 363 XRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLGSAEGAAQXLRHPLPCQWRGL 417
OY 58 EAVLOHGIKRSRGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHE 106	FYEDWSFVMDEERS : : : FYEPNALMMEEE-G	Qy 167 SMLPTWAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLLKES 218 :::: :: :	TQGVSSLFREITASSAVSILIKPEQETDPCLSCPGMSVLMPNAKRSG		Db 260 LESNRKGPKQDRTAEGQALSEARKHLKEETQLRLDVEKE 298 Ov 321 LTPMESEOOLMENXFPVPERGYMVPRAXCFK 341	299 LEMQISMRQEMELAMKMLEKDVCEK	RESULT 14	US-U8-681-219-32 ; Sequence 32, Application US/08681219 ; Publication No. US20020058607A1	; GENERAL INCREMITOR: ; APPLICANT: TARARKI Sato and Junn Yanagisawa ; TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN	TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF; TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF NUMBER OF SEQUENCES: 35	COOPER & Dunham LLP STREET: 1185 Avenue of the Americas	CITY: New York STATE: New York COUNTRY: U.S. A.	S 4	CHELLOW INFE: FLOUPY GISK CHELLOW INFE: TOOPY GISK COMPUTER: DR. PC-DOS/MS-DOS COMPUTER: PC-DOS/MS-DOS	E A	; AFFLICATION NUMBER: US/08/681,219 ; FILING DATE: 22-JUL-1996 ; CLASSIFICATION: 435	; ATTORNEY/AGENT INFORMATION: ; NAME: White, John P ; REGISTRATION UUMBER: 28,678	TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400	; INFORMATION NO SEQ ID NO: 32:	JENOTH: 2843 amino acids	; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECHIE TYPE: nentide		Query Match 4.4%; Score 116.5; DB 8; Length 2843; Best Local Similarity 21.9%; Pred. No. 0.076; Matches 95; Conservative 60; Mismatches 140; Indels 139; Gaps 23;	Qy 156 DWSFVMDEERSSMLPTWAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLL 215

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GenCore version 5.1.6
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2005, 8 June Run on:

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score:

1 cccttctcacagcccaggcc......accgtcgacctcgagggggg 2631 Title: Perfect so Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

8780412 Total number of hits satisfying chosen parameters: 4390206 segs, 2959870667 residues Searched:

seq length: 0 seq length: 200000000 09 09 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04: Database

geneseqn2004as:* geneseqn2004bs:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2001as:* geneseqn1990s:* geneseqn1980s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Re

esult No.	Score	Query	Query Match Length DB	DB	ID	Description
	2553.8	97.1	2631	7	AAV03324	Aav03324 Clone 10
(1)	1851.2	70.4	4596	7	AAV03326	Aav03326 DNA seque
(L)	1850.2	70.3	4596	ហ	AAS79490	Aas79490 DNA encod
4	1850.2	70.3	4596	9	ABK51171	Abk51171 cDNA enco
u)	1850.2	70.3	4596	10	ADE85075	Ade85075 Farnesyl
9	1850.2	70.3	4596	13	ADR25114	Adr25114 Breast ca
٦	1783.4	67.8	4684	. 11	ACN44439	Acn44439 Human mRN
æ	1771.6	67.3	3152	12	ADQ67410	Adg67410 Novel hum
o	1133.4	43.1	3156	~	AAV73917	Aav73917 Human NIK
7	1133.4	43.1	3156	7	AAV71603	Aav71603 Human NF-
1	1133.4	43.1	3156	7	AAV69285	Aav69285 Human NF-
12	577	37.1	2844	7	AAX87842	Aax87842 NF-kB ind
13	973.4	37.0	73967	11	ACN44438	Acn44438 Human gen
14	754.2	28.7	1385	4	AAH99262	Aah99262 Human pro
c 15	691.8	26.3	2760	Ŋ	AAS79491	Aas79491 DNA encod
16	672.8	25.6	2828	11	ACN44437	Acn44437 Mouse mRN
13	588.2	22.4	722	S	AAS79492	Aas79492 DNA encod
18	3 446.8	17.0	2070	12	ADP28582	Adp28582 Human sec
C 13	349.4	13.3	2475	11	ADM03069	Adm03069 Human cDN
20	242.2	9.5	499	σ	ACH15373	Ach15373 Human adu

21 205.8 7.8 476 10 ADF79802 22 188.8 7.2 42566 11 ACN44436 23 88.4 3.4 455 5 ABV22061 24 88.4 3.4 476 5 ABV23061 25 88.4 3.4 476 5 ABV23061 26 28 88.4 3.4 476 5 ABV23478 27 28 88.4 3.4 504 5 ABV23478 29 70 2.7 1024 5 ABV33478 29 70 2.7 1024 5 ABV33478 29 70 2.7 1024 5 ABV33493 31 53.2 2.0 2000 8 ADA71938 32 52.8 2.0 25 6 ABV2298 33 50.4 1.9 50.6 ABV2298 34 50.4 1.9 50.6 ABV2393 35 42.6 1.9 50.6 ABV2393 36 42.6 1.6 1464 6 AAD24766 39 42.4 1.6 1359 11 ABD10419 20 42 4 1.6 1746 11 ABD10312 21 6 128 8 12 ADV89158 22 6 4 40.4 1.5 108 8 AAV333230 23 41.2 1.6 1359 11 AAN60310	Adf79802 Leukaemia	Acn44436 Mouse gen	Abv22061 Human pro	Abv27896 Human pro	Abv12334 Human pro	Abv33478 Human pro	Abv42401 Human pro	Abv03165 Human pro	Aas 79493 DNA encod	Ada71938 Rice gene	Aav03325 Sequence		Aai84793 Human pol	Abz03850 Human leu		Abn46309 Human spl	Ada71938 Rice gene	Aad24766 Beta vulg	Abd10419 Pseudomon	Abd10504 Pseudomon	Abd10381 Pseudomon	Adn89158 Human ITG	Adj92320 Mouse hai	Aca26986 Prokaryot	Aan60310 Canine IF
21 205.8 7.8 476 22 188.8 7.2 42566 24 88.4 3.4 455 25 88.4 3.4 455 26 88.4 3.4 476 27 88.4 3.4 476 28 70.8 2.0 1024 31 53.2 2.0 1024 32 52.8 2.0 65 33 50.4 1.9 50 34 49.1 1.6 11464 42.4 1.6 1746 42.4 1.6 1746 45.4 40.4 1.5 1711	ADF79802	ACN44436	ABV22061	ABV27896	ABV12334	ABV33478	ABV42401	ABV03165	AAS79493	ADA71938	AAV03325	ABN52988	AAI84793	ABZ03850	ABZ02592	ABN46309	ADA71938	AAD24766	ABD10419	ABD10504	ABD10381	ADN89158	ADJ92320	ACA26986	AAN60310
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00000000000000000000000000000000000000	205.8	188.8	88.4	88.4	88.4	88.4	88.4	73.8	70	58.2	53.2	52.8	50.4	20	20	49	43.6	42.6	42.4	42.4	42.4	42	41.2	40.4	40.4
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ALIGNMENTS

Clone 10 cDNA encoding NMP1, a TRAF2 binding protein. BP. AAV03324 standard; cDNA; 2631 (first entry) 15-APR-1998 AAV03324; RESULT 1 AAV0332

Human tumour necrosis factor receptor-associated factor 2; TRAF2; TRAF-2 binding protein; NF-kappaB activity; NF-kappaB induction; intracellular signalling activity; acute hepatitis; autoimmune-induced cell death; 88.

Ношо

WO9737016-A1

09-OCT-1997.

97WO-IL000117. 01-APR-1997; 96IL-00117800. 96IL-00119133. 02-APR-1996; 26-AUG-1996; (YEDA) YEDA RES & DEV CO LTD

Mett I; Kovalenko A, Boldin M, Malinin N, Wallach D,

WPI; 1997-503101/46.

DNA encoding tumour necrosis factor receptor-associated factor binding molecule - used for modulation or mediation in cells of the activity of NF-kB

Claim 4; Fig 4; 127pp; English.

The present sequence encodes a protein designated NMP1, a TRAF2 binding protein. This protein contains Ser/Thr protein kinase motifs. A full length cDNA clone encoding NF-kappas (NIK) was obtained by PCR using the present clone, clone 10. The clone 10 protein is capable of binding to at least amino acids 222-501 of TRAF2. The TRAF-2 binding proteins can be

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840
any other intracellular signalling activity modulated or mediated by TRAF2. TRAF-binding proteins are especially used for prevention or treatment of pathological conditions associated with NF-kB induction, e.g. acute hepatitis, autoimmune-induced cell death, e.g. death of the beta langerhans cells or the pancreas that results in diabetes, the death of cells in graft rejection, the death of oligodendrocytes in the brain in multiple sclerosis, and AIDS-inhibited T cell suicide which causes proliferation of the AIDS virus and hence the AIDS disease. The proteins which are useful for screening of ligands capable of binding to a protein, which are useful for modulating cellular activity modulated/mediated by TRAF2.
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2631; Conservative 0; Mismatches
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The present sequence encodes a NF-kappa inducing kinase (NIK). The full conditions are detectively than TRAF2. Proteins count to induce NF-kappa even more effectively than TRAF2. Proteins capable of binding to TRAF2 and NIK were identified. The NIK or TRAF-2 binding proteins can be used for modulation or mediation in cells of NF-kappaB activity or any other intracellular signalling activity modulated or mediated by TRAF2. TRAF-binding proteins are especially used for prevention or treatment of pathological conditions associated with NF-kappaB induction, e.g. acute hepatitis, autoimmune-induced cell death, and induction, e.g. acute hepatitis, autoimmune-induced cell death, c.g. death of the beta LangerThans cells or the pancreas that results in diabetes, the death of cells in graft rejection, death of cells in graft rejection, the death of cells in graft rejection, death of cells in graft rejection, death of cells in graft rejection, death of cells in graft rejection, death of cells in graft rejection, death of cells in graft rejection, death of cells in graft rejection of the AIDS virus and hence the AIDS disease. The proteins are also useful for screening of ligands cappable of binding to a protein, which are useful for modulating cellular activity modulated/mediated by TRAF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal crivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food of sites expressing (II). (I) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 15294; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published pct sequences
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2000US-00649167.
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                                                     (first entry)
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P-PSDB; ABG15303.
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23-AUG-2000;
                                                                                       DNA encoding
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Matches 2334;
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10	RESULT 4 ABK51171 ID ABK51171 standard; cDNA; 4596 BP. XX AC ABK51171; XX XX DT 30-JUL-2002 (first entry)	cDNA encoding human cellular kinas Human; virucide; cytomegalovirus i RIP; Nck-Interacting kinase; NIK; Homo sapiens.	FH Key Locaton/Qualifiers FT CDS 233. 3076 FT / tag= a / tag= a / product = "Human cellular kina Knase)" XX XX XX XX XX XX XX XX XX XX XX XX XX	02-MAY-2002. 15-OCT-2001; 2001EP-00124604. 16-OCT-2000; 2000US-0240750P. (AXXI-) AXXIMA PHARM AG.	XX WPI; 2002-373930/41. DR WPI; 2002-373930/41. DR P-PSDB; AAU80371. XX Identifying agents for treatment or prevention PT infection, comprises contacting test compound PT detecting change in cellular kinase activity.	XX XX XX XX XX XX XX C The present invention relates to a new method CC for treating and/or preventing cytomegalovirus CC clated diseases. The method of the invention CC compound with at least one of the cellular kin CC activity. The method of the invention CC c durinity. The method of the invention co pecified kinases can also be used for diagnost CC present nucleic acid sequence encodes the human CC present nucleic acid sequence encodes the human CC interacting kinase) protein of the invention, XX XX XX XX XX XX XX XX XX XX XX XX XX	
1261 ACAAAACAGGGATCTTTNTTCTGCCCCTGCTCCAGTNCCAGTTGGCCTGNACCGCTTGG 1320		1621 CACACTTTCAGGTTGTTGCAACACGTCCTGAGTTGACCTCTGGTTCAGCCAAGGACC 1680	1741 GCTACCACTCTTCCCCAGAGCAGCCCCCAGCCCCTTCAGGCCCAGCACTGCCCCAG 1800	1861 CAGGAACAGTCTGTGGACATGATCAGTGCTNAAGGNAAAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAG	1981 GCTNCAGNCATCANCACTTNCACCCTNGCCCTGGCCCANGGCCANGAGGGTACTG 2040		
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hod for identifying compounds irus (CMV) infection and/or ion comprises contacting a test kinases RICK, RIP, NCk-tecting any change in kinase be used to treat and/or prevent mucleotides that can detect the gnosis of infection. The human cellular kinase NIK (Nck-on, as described above
CCGAGACTCCGTGGGGGAGAAGCTCAT 2400
                                                                                   TGCAGCCTTGGTACTGCAGAGTCTG 2520
                                                                 STCCACATTGAGTCAGACTGCTCCC 2460
                                                                                                                                                                                            CMV; cellular kinase; RICK; -2; gene; ss.
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us-09-155-676b-3.rng

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chlorophenyl) (1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-methyl-2-(1H)quinolinone, monitoring the therapy of a partient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTGCACACTGGCCCCTGATGGCAGCTTCGCCTGGAGCTGGAGGGTCAAGCATGGCCAGC 960
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Pred. No. 0;
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                                                                                 Sequence 4596 BP; 1055 A; 1401 C; 1299 G;
                                                       modulated in the presence of FTI.
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                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-[amino(4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
                                                                                                                    CCCAGGGGAGCTANCTCAGGACTCACGTAGCATTAAATCAGCTGTGNAATCGTCAGGGGG
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30-OCT-2001; 2001US-03400B1P.
30-OCT-2001; 2001US-0340938P.
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     according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a pattent similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.
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are associated with Carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of bioactive agent capable of bioactive agent capable of anounlating the activity of CAP; (ii) for screening of evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vii) for inhibiting the activity of CAP; (vii) for treating carcinoma; (vii) for neutralizing the activity of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DAA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA gene sequence. Note: This patent is an equivalent to basic patent
     carcinoma
                                                                                                                                                                                                                                                                                   present invention relates to novel DNA and protein sequences which
Recombinant nucleic acid useful for diagnosis and treatment of comprises a nucleotide sequence.
                                                                                                                                                  SEQ iD NO 887; Opp; English.
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Sequence 4684 BP; 1057 A; 1434 C; 1328 G; 865 T; 0 U; 0 Other;

2209 2329 2569 2629 2749 2269 2509 2689 180 240 300 420 720 480 540 900 099 9 CTGCAGCGGAGCTGGGAGGTGAACCGGGCACTACAGCAAGTGGGGAGGTCTGAAGA GCCCTTGGAGGGAGAATATAAAGAACCAAGACATCCACCGCCAAATCAAGCCAATTACC 2510 TACCTCTGTCCTCCCTGGAGCCAGCCCTGCCAGAAACCCCAGCTCACCAGAGGGAAAG CCCAGCCATTTTCTCTGGAGGAGCAGGAGCAAATTCTCTCGTGCCTCAGCATCGACAGCC CCCTGAGCTCAGGCGTACACTCCTGGAGCAGCCAGGCCGAGGCTCGAAGCTCCAGCTGGA cecercicacageceaagecarecaagagagergaggaaaagagecearecaegegrer 121 GCCCTTGGAGGGGAGAATATAAAGAACCAAGACATCCACCGCCAAATCAAGCCAATTACC ACCAGACCCTCCATGCCCAGCCGAGAGAGACTTTCGCCAAGGGCCCCAGGGCCCCGGCCAG CTGAGGAGACAACAGGCAGAGCCCCTAAGCTCCAGCCTCCTCCCCACCAGAGCCCCCAG CTGAGGAGACAACAACAAGGCCCCCTAAGCTCCAGCCTCCTCTCCCACAGAGCCCCCCAG 2570 CAACCGTCCCGGAGCAGGAACTGCAGCTGGAAATAGAATTATTCCTCAACAGCCTGT TCTCCCTGTCGGATGACAGTGAGAACCCATCAAAGGCCTCTCAAAGCTCGCGGGACA 661 ACATGGTGCTGGCCCGGGGCCCCACCGACACCCCAAGCTATTTCAATGGTGTGAAAG CTGCAGCGGAGCTGGGAAGGTGAACCGGGCACTACAGCAAGTGGGAGGTCTGAAGA ACCAGACCCTCCATGCCCAGCCGAGAGAGCTTTCGCCAAGGGCCCCAGGGCCCCGGCCAG TACCTCTGTCCTCGAGCCAGCCCCTGCCAGAAACCCCAGCTCACAGAGGGGAAAG CCCTGAGCTCAGGCGTACACTCCTGGAGCAGCCAGGCCGAGGCTCGAAGCTCCAGCTGGA CCCCTCTCACAGCCCAGGCCATCCAAGAGGGGCTGAGGAAAGAGCCCCATCCACCGCGTGT **AGCCAAACAAGTCTCCTCCCTTGACTTTGAGCAAGGAGGAGTCTGGGATGTGGGAACCCT** CAACCGTCCCGGAGCAGGAACTGCAGCAGCTGGAAATAGAATTATTCCTCAACAGCCTGT TCTCCCTGTCGGATGACAGTGAGAAGAACCCATCAAAGGCCTCTCAAAGCTCGCGGGACA Score 1783.4; DB 11; Lengt Pred. No. 0; 5; Mismatches 183; Indels 67.8%; 89.3%; Query Match 67.8 Best Local Similarity 89.3 Matches 2297; Conservative

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                                                                                                                                                                                                                                                                                                                                      The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% to 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACCTCTGTCCTCCCTGGAGCCAGCCCCTGCCAGAAACCCCAGCTCACCAGAGCGGGAAAG 1094
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Alzheimer's diseases, Parkinson's diseases, dementi
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                                                                                                                                        Wakamatsu
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Pred. No. 0;
5; Mismatches
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                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 4571; 2449pp; English.
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                                                                                                                                        Otsuki T,
Nagai K,
                                                                                                     (REAS-) RES ASSOC, BIOTECHNOLOGY
                                                21-JAN-2003; 2003JP-00102206.
09-MAY-2003; 2003JP-00131392.
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89.2%;
                2004EP-00001196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the invention.
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Matches 2287; Conservative
                                                                                                                                        Sugiyama T,
, Isono Y,
                                                                                                                                                                                           2004-535376/52.
                                                                                                                                                                                                              P-PSDB; ADQ67717
                21-JAN-2004;
                                                                                                                                                           Yamamoto J,
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This sequence encodes a novel human nuclear factor-kappaB (NFKB)-inducing kinase (NIK) which is used in a method for screening for agents that modulate the interaction of NIK with a NIK-binding target. The encoded protein can be used as a modulator of cellular functions at the NIK level, or for development of such compounds. NFKB is involved in expression of many immune and inflammatory responses and of some important viral genes. The protein may be used diagnostically and therapeutically, in conditions associated with abnormal utilisation of pathways that involve NFKB, e.g. inhibition of signal transduction by tumour necrosis factor (TNF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACCTCTGTCCTCCCTGGAGCCAGCCCTGCCAGAAACCCCAGCTCACCAGAGGGGAAAG 2287
                                                                                                                                                                                                                                                                                                                                                                           Screening agents for modulating interaction of nuclear factor kappaB inducing kinase - with kinase-binding target, useful for controlling levels of the kinase, for treatment and diagnosis of conditions associated with e.g. inhibition of signal transduction by tumour necrosis
tumour necrosis factor; NF-kB-inducing kinase; screening; interaction; modulator; immune response; inflammatory response; viral gene; diagnostic; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2048 ACCAGACCCTCCATGCCCAGCCGAGAGAGACTTTCGCCAAGGGCCCCCAGGGCCCCGGCCAG
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Pred. No. 2.1e-305;
4; Mismatches 43; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3156 BP; 736 A; 991 C; 895 G; 534 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
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43.1%;
Best Local Similarity 94.8%;
Matches 1241; Conservative 4
                                                                                                                                                                                              98US-00032475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Col 11-14; 16pp;
                                                                                                                                                                                                                                                                                                                                           WPI; 1999-094902/08.
                                                                                                                                                                                                                                                                    (TULA-) TULARIK INC
                                                                                                                                                                                                                                                                                                       Rothe M;
                                                                                       Homo sapiens
                                                                                                                                                                                              26-FEB-1998;
                                                                                                                       US5854003-A.
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Probe, vector or recombinant nucleic acid encoding a polypeptide, especially human nuclear factor kappa-B-inducing kinase protein - useful
signal transduction; biopharmaceutical; human; ds.
                                                                       /*tag= a
/product= "NIK polypeptide"
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1. .2844
/*tag= a
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GCCCTTGGAGGGGAGAATATAAAGAACCAACATCCACCGCCAAATCAAGCCAATTACC 2047
                                                                                                              This cDNA encodes a nuclear factor kappa B (NF-kB) inducing kinase (NIK) polypeptide or its fragment has one or more activities selected from kinase activity and inhibitory activity. IkB kinase-alpha and beta binding activity and binding inhibitory activity; IkB tumour necrosis factor (TNF) receptor-associated factor 2 binding activity and binding inhibitory activity; IkB binding activity and binding inhibitory activity. IkB binding activity and binding activity and binding inhibitory activity. We captor-associated factor 2 binding binding inhibitory activity, IkB binding activity and binding activity and binding activity and binding activity and binding activity activity. A vector containing the NIK nucleic acid can be used to transform host cells for the recombinant production of the protein. The NIK nucleic acid and the polypeptide may be used in diagnosis (e.g. genetic hybridisation server from the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the conta
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                                                             NIK; IkB; NF-kB; TNF; kinase; nuclear factor kappa B; inhibition; tumour necrosis factor; binding; genetic hybridisation; screening; signal transduction; biopharmaceutical; immunogen; pharmacological;
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.larity 94.8%; Pred. No. 2.1e-305;
Conservative 4; Mismatches 43; Indels 21;
NF-kB-inducing kinase (NIK) polypeptide encoding cDNA
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This DNA sequence codes for human wild-type NIK (see AAY31665), a NF-kB inducing kinase having serine/threonine kinase activity. The invention relates to: (a) an N-terminus deletion mutant NIK protein (see AAY3166); that inhibit auto-phosphorylation or transphosphorylation. The invention provides the molecular basis for cytokine induction of NF-kB-dependent immune and inflammatory responses, emphasising a role for both NIK-NIK and NIK-IKK (IkB-specific kinase) interactions. A novel and highly specific method for modulating NF-kB-dependent immune, inflammatory and anti-apoptotic responses is based on interruption of the critical protein interaction of NIK and IKK. The mutant NIK proteins are used in claimed methods for inhibiting NF-kB-dependent genession. The kinase-deficient NIK mutant proteins inhibit activation of IKK. The N-terminal deleticion NIK mutant proteins bind to IKK, thus inhibiting NIK/IKK
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                                                                                                                                                                                                                                                    are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of biodactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vii) for inhibiting the activity of CAP; (vii) for treating carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent
Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                         present invention relates to novel DNA and protein sequences which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62363 CCTGGAGCTGGAGGGTCAAGCATGGCCAGGTGGAGAACAGGCCCTAACCCTGCCTTCAC
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                                                                                                                                   SEQ ID NO 886; Opp; English.
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Matches 1487; Conservative
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AAM25563. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antianflammatory; antirheumatic; cardiant; cardiant; encorring; cardiant; cardiant; cardians, virucide; anti-HVV; fungicide; antimutagen; cardiavascular; antianeamic; antigargant; haemostatic; vulnerary; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic neuroprotective; antidepressant; nootropic; antidabetic; cytostatic neuroprotective; antidepressant; nootropic; antidabetic; cytostatic and ingene therapy, antisense therapy and vaccine production, The proteins and polymucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-HTV; fungicide; antimuteden; cardiovascular; antianaemic; anaemia; antiagregant; natmuteden; cardiovascular; antianaemic; accema; dermatological; natialtergic; uninasthmatic; antidiabetic; cytostatic; neuropyrotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosals; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                     63836 AGAACTGCAGCCTTGGTACTGCAGAGTCTGGGGTTGTAGAGAACTCTTTGTAAGCAATAAA
2491 AGAACTGCAGCCTTGGTACTGCAGAGTCTGGGTTGTAGAGAACTCTTTGTAAGCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                            Human, cancer; ulcer; HIV infection; human immunodeficiency virus;
antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
antibacterial; endocrine; cardiant; central nervous system; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
                                                                                                                                                                                                                                                                                                                                                    Human protein encoding cDNA sequence SEQ ID NO:97.
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                                                                                                      GTTTGGGGTGATGACAAATGTT
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
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                                                                                                                                                                                                                                                                                                             (first entry)
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P-PSDB; AAM25321.
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                                                                                                 ggczagggzagggczagggczagrgacacr-----graggaggarggaggaggag
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             infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, perkinson's disease, neurodegenerative and neurological disorders
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                                                                                                                                                                                               1137 GGGGCAAGCNAGAATGCCTCCCAGGATTTCACANCCTGAGCCCNTGCCCCANCCCTGCTG
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                                                                                                            Sequence 1385 BP; 320 A; 410 C; 378 G; 277 T; 0 U; 0 Other;
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                                                                                                                                       Score 754.2; DB 4;
Pred. No. 1.2e-199;
4; Mismatches 159;
  viral,
 neuropathology, cardiac anaphylaxis,
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Best Local Similarity 83.5%;
Matches 1205; Conservative
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ID NO 15295; 103pp; English.

sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed care in diagnostics as expressed sequence tags for identifying expressed cartivity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating at molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Ab564197-Ab54564 represent novel human diagnostic coding sequences. Ab564197-Ab54564 represent novel human diagnostic coding sequences. Ab564197-Ab564564 represent novel human diagnostic coding sequences. Ab564197-Ab694564 represent novel human diagnostic parent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at the invention of the printed specification, but was obtained in the printed specification. invention relates to isolated polynucleotide (I) and polypeptide (II)

Sequence 2760 BP; 486 A; 840 C; 810 G; 624 T; 0 U; 0 Other;

Query Match

5; Length 2760;

267 AAGCTCCAGCCTCCTCTCCCACCAGAGCCCCCAGAGCCAAACAAGTCTCCTCCCTTGACT 326 506 412 626 AACCCATCAAAGGCCTCTCAAAGCTCGCGGGACACCTGAGCTCAGGCGTACACCTCGG 352 989 746 866 CCTGCCAGAAACCCCAGCTCACCAGAGCGAAAGCAACCGTCCCGGAGCAGGAACTGCAG 446 GAGCAAATTCTCTCGTGCCTCAGCATCGACAGCCTCTCCCTGTCGGATGACAGTGAGAAG 566 ACCGACACCCCAAGCTATTTCAATGGTGTGAAAGTCCAAATACAGTCTCTTAATGGTGAA 232 CACCTGCACATCCGGGAGTTCCACCGGGTCAAAGTGGGAGACATCGCCACTGGCATCAGC 172 CCTGCCAGAAAACCCCAGCTCACCAGAGCGGAAAGCAACCGTCCCGGAGCAGGAACTGCAG CAGCTGGAAATAGAATTATTCCTCAACAGCCTGTCCCAGCCATTTTCTCTGGAGGAGCAG CAGCTGGAAATAGAATTATTCCTCAACAGCCTGTCCCAGCCATTTTCTCTGGAGGAGCAG GAGCAAATTCTCTCTCGTGCCTCGACATCGACAGCCTCTCCCTGTCGGATGACAGTGAGAAG AACCCATCAAAGGCCTCTCAAAGCTCGCGGACACCCTGAGCTCAGGCGTACACTCCTGG **ACCGACACCCCAAGCTATTTCAATGGTGTGAAAGTCCAAATACAGTCTCTTAATGGTGAA** CACCTGCACATCCGGGAGTTCCACCGGGTCAAAGTGGGGAGACATCGCCACTGGCATCAGC Gaps ö 12; Indels Score 691.8; DB 5; Pred. No. 4.6e-182; 0; Mismatches 26.3%; Matches 699; Conservative Local Similarity 747 327 387 591 447 531 507 471 411 351 291 231 651 267 627 687 807 8 셤 ò В g 셤 δ ઠે ò ઠે g δ ò 유 ઠે

171 AGCCAGATCCCAGCTGCAGCCTTCAGCTTGGTCACCAAAGACGGGCAGCCTGTTCGCTAC 112 52 111 GACATGGAGGTGCCAGACTCGGGGATCGACTGCAGTGCACACTGGCCCCTGATGGCAGC 977 TTCGCCTGGAGCTGGAGGGTCAAGCATGGCCAGCTGGAGAACAGGCCCTAA 1 TTCGCCTGGAGCTGGAGGGTCAAGCATGGCCAGCTGGAGAACAGGCCCTAA 927 51 ð 셤 ò ద

Search completed: June 10, 2005, 06:10:27 Job time: 914.226 secs

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AC137575 Homo sapi BV184269 sqnm14402 AY091549 Mus muscu BC031942 Homo sapi CQ490185 Sequence CQ490185 Sequence CQ401629 Sequence CQ501629 Sequence CQ510553 Sequence CQ510553 Sequence CQ471290 Sequence AF429315 Homo sapi AF429315 Homo sapi AF429315 Homo sapi AK655393 Sequence AK655393 Sequence AK655393 Sequence AK655910 Sequence

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AXB34630 Sequence AK097219 Homo sapi G27543 human STS S

AK097219 G27543

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121 GCCCTTGGAGGGGGAGAATATAAAGAACCAAGGACATCCACCGCCAAATCAAGCCAATTACC
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Wallach,D., Malinin,N., Boldin,M., Kovalenko,A. and Mett,I.
MODULATORS OF TNF RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR
PREPARATION AND USE
Patent: WO 9737016-A 3 09-OCT-1997;
YEDA RES & DEV (IL)
Other publication AU 2175597 19971022.
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Oy 421 CAACCGTCCCGGAGCAGCAGCTGGAGATGGAAATAGAATTATTCCTCAACAGCTGT 480	Qy 481 CCCAGCCATTTTCTCTGGAGGAGCAAATTCTCTGGTGCCTCAGCATCGACAGCC 540 Db 2579 CCCAGCCATTTTCTCTGGAGGAGCAAATTCTCTCTGTGCCTCAGCATCGACAGCC 2638	Qy 541 TCTCCCTGTCGGATGACAGTGAGAACCCATCAAAGGCTCTCAAAGGTCGGGGACA 600 Db 2639 TCTCCCTGTCGGATGACAGAGAACAACCCATCAAAGGCTCTCAAAGGTCGGGGACA 2698	QY 601 CCCTGAGCTCAGGCGTACACTCCTGGAGCAGCCCGAGGCTCGAAGCTCCAGCTGGA 600 DD 2699 CCCTGAGCTCAGGCGTACACTCCTGGAGCCAGGCCGAGGCTCGAAGCTCCAGCTGGA 2758	QY 661 ACATGGTGCTGGCCGGGGGGGGCGCCCACGGACCCCAAGCTATTCAATGGTGTGAAAG 720 DD 2759 ACATGGTGCTGGCCCGGGGGGGGCCCACGGACCCCAAGCTATTCAATGGTGTGAAAG 2818	Oy 721 TCCAAATACAGTCTCTTAAATGGTGAACACCTGCACATCCGGGAGTTCCACCGGGTCAAAG 780	Oy 781 TGGGAGACATCGCCACTGGCATCAGCAGATCCCAGCTGCAGCCTTCAGCTTGGTCA 840	QY 841 CCAAAGACGGGCAGCTGTTCGCTACGACATGGAGGTGCCAGACTCGGGCATCGACCTGC 900 L	QY 901 AGTGCACACTGGCCCCTGATGGCAGCTTCGCCTTGGAGGGTCAAGCATGGCCAGC 960 Db 2999 AGTGCACACTGGCCCCTGATGGCAGCTTCGCCTTGGAGGTCAAGCATGGCCAGC 3058	QY 961 TGGAGAAAGGCCTAACCCTGCCCTCCACCGCCGGCTCCACAGCAGCTT 1020 DD 3059 TGGAGAACAGGCCCTAACCCTGCCCTCCACCGCGGCTCCACACGGGGGAAAGCAGCCT 3118	Oy 1021 TCCTGCTGCACGATGCTGCCCTGAAAACACAGGCTCAGCGGTTCCCAGGGGATYTG 1080	Oy 1081 NCCAGCCCCGGGCTCARCAGNTGGGAACCAGGCCTCGNCAGCNAAGGTNGGGGG 1140	QY 1141 CAAGCNAGAATGCCTCCCAGGATTTCACANCCTGAGCCCNTGCCCCANCCTGCTGAADA 1200 DD 3230 GCAAGCAGAATGCCTCCCAGGATTTCACACCTGAGCCCTGCCCCACCCTGCTGA 3283	OY 1201 AAACAYTNCCGCCACGTGAAGAGACAGAAGGAGGATGGNCAGGAGTTNNACCTYGGGGAA 1260 Db 3284 AAAACATCGCCACGTGAAGAGACAGAAGGAGGATGGCAGGAGTTACCTGGGGAA 3339	Qy 1261 ACAAAACAGGGATCTTINTTCTGCCCCTGCTCCAGINCGAGTTGGCCTGNACCCGCTTGG 1320	Oy 1321 ANTCAGTGACCATTTGTTGGCAGANCAGGGGAGAGCAGCTTCCAGCCTGGGTCAGAAGGG 1380	Oy 1381 GTGGGCGCTTCGGCCCTCACCTNCCAGGCTGCTGTGAAGAGTGTCAAGTGTA 1440	Qy 1441 AGGENCCCAAANCTCAGGNTTCAGTGCAGAACCAGGTNCAGCAGGTATGCCCGCCGNTA 1500	
Qy 2401 TCCCACATCTTGCCAAGACTTTNGTCCAGCTGTCCACATTGAGTCAGACTGCTCC 2460	Qy 2461 GGGGAGAGAGCCCCGGCCCCAGCACATAAAGAACTGCAGCCTTGGTACTGCAGAGTCTG 2520	Qy 2521 GGTTGTAGAGAACTCTTTGTAAGCAATAAAGTTTGGGGTGATGACAATGTTAAAAAAG 2580 	Qy 2581 GCCTTCGTGGCCTCGAATCAAGCTTATCGATACCGTCGACCTCGAGGGGG 2631 Db 2581 GCCTTCGTGGCCTCGAATCAAGCTTATCGATACCGTCGACGGGGG 2631	. True Co man	HO W	SOURCE unidentified ORGANISM unidentified unclassified.	AUTHORS Wallach, D., Malinin, N., Boldin, M., Kovalenko, A. and Mett, I. TITLE MODULATORS OF TNF RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR PREPARATION AND USE	YEDA RES & DEV (Other publicatio	g o	Query Match Query Match A0.4%; Score 1851.2; DB 6; Length 4596; Best Local Similarity 90.5%; Pred. No. 0; Marches 2318. Conservative Michael No. 01. Can 24.	CATCCAAGAGGGCTGAGGAAGAGCCCATCCACGCGTGT 6	61 CTGCAGCGGAGCTGGAAGGTGAACCGGGCACTACAGGAAGTGGGAGGTCTGAAGA 	121 GCCTTGGAGGAGAATATAAAGAACCAAGACATCCACGCCAAATCAAGCCAATTACC 2219 GCCTTGGAGGAGAAATATAAAGAACAAGAACTACACGCCAAATCAAGCCAATTACC		241 CTGAGGAGACAAGGCGGGGAGCCCTTAAGCTTCCCCAAGGGCCCCGAGGGCCCCCAGGGGGGGG	301 AGCCAACAGTCTCCTCCTTGAGCAGGAGGAGGAGGATCTGGGAACCCTTTGAGCAAGGAGGAGGAGGATGTGGGAACCCTTTGAGCAAGGAGGAGGAGGATGTGGGAACCCTTTGAGCAAGAAGAAGAACAACAACAACAACAACAACAACAAC	361 TACCTCTGCCCCGGAGCCGCCCTGCCAGAAACCCAGCTACAAAGAAAAAAAA	Db 2459 TACCTCTGTCCTCGGAGCCAGCCCTGCCAGAACCCCAGCTCACCAGAGCGGAAAG 2518

AX429240 LOCUS LOCUS LOCUS LOCUS AX429240 AX429240. AX429240. AX429240. VERSION VERSION AX429240. AX429240. AX429240. AX429240. GI:21540550 KEYWORDS SOURCE SOURCE OCHALIC CONSTRUCT OCHAR SEQUENCES: Artificial sequences. ANDTHORS SCHUBART, D., Habenberger, P., Stein-Gerlach, M. and TITLE AUTHORS Cellular kinases involved in cytomegalovirus infectinhibition JOURNAL AXXIMA Pharmaceuticals Aktiengesellschaft (DE) FRATURES Incation/Qualifiers Interpretation/Qualifiers AXXIMA Pharmaceuticals Aktiengesellschaft (DE) AXXIMA Pharmaceuticals AKTIENTALS AKTIENTALS AKTIENTALS AKTIENTALS AKTIENTALS AKTIENTALS AKTIENTALS AKTIENTALS AKTIE	Query M Best Lo Matches	2100	Oy 61 CIGCAGCGAACCIGGAACGGAACGGAACGGAACGGAACG	OY 121 GCCCTTGGAGGGAGAATATAAAGAACCAGGATCCACGCCAAATT 	OY 181 ACCAGACCTCCATGCCCAGCGAGAGAGCTTTCGCCAAGGGCCCCAAGGGCCCCAAGGGCCCCAAGGGCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGCCCCCC	QY 241 CTGAGGAGACAACAGGCAGAGCCCCTAAGCTCCAGCCTCCTCCCCA 	OY 301 AGCCAAACAAGTCTCCCTTGACTTTGAGCAAGAGGAGTCTGGG Db 2400 AGCCAAACAAGTCTCCTCCCTTGACTTGAGCAAGAGAGAG	QY 361 TACCTCTGTCCTGGAGCCAGCCCCTGCCAGAAACCCCAGGTCA	QY 421 CAACCGTCCCGGAGCAGAACTGCAGCTGGAAATAGAATTATTC	Qy 481 CCCAGCCATTTCTCTGGAGGAGCAGGAGCAATTCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	OY 541 TCTCCCTGTCGGATGACAGTGAGAAGCCCTTCAAAGGCCTCTCAAD 541	OY 601 CCCTGAGCTCAGGCGTACACTCCTGGAGCAGCCGAGGCTGGAGGTTGGAGCTCGAGGCTCGAGGCTCGAGGCTTCGAGCTCGGAGCTCGAGCTCGAGCTCGAGCTCGAGCTCGAGGCTCGAGGCTTCGAGGCTACACTCCTGGAGCAGCCAGGCCGAGGCTTCGAGGCTTCGAGGCTACACTCCTGGAGCTAGGCCGAGGCTTCGAGGCTACA	OV 661 ACATGGTGCTGGCCCGGGCGGCCCACCGACCCCCAAGCTATTT
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RESULT 3

CGAAGCTCCAGCTGGA 660 TCAGCATCGACAGCC 540 TCCTCAACAGCCTGT 480 |||||||||||||| |TCCTCAACAGCCTGT 2579 CAGGGCCCGGCCAG 240 661 ACATGGTGGCTGGCCCGGGGGGGGGCCCACCGAGCCCAGCCATTTCAATGGTGTGAAAG 720 rgggaggrcrgaaga 120 |||||||||||||| rgggaggrcrgaaga 2219 ATCAAGCCAATTACC 180 |||||||||||||| ATCAAGCCAATTACC 2279 CCATCCACCGCGTGT 60 34; PAT 21-JUN-2002 d Bevec,D. ection and their .s 81; Gaps th 4596; ò

3060 TGGAGAACAGGCCCTAACCCTGCCCTCCACGGCGGCTCCCACAGCCGGAAAGCAGCCT 3119	TCCTGCTCGGTGCACGATGCTGCCCTGAAAACACAGGCTCAGCGTTCCCAGGGGATT	NCCAGCCCCCGGGCTCARCAGN 1996AACAGGGCCTCGCAGCAGCGAAGGGGGGGGGGCTCGCAGCAGCAAGGTGGGGAACCAGGGCCTCGCAGCAGCAAGGTGGGG	CAAGCNAGAATGCCTCCCAGGATTTCALANCTGAAGCCTNAGCCCANCCANCGAGGA 328 GCAAGCAGAATGCCTCCAGGATTTCACACCTGAGCCCTGCCCCACCCTGCTGA 328	AAACAYTNCGCCACGAGGAACAGAAGAGATAGAATAGAATAGATTINNACTINNACCTIONGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ACAAAAACGGATCTTT TITTTTCCCCCCTGCTCCAGT			3514 AGGCCCAAACTCAGGTTCAGCAGAACAGGGT-CAGCAGTATTGCCCGCCGCCGTAG 3569 1501 GCTTAANNGGGGGCCCTTTAAAACCCCTTGCTTNGGCTTNCACCTNGGCCAGCTC 1560	3570 GTTAAGGGGGCCCTCTAAACCCTTTGCCTGGCCTCACCTGGCGAGCTCA-CCC 3621 1561 CTTTGGGTGTAGGGGAAAGAAGAAGACCCTGGGAAGGCTWCCCTGGTAGAATACAC 1620	3622 CTTTTGGTGGGAAAGAAGAGCCTGGACCTGGGAAGGCT-CCCTGGTAGAATACAC 3680 1621 CACACTTTTCAGGTTGTTGCAACACAGGTCCTGAGTTGACCTCTGGTTCAGCCAAGGACC 1680			3800 GCTACCACTCTTCCCCAGAGCAGCCCCCGAGCCCCAGCACTGCCCAGAGCCCAGAGAGCCCAGAGAGAG			7 1	4033TCAGCATCACACTCACCTGCCCTGCCCTGGCCAGAGGGTACTG 4083 2041 CCGNACGACACTTGCACATCTGATGNACCTCAAACACTTTCATGGCTNGCCTCTNNG 2100
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/mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match 70.3%; Score 1850.2; DB 6; Length 4596; Best Local Similarity 90.5%; Pred. No. 0; Matches 2334; Conservative 4; Mismatches 159; Indels 81; Gaps 34;		61 CTGCAGGGAGCTGGGAAGGTGAACCGGGCACTACAGCAAGTGGAAGTCT 61 CTGCAGCGGAGCTGGAAGGTGAACCGGGCACTACAGCAAGTGGAAGTCT 61 CTGCACCTGCACCAAACCGGAAGACTCAAAACGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGGAAGTGAAACTGGAACTGAACTGGAACTGGAACTGGAACTGGAACTGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGAACTGGAACTGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGAACTGGAACTGGAACTGAACTGAACTGGAACTGAACTGAACTGGAACTGAACTGGAACTAACT	TTACC TTACC	181	241	OY 301 AGCCAAACAAGTCTCCCTTGACTTTGAGGAAGGAGGAGTCTGGGATGTGGGAACCCT 360	OY 361 TACCTCTGTCCTCCTGGAGCCAGCCCTGCCAGAAACCCCAGCTCACCAGAGCGGAAAG 420		OY 481 CCCAGCCATTTTCTCTGGAGGAGCAGGAGCAAATTCTCTCGTGCCTCAGCATGGACAGCC 540	Qy 541 TCTCCCTGTCGGATGACAGAGAACCCATCAAAGGCCTCTCAAAGCTCGCGGGACA 600 Db 2640 TCTCCCTGTCGGATGACAGTGAGAACCCATCAAAGCCTCTCAAAGCTCGCGGGACA 2699	Qy 601 CCCTGAGGCTCAGGCGTACACTCCTGGAGCAGCCGAGGCTCGAAGCTCCAGCTGGA 660 Db 2700 CCCTGAGCTCAGGCGTACACTCCTGGAGCAGGCCAGGCC	OY 661 ACATGGTGGTGGCCGGGGGCCCACCGACCCCAAGCTATTCAATGGTGTGAAAG 720 	Qy 721 TCCAAATACAGTCTCTTAATGGTGAACACCTGCACATCCGGGAGTTCCACGGGTCAAAG 780 	Qy 781 TGGGAGACATCGCCACTGGCATCACCAGATCCCAGCTGCAGCCTTGGTTCA 840 Db 2880 TGGGAGACATCGCCACTGGCATCAGCAGATCCCAGCTGCAGCCTTCAGCTTGGTCA 2939	QY 841 CCAAAGACGGCAGCCTGTTCGCTACGACATGGAGGTGCCAGACTCGGGCATCGACCTGC 900	OY 901 AGTGCACACTGGCCCTGATGGCAGCTTCGCCTGGAGGTTGAGGGTCAAGCCATGGCCAGC 960

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L. Submitted (12-10EC-1996) D. Wallach, The Weizmann Institute, Dept of Membrane Research & Biophysics, Rehovot 76100, ISRAEL

NIK is a serine/threonine protein-kinase, resembling several MAP

Kinase kinase kinase (MAPSK), that binds specifically to TRAF2, an
adapter proteins associated, either directly or through interaction

with other adapter proteins, with several receptors of the TNF/NGF

family. NIK overexpression in cells activates the transcription

factor NF kappa B. Cellular expression of kinase-deficient

NIK-mutants blocks NF kappa B induction by TNF, by either of the

two TNF receptors, by CD95 (Fas/Apo-1) and by TRADD, RIP and

MORTI/FADD, adapter proteins that bind to these receptors. It also

blocks NF kappa B induction by IL-1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                   GCAGGGNCAGGGNCAGTGACANCTGTAGGNAGCATANGCAANGCCAGGAGATGG
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/organism="Homo sapiens"
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                                                               /codon_start=1
/product="NIK, serine/threonine protein-kinase"
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                                                                                            /protein_id="CAA71306.1"
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| db_xref="G0A.09558"
| db_xref="UniProt/Swiss-Prot:099558"
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Pred. No. 0;
4; Mismatches 159;
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/cell_type="B cells"
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/note="lysin-rich reg
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90.5%;
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Matches 2334; Conservative
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PHPLESFLGKLACYDSQKPLPDPHLSKLACYDSPKPLPGPHLEPSCLSRGAHEKFSVE
EYLVHALQGSVSSGQAHSLTSLAKTWAARGSRSREPSPKTEDNEGVLLTEKLKPVDYE
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YPPLYGAVRESPWYNI FREHLEGGSFGQLVEGGCLPEDBALYYLGABLEGLEYLHS
RRILHGDVKANDYLSSDGSHAALCDFGHAVCLQPDGLGKSLLTGDY I PGTETHMAPE
VVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFFRGPLCLKIASEPPPVREI PPSCAP
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HQTLHAQPRELSPRAPGPRPAEETTCRAPKLQPPLPPEPPBBNKSPPLTLSKEESGWM
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YFNGYKVQIQSLNGBHLHIREFHYKVGDIATGISSQIPAAAFSLVTKDGQPVRYDME
VPDSGIDLQCTLAPDGSFAWSWRVKHGQLENRP"
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/db_xref="CDD:smart00220"
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5; Mismatches 191; Indels
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89.0%; Pred. No. 0;
                                                                                                      1286. .2011
/gene="MAP3K14"
                                                    gene="MAP3K14"
                                                                                       /codon start=]
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Best Local Similarity 89.0
Matches 2296; Conservative
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                                                                                          1. (Dassel Lo. Peingold, E.A., Grouse, L.H., Derge, J.G., Klausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raa, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Munny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Genera, E.D., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.D. Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupca,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McClowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505396. Location/Qualifiers
                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC).
                                                          Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/db_xref="LocusID:9020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Conteact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'clone="MGC:45335 IMAGE:5497185"
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/clone_lib="NIH_MGC_85"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                 (bases 1 to 4452)
                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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AUTHORS
TITLE
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1812	RESULT 7 CQ723104 CQ7
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Matches 2287; Conservative 5; Mismatches 186; Indels 87; Gaps 35;	y 1 CCCTCTCACAGCCATCCAAGAGGGGTGAGGAAAGAGCCCATCCACCGGTGT 60	QY 61 CTGCAGCGGAGCTGGGGAAGGTGAACCGGGCACTACAGCAAGTGGGAGGTCTGAAGA 120 DD 735 CTGCAGCGGAGCTGGGAAGGTGAAAGCCGGGCACTACAGCAAGTGGGAAGGTCTGAAGA 794	OY 121 GCCCTTGGAGGGAGAATATAAAGAACCAAGACATCCACCGCCAAATCAAGCCAATTACC 180	Oy 181 ACCAGACCCTCCATGCCCAGAGAGGTTTCGCCAAGGGCCCCAGGGCCCCGGCCAG 240	Oy 241 CTGAGGAGACACAGCCCCTAAGCTCCAGCTCCTCTCCCCAGAGCCCCCAG 300	Oy 301 AGCCAAACAACTACTCCTTGACTTTGACCAAGGAGGAGTCTGGGATGTGGGAACCCT 360 Db 975 AGCCAAACAAGTCTCCCTTGACTTTGACTTTGAGAAGGAGTGTGGGAATGTGGGAACCCT 1034	OY 361 TACCTCTGCTCCTGGAGCCAGCCTGCCAGAAACCCCAGCTCACCAGAGCGAAAAG 420	OY 421 CAACCGTCCCGGAGCAGGAACTGCAGCTGGAAATAGAATTATTCCTCAACAGCTGT 480	QY 481 CCCAGCCATTTTCTCTGGAGGAGCAAATTCTCTCGTGCCTCAGCATCGACCACCG 540 L	OY 541 TCTCCTGTGGGATGACAGTGAGAAGAACCCATCAAAGGCCTCTCAAAGCTCGCGGGGACA 600	Qy 601 CCCTGAGCTCAGGCGTACACTCCTGCAGCCAGGCCGAGGCTCGAAGCTCCAGCTCCAGCTGCA 660 Db 1275 CCCTGAGCTCAGGCGTACACTCCTGGAGCCAGGCCAGGC	
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GLAADNVLLSSDGSHAALCDFGHAVCLQPDGLGKSLLTGDY IPGTETHMAPBVVLGRS
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QCGLRKEPIHRVSABELGGKVNRALQQVGGLKSPWRGEYKEPRPPPPRQANTGTLHA
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SLEPRPARNDSSPERKATVPRGELQQLEIELFLNSLSQPFSLEEGGGLILSCLSIDSLS
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                                            TCTCCCTGTCGGATGACAGTGAGAAGAACCCATCAAAGGCCTCTCAAAGCTCGCGGGACA
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Unclassified.
In (bases 1 to 3156)
In (bases 1 to 3156)
Rothe, M. and Wu, L.
Screening method for agents that modulate human NIK activity
Patent: US 5854003-A 1 29-DEC-1998;
Location/Qualifiers
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Sequence 1 from p
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AR068515.1 GI:60
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Pred. No. 1.2e-279;
4; Mismatches 43;
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Rothe, M. and Wu, L.
Human NIK proteins
Patent: US 5844073-A 1 01-DEC-1998;
Location/Qualifiers
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Sequence 1 from patent US 5844073.
AR063065.
AR063065.1 GI:5990754
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94.8%;
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Matches 1241; Conserv
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Rothe, M. and Wu, L.
NIK proteins, nucleic acids and methods
Batene: JP 2001510348-A 1 31-JUL-2001;
PN JP 2001510348-A/1
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PD 31-JUL-2001
PD 31-JUL-1998 JP 1999507409
PR 03-JUL-1997 US 08/887518
PI MIKE ROTHE, LIN WU
PC
C07K7/06, C07K7/08, C07K14/47, C12N1/00, C12N5/10, C12N15/12, C12N15/
                                                                                                                  2888 TCCTGCTCGGTGCACGATGCTGCCCTGAAACACACAGGCTCAGCCGTTCCCAGGGGATT--
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larity 94.8%; Pred. No. 1.2e-279;
Conservative 4; Mismatches 43;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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/mol_type="unassigned DNA"
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OY 1261 ACAAACGGGGATCTTITTTCT DD 3109 ACAAACGGGGATCTTT-TTCT		ACCESSION AR429673 VERSION AR429673.1 GI:40189976 KEYWORDS TINKTOWN	NISM		ψ.	Query Match 37.1%; Sc Best Local Similarity 100.0%; I Matches 977; Conservative 0;	Oy 1 CCCCTCTCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCA		121	181		301		421 2288	481	Oy 541 TCTCCCTGTCGGATGACAGTG	Oy 601 CCCTGAGCTCAGGCGTACACT
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Subramanian, A., Sydney, K., Tang, L., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and Zody, M. Direct Submission
Submitted (28-MAR-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAT 28, 1998 this sequence version replaced gi:2978476.
All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                 Only the last 48 kilobases of this clone are being submitted. The remainder overlaps accession number AC003070 (WICGR project L266). Location/Qualifiers
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Birren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Boutwell, C., Brown, A., Byrne, S., Cantu, C., Castle, A., Cerny, J., Cooke, P., Daly, M. J., Depayre, E., Devon, K., Dewar, K., Donelan, L., Durkette, B., Etemadi, S., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gensbeiner, S., Geragoery, K., Gilmartin, T., Gardt, G., Gray, D., Hagos, B., Harris, K., Horton, L., Howland, J. C., Hui, L., Jacotot, L., Kann, L., Linton, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., Maylor, J., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rollins, G., Rossello, R., Strickland, C., Strickland, C., Strickland, C.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 17, clone HRPC1169K15, complete sequence.
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                                                                       811 AGATCCCAGCTGCAGCCTTCAGCTTGGTCACCAAAGACGGGCAGCCTGTTCGCTACGACA
                                                       87;
                                       Length 48032;
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                                       Query Match
Best Local Similarity 84.4%; Pred. No. 1.3e-238;
Matches 1487; Conservative 5; Mismatches 183;
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/rpt_family="AluSx"
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Sequence 2, Appli
Sequence 30582, A
Sequence 11289, A
Sequence 11289, A
Sequence 1432, App
Sequence 14316, A
Sequence 14310, Sequence 14310, Sequence 219170, A
Sequence 219170, A
Sequence 219170, A
Sequence 219170, A
Sequence 11970, A
Sequence 11970, A
Sequence 11970, A
Sequence 1554, A
Sequence 1567, A
                                                                                           June 7, 2005, 11:57:41; Search time 30.0772 Seconds (without alignments) 2390.553 Million cell updates/sec
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1: /cgn2_6/ptodata/1/paa/NSO6_NEW_COMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-110-450-765-30582
US-11-097-143-11289
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Sequence 1425, Ap Sequence 10758, A Sequence 10759, A Sequence 2013, Ap Sequence 45794, A Sequence 34486, A Sequence 1186, Ap Sequence 25559, A Sequence 23, Appl Sequence 23, Appl Sequence 42824, A Sequence 47387, A Sequence 1655, Ap Sequence 1655, Ap Sequence 1655, Ap Sequence 16757, A App Sequence 16757, A App Se	ATED FACTOR (TRAF), THEIR	g amino acid g amino acid g amino acid
PCT-US03-10870-1425 US-10-990-328A-10759 US-10-990-328A-10759 US-11-097-143-2013 US-10-450-763-4621 US-10-459-489-486 US-10-489-489-1186 US-11-097-143-29559 PCT-US03-10870-1655 US-11-097-143-2959 US-11-097-143-2959 US-11-097-143-2959 US-11-097-143-1774 US-11-097-143-1774 US-11-097-143-1774 US-11-097-143-1774 US-11-097-143-1786-1786 PCT-US04-177965-943	ALIGNMENTS nu US/09155676B aavid Nikolai lark .r Andrei r TOPIC TOPE CH=21 1999-01-04 BER: PCT/L197/00117 197-04-01 BER: IL 117800 96-04-02 BER: IL 119133 96-08-26 122 rxsion 3.3	can be any naturally occurring amino acid can be any naturally occurring amino acid can be any naturally occurring amino acid
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26 120 2 2 110 5 2 9 110 5 5 110 5	RESULT 1 US-09-155-676B-2 Sequence 2, Application of GENERAL INFORMATION: APPLICANT: WALLACH, APPLICANT: MALININ, APPLICANT: MALININ, APPLICANT: MALININ, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: CURRENT FILING DATE: CURRENT FILING DATE: PRIOR PILING DATE: NUMBER OF SEQ ID NOS SUFFRMENT FOR PRICATION NUMBER OF SEQ ID NOS SUFFRMENT FOR PAPELICATION NUMBER OF SEQ ID NOS SUFFFMENT FOR PAPELICATION NUMBER O	LENGTH: 604 TYPE: PRT ORGANISM: Homo sapi FEATURE: NAME/KEY: misc_feat LOCATION: (1)(1) OTHER INPORMATION: FEATURE: NAME/KEY: misc_feat NAME/KEY: misc_feat NOTHER INFORMATION: FEATURE: NAME/KEY: misc_feat LOCATION: (6)(6) OTHER INFORMATION: FEATURE:

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NAME/KEY: misc feature
LOCATION: (13)...(13)
OTHER INFORMATION: Xaa CR
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NAME/KEY: misc feature

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LOCATION: (15)...(15)...
OTHER INFORMATION: Xaa can be any naturally occurring amino PEATURE:
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: OTHER INFORMATION: Xaa can be any naturally occurring amino acid

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LOCATION: (405)..(405)
OTHER INFORMATION: Xaa can
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OTHER INFORMATION: Xaa can
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OTHER INFORMATION: Kaa can
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NAME/KEY: misc feature
LOCATION: (274)...(274)
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LOCATION: (274)...(274)
OTHER INFORMATION: Xaa of
FEATURE:
NAME/KEY: misc feature
LOCATION: (334).
OTHER INFORMATION: Xaa of
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OTHER INFORMATION: Xaa
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LOCATION: (354)..(355)
OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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LOCATION: (363)..(363)
OTHER INFORMATION: Xaa
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PEATURE:
NAME/KEY: misc feature
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NAME/KEY: misc_feature
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481
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EXPRESSION OF 10,000 OR MORE
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                                                                                                                                 482 VAMMURKDELEEENRSLRNLLDGEMEHSAALRQEVDTLKRKVAEQEERQGMKVQALASYL
                                                                                                                                                                                                         CYFVRRFXPHVRTMWWRNGGREKSNSSXXSHLSSWIQSFLKLCFLWTFHVCEPINCFHSL
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                                                                               Gaps
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J GENERAL INCREMILE.

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 790C193/US
FILE REPERENCE: 790C193/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SED ID NOS: 60736
SEQ ID NO 30582
LENGTH: 91
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Pred. No. 7.4e-22;
0; Mismatches 3;
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TITLE OF INVENTION: DRRAYS, FOR DETECTING EXE
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXE
FILE REFERENCE: CLOO0728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
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US-11-097-143-11289
; Sequence 11289, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 30582, Application US/10450763; GENERAL INFORMATION:
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96.3%;
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Best Local Similarity 96.3
Matches 79; Conservative
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US-10-450-763-30582
                                                                                                                                                                                                                                                                                                                              602 KKK 604
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381 REATGREHLPLPDAQ---LGSAEGAAQXLRHPLPCQWRGLLQPS-----RC---PPRKP 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 T--ORHNPFNEBÓAET-----ASSDTTPVHTTSQEKEBA-----QAPDQPDA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ALLYGLO-------DLSSGYWVLVVHFTRREAIRQIEVLOHVATN
           46 PETEPASAYGPFSPTETAGCAEAGNSPQP--WLN----KRCPPRKPGERDRTRGPRSPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 VLOHGLKRSRGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 VGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSI
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                                                                                                                                                                                                  Sequence 344, Application US/11090997
GENERAL INFORMATION:
APPLICANT: Betsholtz, Christer et. al.
TITLE OF INVENTION: Glomerular Expression Profiling;
FILE REPERENCE: 04-1059
CURRENT APPLICATION NUMBER: US/11/090,997
CURRENT FILING DATE: 2005-03-25
NUMBER OF SEQ ID NOS: 2985
SOFTWARE: Patentin version 3.3
SEQ ID NO 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.3%; Score 193.5; DB 7; Best Local Similarity 21.3%; Pred. No. 6.6e-06; Matches 129; Conservative 82; Mismatches 232;
                                                                             443 WISVQCGSQLSRPRKSSEQPVT---SASVPES 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          489 DELEEENRSLRNLLDGEMEH-
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CORGANISM: Mus musculus
US-11-090-997-344
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US-11-090-997-344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 MSGSXNXDKRQFLLERLLDAVKQCQIRFXGRKEIASDSDSRVTCLCAQFEAVLQHGLKRS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 LAGSTFGQRREDIFRRLQESAHKISQKFSG-KELATERDESVQELCESLEELMSYGLRQS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
9.8%; Score 302; DB 7; Length 520;
Best Local Similarity 29.4%; Pred. No. 1.9e-14;
Matches 75; Conservative 59; Mismatches 99; Indels
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FILE REPRENCE: 790CIP3/US
FILE REPRENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR REPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-08-23
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-12-28
PRIOR PILING DATE: 1999-12-28
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: PASTESEQ FOR WINDOWS VERSION 4.0
SOFTWARE: PASTESEQ FOR WINDOWS VERSION 4.0
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Best Local Similarity 57.67
Matches 53; Conservative
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US-10-450-763-58372
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APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                           EAVLOHGIKRSRGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELORFYSLRHIA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 SDVGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTWAAGLN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SILFAINIDNKDLNGQSKFAPTVSDLLK-ESTQNVTSLLKESTQGVSSL----FREITAS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 NLEWDDSAIAPSSEDYDFGDVFPAVPS----VPSTDWEDGDLTDTVSGPRS----TASDL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 MMRKWSRTLGTCLKRHLGQGRAQRTTPTAPLSISCPPLK--APSGLTPMESEQQLMENXF 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 TSSKASTRSPT-----QRQNP-----FNEEPAETVSSSDTTPVHTTSQEKE--- 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 PVFERGVWVPEAXCEKHRXXRCGXKRRXRVWKLIRKEAQGPLGVAREATGREHLPLPDAQ 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 LGSAEGAAQXLRHPLPCQWRGLLQPSRCPPRKPGERDRTRGPRSPGSWTSVQCGSQLSRP 455
                                                                                                                                                                                                                                                                                                                                       3 GPGXGXMSGSX--NXDKRQFLLERLLDAVKQCQIRFXG-RKEIAS--DSDSRVTCLCAQF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---EAQALDPPDACTELEVIRVTKKK-----KIGKKK-----KSRSDEEASPL---- 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  456 RKSSEQPVTSASVPESMTISELRQATVAMMNRKD-ELEEENRSLRNLLD---GEMEHS 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14316, Application US/11097143
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REPERENCE: CLO00728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/150,191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAV--SILIKPEQET----DPCLSCPGMSVLMPNA-----KRSGRRKRKXPTXSHL
                                                                                                                                                                                                                                                                     Query Match
6.1%; Score 189; DB 7; Length 1094;
Best Local Similarity 22.3%; Pred. No. 1.5e-05;
Matches 120; Conservative 77; Mismatches 207; Indels 134; Gaps
            Sequence 1432, Application US/11090997
GENERAL INFORMATION:
TYPLICANT: Betablitz, Christer et. al.
TITLE OF INVENTION:
FILE REFERENCE: 04-1059
CURRENT APPLICATION UNDERS: US/11/090,997
CURRENT PILING DATE: 2005-03-25
NUMBER OF SEQ ID NOS: 2985
SOFTWARE: PatentIn version 3.3
SEQ ID NO 142
                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-090-997-1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-11-097-143-14316
US-11-090-997-1432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 HSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNS----ILFAINIDNKD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LTPMESEQQLMENXFPVFERGVWVP-------EAXCEKHRXXR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 QISWSGDLEATPTSPTEELTGSRF--FORSVSVSSSVSLRSPTTDRCSYNALLRKHESNR 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 NXDKRQFLLERLLDAVKQCQIRFXGRKEIASDSDSRVTCLCAQFEAVLQHGLKRSRGLAL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 NENAREIEFE----VKOKSLEVLGVCE-----QTSALCTTLEALFLHGLKDS----F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------ESTQNVTSLLKES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 5.9%; Score 183.5; DB 7; 1 Similarity 21.8%; Pred. No. 2.2e-05; 97; Conservative 61; Mismatches 162;
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 1999-12-28
PRIOR PILING DATE: 1999-12-28
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-2
PRIOR FILING DATE: 2000-01-3
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2001-03-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 ESGAGWSEIWEKFRASASN-LNVAQ 424
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McCarter, James
Miller, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams, Deryck
Vaudin, Mark
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Guo, Liang
Kovalic, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DROSOPHILA
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Best Local Similarity
Matches 97; Consery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: DROSOF
US-11-097-143-14316
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p-value=
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OTHER INFORMATION: Phorbol esters / diacylglycerol binding domain proteins
OTHER INFORMATION: domain identified by eMATRIX, accession number BL00479B,
OTHER INFORMATION: 7.429e-09, raw score of 12.57
                                                                                                                                                                  110 FYSLRHIASDVGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSML 169
                                                                                                                                                                                                                                                              170 PTMAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLLK--ESTQGVSSLFR 227
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                                                                                                                                EAVLOHGLKR----SRGLALTAAAIK-QAAGFASKTETEPVFWYYVKEVLNK---HELQR 109
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                                                               14 GGGGGGGKKSLSARNAAVER-RNLITVC--RFSVKTLIDRSCFETIDDSSPEFNNFAAIL 70
                                  57
                                  GXGXMSGSXNXDKRQFLLERLLDAVKQCQIRFXGRK-----EIASDSDSRVTCLCAQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             name
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 51537, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TILLE OF INVENTION:
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450, 763
CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
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; LOCATION: (1)...(1006)
; OTHER INFORMATION: Xaa = X or * as defined in Table
US-10-450-763-51537

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OTHER INFORMATION: PH domain identified by
OTHER INFORMATION: -09, PFam score of 38.4
                                                                                                                                                                                                                                                                                                                                                                                                                                         228 EI-TASSAVSILIKPEQETDPCL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELRTLGSSGSESSTPENVGPPFL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(1006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: DOMAIN
LOCATION: (476)..
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LENGTH: 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Homolog annotation: Hit_ID=NP_496906.2; Match level="QueryCoverage; OTHER INFORMATION: =96%, HitCoverage=41%, E-value=2e-49, Identity=41%"; Hit descript orther INFORMATION: =RUN domain containing protein (20146) [Caenorhabditis elegans]; OTHER INFORMATION: emb|CAA21666.2| Hypothetical protein Y51H1
                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID 81293; Strand=-; Position=1
OTHER INFORMATION: -166,1016-1128,1249-1344,1396-1475,1529-1639,1721-1805,3272-3393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 KQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGR-----AWLRCA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---KGSRHSNRPSPNFWPFVSKYTQRSIKTQISTLNQIHTEIGRARAWIRIVLNAWIRIV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNEHSLERYLHMLLADRCRL----STFYEDWSFVMDEERSSMLPTMAAGLNSILFAINID 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- CVNSLGVH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 DAVKQCQIR-----FXGRKEIASDSDSRVT-CLCAQFEAVLQHGLKRSRGLALTAAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (241)..(241)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.9%; Score 181.5; DB 8; Length 269; Best Local Similarity 26.9%; Pred. No. 8.9e-06; Matches 60; Conservative 33; Mismatches 81; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 473;
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APPLICANT: Mitchory, Inc.

APPLICANT: Buck Institute

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Taylor, Eoin D.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Glosn, Gary W.

APPLICANT: Warnock, Dale E.

TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

FILE REFERENCE: 660088.465PC

CURRENT APPLICANTON NUMBER: PCT/US03/10870

CURRENT FILING DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 3025

SOUTHWARE: PSESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 NKDLNGQSKFAPTVSDLLKESTQNVTSL--LKESTQGVSSLFR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||:||:||:||:||:|
LNEYSLDHYISMFVXDTRQMKQFYAQFYADDAFLRDSE-----
TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
FILE REFERENCE: 38-21 (53885)
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-24
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 154870
LENGTH: 269
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28.5%; Pred. No. 5.2e-05;
iive 35; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2491, Application PC/TUS0310870 GENERAL INFORMATION:
                                                                                                                                                                                  TYPE: PRT
ORGANISM: Heterodera glycines
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Best Local Similarity 28.55
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32
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----LFREITASSAVSIL 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 WY---YVKEVLNKHELQRFYSLRHIASDVGRGRAWLRCALNEHSLERYLHMLLADRCRLS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 TFYEDWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLN-----GQSKFAPTVSDLL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SSLFREITASSAVSIL 238
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                                                                                                                                         ALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLRCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: | || : | || : |
131 NDCLLSSYLMSIRQDSSSLKSYYKVNAYVRDGELLDVAQRLIEGVEAF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.0%; Score 154; DB 6; Length 388; 25.7%; Pred. No. 0.0016; live 29; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION THOUSEN TO THE REPERTIDES
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 790CTB2/US
FILE REPERENCE: 790CTB2/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR PLILOR DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/549,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 51533
LENGTH: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 931, Application US/60680002
GENERAL INFORMATION:
APPLICANT: JOSELO-FF, Elizabeth et al.
TITLE OF INVENTION: KIDNEY DISEASE TARGETS AND USES THEREOF
FILE REFERENCE: CL001661
CURRENT APPLICATION NUMBER: US/60/680,002
CURRENT FILING DATE: 2005-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 IKPEQETDPCLSCPGMSVLMPNAKRSGRRK 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNFENSSDTASIC---SVMSYNSQSSGLRQ 259
                                                                                                                                                                                                                                                                                                                                    192 GOSKFAPTVSDLLKESTQNVTSLLKESTQGVSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 IKPEQETDPCLSCPGMSVLMPNAKRS 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L---NSDSCL-----LQENGSKS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-10-450-763-51533
Sequence 51533, Application US/10450763
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 KESTQNVTSLLKESTQGV-----
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Best Local Similarity 25.7%
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-450-763-51533
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US-60-680-002-931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam annotation: Pfam ID=RUN; Match level="Score=108.7, E-value=1-29, Copies=1"; Pfam description=RUN domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_1074; Strand=+; Position=317
278 MMRKMSRTLGTCLKRHLGQGRAQRT---TPTAPLS-----ISCPPLKAPSGLTPME 325
                                                                                                                                                                                                                                              304 AASGTQD------GVHVQEP--------RPQAPSPLDLQQPVES 333
                                                                                           ----SCPGMSVLMPNAKRSGRRKRKXPTXSHL 277
                                                                                                                                                                                                                                                                                                                           326 SEQQLMENXFPVFERGVWVPEAXCEKHRXXRCGXKRRXRVWKLIRKEAQGPLGVAR--EA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                            TGREHLPLPDA-----QLGSAEGAAQXLRHPLPCQWRGLLQPSRCPPRKPGERDRTRG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GAGLKLVVSS 373
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                                                                                                                                         198 ASSSQLSCSLNSDSCLLQENGSKSPDHCEEPMSCDS-DLGTANAEDSDRSLQE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRSP -- GSWTSVQCGSQLSRPRKSSEQPVTSAS 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTSPKNKSWIS---EDDFYRP--SREQPLESAS 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 TSGQQ---PSSTVSETAREVGQGNGLQKAQAHD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21377, Application US/60669175 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baum, James A
Glibertson, Larry A
Kovalic, David K
LaRosa, Thomas J
Lu, Maolong
Munyikwa, Tichifa R. I
Roberts, James K
Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Monsanto Technology LLC
APPLICANT: Baum, James A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Diabrotica virgifera
                                                                                        AVSILIKPEQETDPCL-
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Best Local Similarity
Matches 62; Conserv
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OTHER INFORMATION:
US-60-669-175-21377
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            384
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APPLICANT:
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APPLICANT:
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; TYPE: PRT
; ORGANISM: Homo s
US-10-450-763-51534
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                                                                                                                                                                                        56 QFEAVLOHGIKKSRGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRH 115
                                                                                                                                                                                                                                                       116 IASDVGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAG 175
                                                                                                                                                                                                                                                                       288 TCLKRHLGQGRAQRTTPTAPLSISCPPLKAPSGLTPMESEQQLMENXFPVFERGVWVPE- 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :: | | : | | : | | 320 TKQDTKVELETYKQTRQGLDEMYSDVWKQLKEEKKVVRLELEKEL------ELQIGMK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SAEGAAQXIRHPLPCQWRGILQPSRCPPRKPGERDRTRGPRSPGSWTSVQCGSQLSRPR 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457 KSSEQPVTSASVPESM-----TISELRQATVAMMNRKDELEEENRSLRNLLDGEMEHSA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AINLOMFHKAQNAESSLQQKNEAITSFEGKTNQVMSSMKQMEERLQHSERARQGAEERSH 412
                                                                                                                                                                                                                                                                                                                  LNSILFAINIDNKDLNGQ-----SKFAPTVSDL--LKESTQNVTSLLKESTQGVSSLFR 227
                                                                                                                                                                                                                                                                                                                                                                              228 EITASSAVSILIKPEQETDPCLSCPGMSVLMPNAKRSGRRKRKXPTXSHLMMRKMSRTLG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 -----AXCEKHRXXRCG-XKRRXRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLG-- 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EKD-THEKOD----TLVALROOLEEVK 352
                                                                                                                                                                                                                       QFFVVMEHCLK--HGLKVKKSFIGQNKSFFGPLELVEKLCPEASDIATS-----VRNLPE 91
                                                                                                                                                                                                                                                                                                                                      ------SLQEEQQQLREQNELIRERSEKSVEI
                                                                                                                           4.9%; Score 151; DB 8; Length 600;
21.3%; Pred. No. 0.0048;
tive 71; Mismatches 190; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 4.9%; Score 151; DB 8; Length 601; Local Similarity 21.3%; Pred. No. 0.0048; hes 111; Conservative 71; Mismatches 190; Indels 150;
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GENERAL INFORMATION:
APPLICANT: Win Van Criekinge
APPLICANT: Win Van Criekinge
APPLICANT: Josef Straub
TITLE OF INVENTION: METHYLATION MARKERS FOR DIA
TITLE OF INVENTION: METHYLATION MARKERS
FILE REFERENCE: 006/91,00011
CURRENT APPLICATION NUMBER: US/60/671,501
CURRENT FILING DATE: 2005-04-15
NUMBER OF SEQ ID NOS: 420
SOFTWARRE: FASICED for Windows Version 4.0
SEQ ID NO 404
NUMBER OF SEQ ID NOS: 2417
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 TEMÉLÁMKLĽ------
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                                                                                                                                                           Matches 111; Conservative
                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-680-002-931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511 ALRQEV----
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56 QFEAVLQHGLKRSRGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRH 115

ŝ 287 346 457 KSSEQPVTSASVPESM-----TISELRQATVAMMNRKDELEEENRSLRNLLDGEMEHSA 510 67 TFVNMDVGRCRAWLRLALNNGLMECYLKLILQEQARLQL------QRKESLDSIS 115 AGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLLKESTQGVSSLFREITASS 233 243 IC------SLOEEQQLREQNELIRERSEKSVEI 270 -----AXCEKHRXXRCG-XKRRXRVWKLIRKEAQGPLGVAREATGREHLPLPDAQLG-- 397 -SAEGAAQXLRHPLPCQWRGLLQPSRCPPRKPGERDRTRGPRSPGSWTSVQCGSQLSRPR 456 54 CAQFEAVLQHGLKRSRGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSL 113 114 RHIASDVGRGRAWIRCAINEHSLERYLHMILADRCRISTFYEDWSFVMDEERSSMLPTMA 173 116 IASDVGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAG 175 271 TKQDTKVELĖTYKQTROGLDEMYSDVWKQLKEEKKVRLELEKEL------ELQIGMK 321 322 TEMBIAMKLL-----TLVALRQDEEVK 353 99 QFFVVMEHCLK--HGLKVKKKSFIGQNKSFFGPLELVEKLCPEASDIATS----VRNLPE **EITASSAVSILIKPEQETDPCLSCPGMSVLMPNAKRSGRRKKKYPTXSHLMMRKMSRTLG** CTPSTSKLOPGGKR-----KKSA--HOKPLPOPVFWPLLKAVTPKHIISELEHL LNSILFAINIDNKDINGQ----SKFAPTVSDL--LKESTQNVTSLLKESTQGVSSLFR 288 TCLKRHLGQGRAQRTTPTAPLSISCPPLKAPSGLTPMESEQQLMENXFPVFERGVWVPE-28; GENERAL LICATION AND ADDRESS AND POLYPEPTIDES TITLE OF INVERTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES TITLE REFERENCE: 190CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 51534
LENGTH: 183 80; Indels 511 ALROEV-------511 ALROEV-AROEBROGMK 533 | | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : Score 143; DB 6; Pred. No. 0.0042; 24; Mismatches ; Sequence 51534, Application US/10450763 ; GENERAL INFORMATION: Query Match
Best Local Similarity 28.6%;
Matches 53; Conservative 2. ð

116 HSSGSEDIEVHHSGHKIRRNQK--PTASSLSLDTAS--SSQLSCSLNCDSCLLQENGSKS 171 g &

234 AVSIL 238 :| 172 PDHVL 176

셤

Search completed: June 7, 2005, 12:21:16 Job time : 31.0772 secs

OM protein

Run on:

Sequence:

Searched:

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June 7, 2005, 11:52:21; Search time 269.467 Seconds (without alignments) 2618.037 Million cell updates/sec
                                                                                                                   US-09-155-676B-2
3093
1 XTGPGXGXMSGSXNXDKRQF......FLWTFHVCEPINCFHSLKKK 604
                                                                                                                                                                                                                                                                                                                              6959266
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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6/ptodata/1/paa/US103_COMB.pe
6/ptodata/1/paa/US103_COMB.pe
6/ptodata/1/paa/US105_COMB.pe
6/ptodata/1/paa/US107_COMB.pe
6/ptodata/1/paa/US108_COMB.pe
6/ptodata/1/paa/US108_COMB.pe
6/ptodata/1/paa/US108_COMB.pe
                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                          6959266 segs, 1168006243 residues
                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              - protein search, using sw model
                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                    Title:
Perfect score:
                                                                                                                                                                      Scoring table:
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Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ription	74 6 9000000	equence 2. Ar	equence 7. Ar	equence 9, Ap	equence 8, Ap	equence 14017	equence 14017	equence 18638	equence 5854,	equence 5854,	equence 236,	equence 203,	equence 294,	Sequence	quence 30582,	equence 6178,	equence 456, equence 6243	equence 11289	edience 11289	equence 11318	equence 9160.	equence 11321	equence 8867,	Sequence 17822	quence 58372,	equence 66567,	equence 66567,	equence 14316.	equence 14393,	equence 14357,	ence 66	equence 66566,	equence 66557,	equence 66558,	equence 66559,	equence 66560,	equence 66562	equence 66563.	equence 66564,	equence 66565,	equence 66557,	equence 66558,								CIATED	ION AND USE					
	71.00.	-03-153-67	-10-070-25	-10-070-25	-10-070-25	-09-629-469A-14	-10-917-503-14017	-10-170-205E-186	-09-758-472-58	-10-235-926-585	-60-212-356-23	-60-212-356-20	-60-229-525-294	70-20	-US01-08631-3058	-10-1/0-2058-61/	-60-229-525-456 -10-170-205E-624	-09-614-150-1128	-09-614-150A-112	-60-167-217-11318	-60-173-464-9160	-60-191-637-113	-60-191-681-8867	-10-170-205E-178	US01-08631-5837	-09-724-676-66567	- U9- /24-6 /6A-665 - U9-614-150-1431	-09-614-150A-143	-60-167-217-14393	-60-191-637-1435	-09-724-676-66566	-09-724-676A-665	-09-724-676-6655	-09-724-676-6655	-09-724-6/6-6655 -08-724-6/6-6655	000-0/0-47/-00	-03-724-676-6636	-09-724-676-6656	-09-724-676-6656	-09-724-676-6656	-09-724-676A-665	-09-724-676A-6655	ALIGNMENTS	i i	5676			- - -		E E	7, THEIR PREPARA	,	MAR,	וויא מחורם זח		
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* Query Match Leng			1.6	7 7.6	9.7 8	8.7 3	8.7 3	8.6 2	3.3	8.3	2.4	2.2	1.5	16.1	٠. د.	1.7 5.1	J 4	1 0			. 60	. 8.	.8	۰.	9.	ທຸ	00		. 6	.9	6.	0.0	6.0	. r	, ,	, ,		. 6	6	.9	.9	7 6.		676-2	lication ATION:	MALLACH,	MALININ,	BOLDIN, M KOVALENKO	METT, Igo	ENTION:	ENTION: QUENCES:	CE ADDRES	BROWDY 24 Ninth	hington	ن ن	401
Score	305	305	1594.	1537.	1537.	119	119	119	72	72	693	685.	663.	498	. ה ה	. 4. 4	. 40.		9 6	9 6	30	30	30	242.	23	199.	182	183.	183.	183.	18	81	80.	20 6	5 6	9 6	9 6	18	18	18	18	18		1 155-676-2	ence z, Apj RDAI INFOR	PPLICANT:	PPLICANT:	; APPLICANT:	PPLICANT:	ITLE OF IN	TILE OF IN	ORRESPONDE	ADDRESSEE STDFFT.	CITY: War	STATE: D	
Result No.		10	ım	4	S	9	7	8	σ,	10	11	12	13	LT L	CT	0 F	÷ -	9 -	200	2 5	22	23	24	25	26	27	9 0	308	31	32	33	34	35	3.0	7 0 0	0 0	2 4	41	42	43	44	45		SES.	; seque	A A	A	Ā Ā		H i		ŭ 			. . .	

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QHGLKRSRGLALTAAAIKQAAGFASKTETEPVFWYVKEVLNKHELQRFYSLRHIASDVG 121
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                     542 CYFVRRFXPHVRTMWWRNGGREKSNSSXXSHLSSWIQSFLKLCFLWTFHVCEPINCFHSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGPGXGXMSGSXNXDKRQFLLERLLDAVKQCQIRFXGRKEIASDSDSRVTCLCAQFEAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MODULATORS OF THE RECEPTOR ASSOCIATED TITLE OF INVENTION: FACTOR (TRAF), THEIR PREPARATION AND USE UNMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 604;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DetentIn Release #1.0, Version #1.30
SOFTWARE: DetentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,676A
FILING DATE: 04-JAN-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IL97/00117
FILING DATE: 01-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3058; DB 15;
Pred. No. 4.2e-259;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C.
STREET: 624 Ninth Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25,618
R: WALLACH=21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: IL 117800
FILING DATE: 02-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 119133
FILING DATE: 26-AUG-1996
ATTORNEY/AGBNT INPORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                  Sequence 2, Application US/09155676A
GENERAL INFORMATION:
APPLICANT: MALLACH, David
APPLICANT: MALININ, Nikolai
APPLICANT: BOLDIN, Mark
APPLICANT: ROVALENKO, Andrei
APPLICANT: METT, IGO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 98.9%; Sco
Best Local Similarity 100.0%; P:
Matches 603; Conservative 0;
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amino acid
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MOLECULE TYPE: protein
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                                                                                                            KKK 604
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US-09-155-676A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 AINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLLKESTQGVSSLFREITASSAVSILIKP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQETDPCLSCPGMSVLMPNAKRSGRRKRKXPTXSHLMMRKMSRTLGTCLKRHLGQGRAQR 301
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         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRAING SYSTEM: PC-DOS/MS-DOS
SPERAITING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,676
FILING DATE: 04-JAN-1999
CLASSITCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IL97/00117
FILING DATE: 01-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117800
FILING DATE: 26-APR-1996
PRIOR APPLICATION NUMBER: IL 119133
FILING DATE: 26-APR-1996
APPLICATION NUMBER: IL 119133
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: WALLACH=21
FELEROMENNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-737-3528
INFORMATION FOR SEG ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-155-676-2
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COMPUTER READABLE FORM
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STRANDEDNESS: si
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239
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                                                                                                          DLNGQSKFAPTVSDLLKESTQNVTSLLKESTQGVSSLFREITASSAVSILIKPEQETDPC 248
                                                                                                                                                                                                      -----TTPTAPLS----ISCPPLKAPSGLTPME----SEQQLMENX 334
                                                                                                                                                                                                                                                                                                                            335 FPVFERGVWVPEAXCEKHR-----XXRCGXKRRXRVWKLIRKEAQGPLGVARE- 382
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   RGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLR 120
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GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: WALLACH, David
APPLICANT: MALININ, Nikolay
APPLICANT: EU, SERFA
APPLICANT: ELU, SERFA
APPLICANT: LEU, SERFA
APPLICANTON: IREN PROTEIN, ITS PREPARATION AND USE
FILE REFRENCE: WALLACH=28
CURRENT APPLICATION NUMBER: US/10/070,255
CURRENT FILING DATE: 2002-12-16
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 1999-09-02
NUMBER: OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 784
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QHGLKRSRGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVG 121
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                                   RGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSILF
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APPLICANT: WALLACH, David
APPLICANT: WALLACH, David
APPLICANT: MALININ, Nikolay
APPLICANT: SINHA, Indranil
APPLICANT: ESTARA
TITLE OF INVENTION: IREN PROTEIN, ITS PREPARATION AND USE
FILE REPRENCE: WALLACH=28
CURRENT APPLICATION NUMBER: US,10/070,255
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PT/IL00/00517
PRIOR APPLICATION NUMBER: IL 131719
PRIOR APPLICATION NUMBER: IL 131719
PRIOR FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 7
SEQ ID NO 7
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ORGANISM: Homo sapiens
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Matches 366;
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APPLICANT: IGHII, SHIZUKO

APPLICANT: WAKAMATSU, AI

APPLICANT: WAGAMATSU, AI

APPLICANT: OTSUKI, TETSUVII

TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE

FILE REFERENCE: 084335/0123

CURRENT FILING DATE: 2000-07-28

PRIOR FILING DATE: 1999-00-29

PRIOR FILING DATE: 1999-00-29

PRIOR FILING DATE: 1999-06-27

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 1999-06-27

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 1990-06-09

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                                                                                                      295 NSDRSSVNIMSAFESPFGPNSNGSQSSNSWKIDSLSLNGEFGYQKLDVKSIDDEDVDENE 354
                                                                                                                                                                                                                                                                                                            ---XXRCGXKRRXRVWKLIRKEAQGPLGVARE- 382
181 DLNGQSKFAPTVSDLLKESTQNVTSLLKESTQGVSSLFREITASSAVSILIKPEQETDP- 239
                                                                                                                                                                                   ---ISCPPLKAPSGLTPME----SEQQLMENX 334
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                                                            249 LSCPGMSVLMPN-----AKRSGRRKRKXPTXSHLMMRKMSRTLGTCLKRHLGQGRAQR-
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hes 30;
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GENERAL INFORMATION:
APPLICANT: OTA, TOSHIO
APPLICANT: ISOGAI, TAKAO
APPLICANT: NISHIKAWA, TETSUO
APPLICANT: HAYASHI, KOJI
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YAMAMOTO, JUNICHI
ISHII, SHIZUKO
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Best Local Similarity 82.2
Matches 244; Conservative
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SEQ ID NO 14017
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APPLICANT:
APPLICANT:
APPLICANT:
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         CALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTWAAGLNSILFAINIDNK 180
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Best Local Similarity 61.2%; Pred. No. 4.2e-125;
Matches 356; Conservative 22; Mismatches 101; Indels 103;
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US-10-070-255-8

US-11-070-255-8

SEQUENCE 8, Application US/10070255

GENERAL INFORMATION:
APPLICANT: WALININ, Nikolay
APPLICANT: SINHA, Indranil
APPLICANT: SINHA, Indranil
APPLICANT: SINHA, Indranil
APPLICANT: LEU, Stefan
ITILE OF INVENTION: INER: NOTIEIN, ITS PREPARATION AND USE
FILE REPERENCE: WALLACH-28
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/10/000517
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2009-08-31
PRIOR FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 14

SOSTWARE: PatentIn version 3.1
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US-10-070-255-8
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LENGTH: 813
TYPE: PRT
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61 RGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLR 120
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GENERAL INFORMATION:
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Best Local Similarity 98.7%;
Matches 236; Conservative
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US-10-170-205E-18638
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ORGANISM: Homo sapiens
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APPLICANT: SALTO, KAORU
APPLICANT: SALTO, KAORU
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APPLICANT: MAKAMATSU, AI
APPLICANT: MAKAMATSU, AI
APPLICANT: MACAMATSU, AI
APPLICANT: MACAMATSU, AI
APPLICANT: OTSUUI, TETSUUI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE
CURRENT PELICATION NUMBER: US/10/917,503
CURRENT PILING DATE: 2004-08-13
PRIOR PELING DATE: 2000-07-28
PRIOR PELING DATE: 1999-00-27
PRIOR PELING DATE: 2000-01-11
PRIOR PELING DATE: 2000-01-11
PRIOR PELING DATE: 2000-01-11
PRIOR PELING DATE: 2000-06-09
PRIOR PELING DATE: 2000-06-09
PRIOR PELING DATE: 2000-06-09
PRIOR PELING DATE: 1999-10-18
PRIOR PELING DATE: 1999-10-18
PRIOR PELING DATE: 2000-06-09
PRIOR PELING DATE: 1999-10-18
PRIOR PELING DATE: 2000-06-09
PRIOR PELING DATE: 2000-06-09
PRIOR PELING DATE: 1999-10-18
PRIOR PELING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 1903-27
SEG ID NO 14017
FENERMATH. 775
                                                                                                                                    61 RGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLR 120
                                                                                                                                                                                                                                       RGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELQRFYSLRHIASDVGRGRAWLR 128
                                                            RGLALTAAAIKQAAGFASKTETEPVFWYYVKEVLNKHELORFYSLRHIASDVGRGRAWLR 128
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1 MSGSQNNDKRQFLLERLLDAVKQCQIRFGGRKEIASDSDSRVTCLCAQFEAVLQHGLKRS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                 , Application US/10917503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OTA, TOSHIO
APPLICANT: ISOGAI, TAKAO
APPLICANT: NISHIKAWA, TETSUO
APPLICANT: HAYASHI, KOJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-503-14017
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APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SEQ ID NO 18638
LENGTH: 250
                                                                                                                                                  189 DLNGQSKFAPTVSDLLKESTQNVTSLLKESTQGVSSLFREITASSAVSILIKPEQETDPC 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 CALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSILFAINIDNK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSGSQNNDKRQFLLERLLDAVKQCQIRFGGRKEIASDSDSRVTCLCAQFEAVLQHGLKRS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 LSCPGMSVLMPN-----AKRSGRRKRKXPTXSHLMMRKMSRTLGTCLKRHLGQGRA 299
                                                                                                                                                                                                                                                                         CALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSILFAINIDNK
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFRENCE: PHOOL
CURRENT APPLICATION NUMBER: US/09/758,472
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9632
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1194; DB 27;
Pred. No. 1.2e-95;
0; Mismatches 3;
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US-60-212-356-236
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SEQ ID NO 236
LENGTH: 548
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FEATURE:
NAME/KEY: SITE
LOCATION: (3)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                        NAME/KEY: SITE
COCATION: (308)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-758-472-5854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 PTWAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLLKESTQGVSSLFREI 138
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                                                                                                                                      equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                    occurring L-amino acids
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; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PHONICIN
CURRENT APPLICATION NUMBER: US/10/235,926
CURRENT FILING DATE: 2002-09-06
PRIOR PAPLICATION NUMBER: 09/758,472
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9632
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 23.3%; Score 721; DB 22; Length 320; Best Local Similarity 50.3%; Pred. No. 7.1e-54; Matches 167; Conservative 21; Mismatches 64; Indels 8
                                                                                                                                                                                                    equals any of the naturally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 VPEAXCEKHRXXRCGXKRRXRVWKLIRKEAQGPLG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 SGRKHRGHSESPRSHWKGTPAFPDAQVGSXEG 310
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                                                                                                                LOCATION: (198)
OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (267)
OTHER INFORMATION: X
                                                                                                                                                                                                                                                                                                              LOCATION: (312)
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US-10-235-926-5854
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LENGTH: 320
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LOCATION: (198)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
                                                                                                                                                                                                                                                               NAME/KEY: misc_feature; LOCATION: (312); LOCATION: (312); OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-235-926-8854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NGSQSSNSWKIDSLSLNGEFGYQKLDVKSIDDEDXDENEDDVYGNS 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 FYSLRHIASDVGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSSML
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                                                                                                                 equals any of the naturally occurring L-amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                   64; Indels 80;
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                                                                                                                                                                                                                                                                                                                                                                                 Length 320;
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                                                                                                                                                                                                                                                                                                                                                                                 23.3%; Score 721; DB 28;
50.3%; Pred. No. 7.1e-54;
tive 21; Mismatches 64;
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES EN
TITLE OF INVENTION: PROTEINS, AND USES THERES
FILE REPERENCE: CLOOG677
CURRENT APPLICATION NUMBER: US/60/212,356
CURRENT PILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 411
SOFTWARE: FastSEQ for Windows Version 4.0
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OTHER INFORMATION: Xaa = Any Amino Acid
-60-212-356-236
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                           FEATURE:
NAME/KEY: misc feature
LOCATION: (308)
OTHER INFORMATION: Xaa ee
                                                                    NAME/KEY: misc feature
LOCATION: (267)
OTHER INFORMATION: Xaa
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Best Local Similarity
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                                                                                       204 LKESTQNVTSLLKESTQGVSSLFREITASSAVSILIKPEQETDPCLSCPGMSVLMPN--- 260
                                                                                                                                                                                                                                     108 QRFYSLRHIASDVGRGRAWLRCALNEHSLERYLHMLLADRCRLSTFYEDWSFVMDEERSS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLPTMAAGLNSILFAINIDNKDLNGQSKFAPTVSDLLKESTQNVTSLLKESTQGVSSLFR 227
                                 135 QNQWTASLKIASILSSTEGGLCAVLVDCCWGDGFEATSAASSNVTSRRALVAAVLGSAIV 194
                                                                                                                                          LADRCRLSTFYEDWSFVMDEERSSMLPTMAAGLNSILFAINIDNKDLNGQSKFAPTVSDL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EITASSAVSILIKPEQETDPCLSCPGMSVLMPN----AKRSGRRKRKXPTXSHLMM--RK 281
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QIRFXGRKEIASDSDSRVTCLCA------QFEAVLQHGLKRSRGLALTAAAIKQAAG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000677
CURRENT APPLICATION NUMBER: US/60/212,356
CURRENT PILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 411
SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE;
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
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                                                                                                                                                                                                                                                                                    261 ---AKRSGRRKRKXPTXSHLMMRKMSRTLGTCLKRHLGQGRA 299
                                                                                                                                                                                                                                                                                                            355 DAKCKKRRKKKKQVTNINSFDDEEDEQNSGDMFKKTPGAGES 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.2%; Score 685.5; DB 37; 73.7%; Pred. No. 2.1e-50; iive 12; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(544)
CTHER INFORMATION: Xaa = Any Amino Acid
US-60-212-356-203
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 203, Application US/60212356 GENERAL INFORMATION:
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Best Local Similarity 73.77
Matches 146; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-60-212-356-203
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US-60-229-525-294
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APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SEQ ID NO 22102
LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30582, Application PC/TUS0108631
GENERAL INFORMATION:
APPLICANT: Hyseq.
TITLE OP INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT FILIAG DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
                                                                                                                                                                                                                                                                                                                                        Score 663.5; DB 37
Pred. No. 2.7e-48;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.1%; Score 498.5; DB 2'96.2%; Pred. No. 5.6e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
FILE REFERENCE: CL000772
CURRENT APPLICATION NUMBER: US/60/229,525
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 819
SOFTWARE: FastSEQ for Windows Version 4.0
SQ ID NO 294
LENGTH: 692
TYPE: RRT
TYPE: RRT
FEATURE:
                                                                                          FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                        ; LOCATION: (1)...(692)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-229-525-294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 22102, Application US/10170205E; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 EITASSAVSILIKPEQETDP 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         508 EITASSAISILIKPEQETDP 527
                                                                                                                                                                                                                                                                                                                                        21.5%;
95.0%;
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Best Local Similarity 95.0°
Matches 133; Conservative
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US-10-170-205E-22102
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Best Local Similarity
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Best Local Similarity 96.3%; Pred. No. 2e-25;
Matches 79; Conservative 0; Mismatches 3; Indels
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 30582
LENGTH: 91
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-08631-30582
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Search completed: June 7, 2005, 12:19:32 Job time: 271.467 secs

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BV5047 YZ10607.81
BQ8Z7984 LL6102200
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OM nucleic

Run on:

Sequence:

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CR749592 3971 bp mRNA linear HTC 19-AUG-2004
Homo sapiens mRNA; cDNA DKFZp686J04131 (from clone DKFZp686J04131).
CR749592
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/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfiIA + SfiIB"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686J04131"
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N50047
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AUTHORS
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                           87;
                                                                                                                                                                                                                                                Length 1640;
                                                                    /mol_type="mRNA"
/db_xref="texon:9606"
/clone="CSODKOllYM14"
/tissue type="Heia cells Cot 25-normalized"
/plasmid="pcMVSPORT_6"
                                                                                                                                                                                                                                                                                                Indels
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Pred. No. 1.4e-233;
5; Mismatches 183;
     Location/Qualifiers
                           1. .1640
/organism="Homo
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84.1%;
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                         CCGNACGGCACTTTGCACNTCTGATGNACCTCAAAGCACTTTCATGGCTNGCCCTCTNNG 2100
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TCCGGCGCCCCCACCTATCAGTGT---CCAGCGTGCTGGTTCCC-----CAGA 3341
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                        GGTGNDAGGGANCACAGTCTTGAGCTGTCCANCATGCATGTGACTNCCTCAAACCTCTTN
                                                GCTNCAGNCATCANCACTGACACTNCACCCTNGCCCTTGCCCCTNGGCCANGAGGGTACTG
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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HTC; CNSLT cDNA.
Homo sapiens (human)
Homo sapiens
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Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2002) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2273 CACCAGAGGGGGAAAGCAACCGTCCCGGAGCAGGAACTGCAGCAGCTGGAAATAATTAT
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Pred. No. 3.8e-216;
); Mismatches 0;
                                                      gene trios
Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                         1. 284.
/organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"
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100.0%; Pre
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Matches 872; Conservative
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Eukarycis, metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 2844)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
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2014 CAGGGCCCCGGCCAGCTGAGGAGAACAAGCAGAGGCCCCTAAAGCTCCAGCCTCTCTCC
                                                    2074 CACCANAGCCCCCAGAGCCAAACAAGTNTCCTCCCTTGACTTTGAGGAGGAGGAGGAGGAGTCTG
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                                  CACCAGAGCCCCCAGAGCCAAACAAGTCTCCTCCCTTGACTTTGAGCAAGGAGGAGTCTG
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Pan troglodytes MAP3K14 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritera, S., Wango, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                  2633 TCCACCGGGTCAAAGTGGGAGACATCGCCACTGGCATCAGCAGCCAGATCCCAGCTGCAG
                                                                                                      CCTTCAGCTTGGTCACCAAAGACGGGCAGCCTGTTCGCTACGACATGGAGGTGCCAGACT
                                                                                                                                                                         CGGCCATCGACCTGCAGTGCACTGGCCCCTGATGGCAGCTTCGCCTGGAGGGG
                                                                                 CCTTCAGCTTGGTCACCAAAGACGGGCAGCCTGTTCGCTACGACATGGAGGTGCCAGACT
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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Science 302 (5652), 1960-1963 (2003)
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/locus_tag="HCM4937"
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911 bp mRNA linear EST 04-SEP-2002
AGENCOURT 7964504 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6169272
5', mRNA sequence.
BUJ95099
                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 911)
                                                                                                                                                                                                                                                                                                                                                                                                                           NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed Dy: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
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AACAAAACAGGGATCTTTNTTCTGCCCCTGCTCCAGTNCGAGTT-GGCCTGNACCCGCTT 1318
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GCAAGCAGGAATGCCTCCCCAGATTTCACACCTGAGCCCT--GCCCCACCCTGGCTGAG 770
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11 HMG Thtp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 AACTGCAGCAGCTGGAATAGAATTATTCCTCAACAGCCTGTCCCAGCCATTTCTCTGG
                                                                                                                                                      771 AAAACACTCCGCCCACGTGAAGAGACA-AAGGAGGATGGCAGGAAGTTA---CCTCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the In.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LiAM11260 row: o column: 08
High quality sequence stop: 760.
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                                                                                          AAAACAYTNCCGCCACGTGAAGAGACAGAAGGAGGATGGNCAGGAGTTNNACCTYGGGGA
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Pred. No. 1.1e-172;
0; Mismatches 15; Indels
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llarity 97.6%;
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Homo sapiens
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                                                                                                                                                                                                                                                                                                   /clone="IMAGE:6169272"
/tissue type="melanotic melanoma"
/lab.host="DH10B (phage-resistant)"
/clone lib="NHH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
site_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Average insert size 2 kb. Library constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TCCCAGCCATTTTCTCTCTGGAGGAGCAGGAAATTCTCTCGTGCCTCAGCATCGACAGC 120
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Clone distribution: MGC clone distribution information can | found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Plate: LIAM13534 column: 01
High quality sequence stop: 556.
Location/Qualifiers
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                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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VEKSPVFCCKWEILNDVITKGTAKOGSEGGPPAISIIAQAECENSQEFSPTFSERIFI
AGRQQYSQSESLDQIPNNVAHATEGKMARVCRRGKRGKRKRKRSKSLAQAGVA
LAKPLPRTPEQESCTIPVQSDESPLGNLYARNVSQFTKPLGGFGLGHLCFKKQDBGLR
PVLPRPELHKLISPLQCLNHVWKLHHPQATGPRPHPTHPFPYSGMPHPFPYPLEPWK
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. SHIKEN integrated sequence analysis (RISA) system--384-format genome Res. 10 (11), 1757-1771 (2000)
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Clone lib="RiKEN full-length enriched mouse cDNA library"
/dev_stage="16 days neonate"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 tull-length cDNAs
Nature 420, 563-573 (2002)
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kinase kinase kinase 14 (MGD|MGI:1858204, GB|NM_016896,
evidence: BLASTN, 100%, match=2829)
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Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://ganome.ggc.riken.jp/
URL:http://fantom.ggc.riken.jp/.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="9630045G21"
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/strain="C57BL/6J"
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Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone: 9630045621 product:mitogen-activated protein kinase kinase kinase 14, full insert sequence.
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High-efficiency full-length CDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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YEY REREWHWHIQPRVGRSGSFGEVHWKDKOYGTGSCANKLEFFKRLEVPRAGLS
YER REHWHWHIQPRVGRSGFGEVHWKDKOYGTGSCANKLEFFKRLEVPRAGLS
YER ILHGDVANKEGPRWYLLFGGSLGGLIKQMGCLFEDBALYYLLGGLESLTSL
HTRRILLHGDVKADNVLLSSDGSRAALCDFGHALCLQPDGLGKSLLTGDYIFGFTHM
APLYWGKFRODTCKALTAGSTGCTCANLHMLANGCHPWTGYFRGPLCTKLASEPPPIRETPBSC
APLTRAAIQEGLKREPHRASAMELRRKVGKALQFVGGLKSPWGGFYKEPPPQQQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.6%; Score 698.6; DB 3; 80.7%; Pred. No. 9.3e-171;
                                                                                                                                                                                                                                                                                                                    /note="putative"
4174
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5. mENA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Low Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM12128 row: c column: 03
High quality sequence stop: 724.
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NIH-MGC http://mgc.nci.nih.gov/.
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/lab_host="NHDMOB (phage-resistant)"
/clone_lib="NIH_MGC_85"
/note="Gragan: lymph, Vector: pCMV-SPORT6, Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size_1:867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
2717 IGGGAGACATTGCCACCGGCATCAGCAGCCAGACCCAGCCACGCATTCAGCCTGGAGA
                                                                                                                2777 CCAAAGATGGACAGCCTGTTTGCTATGACATGGAGGTGCCAGACTCGGGCATCGACCTGC
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                                                                                                                                                                                            AGTGCACACTGGCCCCTGATGGCAGCTTCGCCTGGAGCTGGAGGGTCAAGCATGGCCAGC
                                                                                                                                                                                                                                                    AGTGCACCCTGGCCCCTGATGGCAGCTTTGCTTGGACCTGGAGGGTCAAGCATGGTCAGC
                                                                               CCAAAGACGGGCAGCCTGTTCGCTACGACATGGAGGTGCCAGACTCGGGCATCGACCTGC
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Pred. No. 3.1e-166;
1; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                      CCTTCCTGCTCGGTGCACGATGCTGCCCTGAAA 1050
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/db_xref="taxon:9606"
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83.2%;
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Tegeagercreaaaaecccrreaaaaeaaaaaaararaaaaaaccaaeaccrecaae. 2038
2 (bases 1 to 2829)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submitsion
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTCAACAGCCTGTCCCAGCCGTTCTCTGGAGGAACAGGAACAAGAATCCTCTCCTGCC
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Pred. No. 1.4e-144;
0; Mismatches 138;
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                            /gene="MAP3K14"
/locus_tag="HCM4937"
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Best Local Similarity 81.7%;
Matches 712; Conservative (
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Mus musculus MAP3K14 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musinae; Musamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Lo 2829)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ferriera, S., Wanghy, B., Ferriera, S., Wanghy, B., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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       AGCCTGGGTCAGAAGGGGTGGGCGAGCCCCTCGGCCCTCACCCT-CCAGGCTGT-T
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AY413579
AY413579.1 GI:39769541
GSS.
Mus musculus (house mouse)
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602865208F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019481 5',
       GGGACATGGGACCCACTGCCCCTGTCCTCCTGGATCCTGCCCCCGCCAGGAACCCCACC 122
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Bukaryogia.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 806)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                              TCACCCGAGGGAAAGGCAACCTTTCCTGAACAGGAGCTACAGCAGCTGGAGGTAGAGTTA
                                                                                                                                                                       183 TITCTGAACAGCCTGTCCCAGCCGTTCTCCCTGGAGGAGCAGGAGCAGAACCTCTCGTGC
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLCM1834 row: o column: 02
High quality sequence stop: 600.
Location/Qualifiers
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/dev stage="Multiple"
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/lab_host="DH10B T1 phage resistant"
/clone lib="BARC 9BOW"
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Site_2: NotI; Equimolar amounts of mRNA extracted from fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Ostertagia ostertagi was initiated at 15 weeks of age. fundic and pyloric abomasum"
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Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay, Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay, S.P., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically activated bovine gut
Unpublished (2004)
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Boly 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048414
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Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt " -trim_fasta. Vector identified
by cross match using options -minmatch 12 -minscore 18
Plate: 40 row: A column: 19
Seq primer: CCGACTACACGTTCTAAAACG
High quality sequence stop: 702.
Location/Qualifiers
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
CTTTCAGCCTGGTGACCAAAGATGGACAGCCTGTTTGCTATGACATGGAGGTGCCAGACT
                                                                                                  2738 CGGCATCGACCTGCAGTGCACCCTGGCCCCTGATGGCAGCTTTGCTTGGACTGGAGGG
                                                                     CGGCCATCGACCTGCACACTGGCCCCTGATGGCAGCTTCGCCTGGAGCTGGAGGG
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/strain="Holstein"
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CK979910.1 GI:45497890
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/tissue_type="epithelioid carcinoma cell line"
/tissue_type="epithelioid carcinoma cell line"
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/note="Torgan: pancreas; Vector: poTB7; Site 1: Xho1;
/note="Torgan: pancreas; Vector: poTB7; Site 1: Xho1;
/note="Torgan: pancreas; Vector: poTB7; Site 1: Xho1;
/note: note: pancreas; Vector: poTB7; Site 1: Xho1;
/note: this is a NIH_MGC Library. |" (Life Technologies).
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                                                                                                                                                                                                      Indels
                                                                                                                                                                                 Score 568.2; DB 4;
Pred. No. 6.8e-137;
0; Mismatches 48;
                                                                                                                                                                                   Query Match 21.6%;
Best Local Similarity 91.9%;
Matches 701; Conservative
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580 bp mRNA linear EST 16-SEP-2004
ary, thyroid JTH Homo sapiens CDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="thyroid"
/cell line="JTH"
/clone lib="Sugano cDNA library, thyroid JTH"
/note="thyroid tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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99.3%; Pred. No. 6.8e-136;
iive 0; Mismatches 3;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
            bec 282 bec 282 bec 282 bec 282 bec 282 bec 282 because JTH06618, mRNA sequence.
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BP267282.1 GI:52182514
                                                                                                                                                                                      Homo sapiens (human)
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Matches 577; Conservative
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955 bp mRNA linear EST 13-SEP-2002
AGENCOURT 10326204 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:6572558
5', mRNA sequence.
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Homo sapiens
Bukaryotas, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria; Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 955)
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GAGCAGCAGCCCCGAGCCCCTTNAGGCCCAGNACTGCCCCAGANCTNGNTGGNACTCAG
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                                                           GAGCAGCAGCCCCGAGCCCCTTCAGGCCCCAGCACTGCCCCAGA-CTCGCTGGCACTCAG
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                                                                                                                                                                                                                                   633 ATGGACATGATCAGTGCTAA--GGAAAGCAGCAGAGAGAGAGAGACGTCCGGCGCCCCAGCCC
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecox V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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Homo sapiens
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31316669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.'
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1095 bp mRNA linear LA578455 Homo sapiens HELA CELLS COT 25-NORVALIZED CDNA clone CSODKOllYM14 3-PRIME, mRNA sequence. AL578455
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Pred. No. 7e-133;
9; Mismatches 129; Indels
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/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
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                                                                                         541 ACACTGCCGG-AAGCAGCCTTCCTGCTCGGTGCACGATGCT
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/mol_type="mRNA"
/db_xref="taxon:9606"
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CNDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM2764 row: n column: 14

High quality sequence start: 31

High quality sequence store: 630.

Location/Qualifiers
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                    2162 GIGNAAGGGANCACAGICITGAGGIGTCCANCAIGCAIGIGACINCCICAAACCICIINN
                                                              2222 CCAGNATITCTCTAAGAATAGCANCCCCTTNCCCCATTGCCCCAGCTTAGCCTCTTCTC
                                                                          -ccagatttctctaagaatagcacccc--trccccattgccccagcttagcctcttctc
                                                                                                                                                   GTCTGCTAGCCTCAACCTCCTGGGGCAGGGACGCCGAGACTCCGTGGGAAAGCTCATT
----GIAGGAGCATAGCAAGCCAGGAGATGGG
                               CCAGGGGAGCTANCTCAGGACTCACGTAGCATTAAATCAGCTGTGNAATCGTCAGGGGGT
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Job time : 5555.69 secs
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1 (bases 1 to 1906)
MABLACH, D., Malinin, W., Boldin, M., Kovalenko, A. and Mett, I. MODULATORS OF THE RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR PREPARATION AND USE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Wallach,D., Malinin,N., Sinha,I.W. and
Iren protein, its preparation and use
Parent: WO 0116314-A 6 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT CO. LTD.
Location/Qualifiers
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Local Similarity 99.6%; Pred. No. 0;
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    /organism="Homo sapiens"
/mol_type="unassigned DNA"
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                                                                                        GAAACAGAGCCCGTGTTCTGGTACTACGTGAAGGAGGTCCTCAACAAGCACGAGCTGCAG
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/ LE TABLAI LI CON "MESCONNDKROPILLERILDAVKOCQIRFGGRKEIASDSDSRVTC
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/mol_type="unassigned DNA"
/db_rref="taxon:9606"
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ACATCGCCTCAGACGTGGGCCGGGGTCGCGCTGGCTGTGCCCTCTCAACGAACACT	382 ACALICACCICAGACCIGAGCCIGGCCIGGCCIGGCCCICAACGAACACT 441 497 CCCTGGAGCGCTACCTGCAACATGCTCCTGGCCGACCGCTGCAGCTGAGCACTTTTTATG 556 [557 AAGACTGGTCTTTTGTGATGGATGAAAGAAAGGTCCAGTATGCTTCCTACCATGGCAGCAG 616 	617 GTCTGAACTCCATACTCTTTGCGATTAACATCGACAAGATTTGAACGGGCAGAGTA 676 	677 AGTITIGCICCCACCGITICAGACCTCTIAAAGGAGTCAACGCAGAACGIGACCTCCTIGC 736 	737 TGAAGGAGTCCACGCAAGGAGTGAGCCGCTGTTCAGGGAATCACAGCCTCCTCTGCCG 796 	797 TCTCCATCCTCATCAAACCTGAACAGAGACCGA-CCCTTGCCTGTCGTCGTCCAGGAATG 855 	856 TCAGTGCTGATGCCAAATGCAAAAAGGAGGGAAGAAAAAAAA	916 TCTCATTTGATGAGGAAGATGAGCAGAACTCTGGGGACGTGTTTAAAAAGACACCTG 975 	976 GGGCAGGGGAGAGCTCAGAGGACAACTCCGACCGCTCCTCTGTCAATATCATGTCCGCCT 1035	1036 TTGAAAGCCCCTTCGGGCCTAACTCCAATGGAA-TCAGAGCAGCACTCATGGAAAATTG 1094 	1095 ATTCCCTGTCTTTGAACGGGGGAGTTTGGGTACCAGAAGCTTGATGTGAAAAGCATCGATG 1154 	1155 ATGAAGATGGAAGAAGGAAGATGACGTGTATGGAAACTCATCAGGAAGGA	1215 GGGCCACTCGGAGTCGCCCGAGAAGCCACTGGAAGGGAACACCTGCCTCTCCCAGATGC 1274	1275 ACAGCTGGGCTCCGCTGAAGGTGCTGCACAATGACTCCGACATCCTCTTCCCTGTCAGTG 1334	1335 GC 1336 1262 GC 1383	T 7 425 AK022 ITION HOMO SION AK022 ON AK022 RDS oligc
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Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sakine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanka, T., Isono, Y., Nakamura, Y. Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Isono, T., Wagatsuma, M., Shizatori, A., Sudo, H., Hosoliri, T., Kakui, Y., Kodaira, H., Kondo, H., Sugawara, M., Yakahashi, M., Ninomiya, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Takibashi, T., Faruya, T., Furuya, T., Furuya, T., Kikawa, E., Omura, Y., Abe, K., Kamihara, K., Kananabe, M., Namazaki, M., Ninomiya, K., Takiguchi, S., Watanabe, N., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, N., Takeuchi, K., Tanikawa, M., Yamazaki, M., Moura, Y., Togiya, S., Komai, F., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, H., Sasaki, N., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Takeuchi, K., Arita, M., Imose, N., Momiyama, H., Satoh, N., Takami, S., Momiyama, H., Satoh, N., Takami, S., Momiyama, H., Satoh, N., Takami, S., Momiyama, H., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Momiyama, H., Sanda, M., Shindara, Y., Shindura, F., Wakebe, H., Hishigaki, H., Watanabe, K., Suzuki, O., Nakagawa, S., Senba, A., Takausa, M., Fujiwara, T., Otaki, Y., Kawakami, T., Kobatake, N., Inagaki, H., Hitao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Matanabe, M., Komatsu, M., Hata, H., Watanabe, M., Komatsu, Y., Wasashita, R., Nakashita, Y., Nakajima, Y., Nakajima, Y., Nakanura, N., Kakhani, H., Wasanura, N., Kakanura, N., Kananura, N., Kakanura, N., Kananura, N., Kakanura, Y., Nagase, T., Nomura, N., Kikuchi, H., Wasaulo, Y., Nagase, T., Nagase, T., Nagase, T., Nagasu, K., Yada, Y., Otana, Conslete sequencing and character
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Craniata; Vertebrata; Euteleostomi;
     aryoča; Metazoa; Chordata; Craniata; Vertebrata; Eutele
malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="unnamed protein product"
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/tissue type="Mammary gland"
/clone_lib="MAMMA1"
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/db_xref="taxon:9606"
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gai, T. and Otsuki, T.
ect Submission
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TTGAAAGCCCCTTCGGGCCTAACTCCAATGGAAGTCAGAGCAGCAACTCATGGAAAATTG
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      TCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGACGTGTTTAAAAAAGACACCTG
                                                                         TTGAAAGCCCCTTCGGGCCTAACTCCAATGGAA-TCAGAGCAGCAACTCATGGAAAATTG
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                             GGGCAGGGGAGAGCTCAGAGGACAACTCCGACCGCTCCTCTGTCAATATCATGTCCGCCT
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Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority
humanexons or transcripts, for detecting expression and c
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Catarrhini; Hominidae;
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Pred. No. 2.9e-214;
0; Mismatches 5;
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Sequence 226 from Patent WO02068579.
CQ714292
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PE Corporation (NY) (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates,
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Location/Qualifiers
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                                                                                                                                  DB 9; Length 2248;
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                                                                                                                               Score 1138.2; DB 9;
Pred. No. 5.4e-271;
0; Mismatches 65;
                                                                                                                             Query Match
Best Local Similarity 94.7%;
Matches 1195; Conservative
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Euteleostomi;

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Gaps

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304 180 364

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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ò	365 AGCCCGTGTTCTGGTACTACGTGAAGGAGGTCCTCAACAAGCACGAGCTGCAGGGGCTTCT 424	REFERENCE AUTHORS
qq	. 238 237	CONSRIM
ò	425 ACTCCCTGCGCCACATCGCCTCAGACGTGGGCCGGGGTCGCGCCTGGCTGG	JOURNAL
Ор	238CAGACGIGGGCCGGGCCGCCCTGCCTGCCTGCCC 276	COMMENT
<u>ک</u> و	485 TCAACGAACACTCCCTGGAGCGCTACCTGCACATGCTCCTGGACCGACC	. w щ с
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e 6	337 GCACTITITIATGAAGACTGGTCTTTTGTGATGGATGAAGAAAGGTCCAGTATGCTTCCTA 804 337 GCACTITITIATGAAGACTGGTCTTTTGTGATGGATGAAGAAAGGTCCAGTATGCTTCCTA 396	ш *1
È	605 CCATGGCAGCAGCTCTGAACTCCTTTGCGATTAACATCGACAACAAGATTTGA 664	FEATURES SOURCE
d d	397 CCATGGCAGCAGTCTGAACTCCATACTCTTTGCGATAACATGACAACAACAAGGATTTGA 456	
ò	665 ACGGGCAGAGTATGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGAACG 724	
Op	457 ACGGGCAGAGTAAGTTTGCTCCCACCGTTTCAGACCTCTTAAAGGAGTCAACGCAGAACG 516	
ò	725 TGACCTCCTTGCTGAAGAGTCCACGCAAGGAGTGAGCAGCCTGTTCAGGGAGATCACAG 784	
qq	517 TGACCTCCTTGCTGAAGGAGTCCACGCAAGGAGTGACCTGTTCAGGGAGATCACAG 576	polyA_gi
ò	785 CCTCCTCTGCCGTCTCCATCCTCAACCTGAACAGGAGACCGA-CCCTTGCCTGTCG 843	polya_si ORIGIN
qq	577 CCTCCTCTGCGTCTCCATCCTCATCAACCTGAACAGAGACCGACC	Query Match
ò	844 TGTCCAGGAATGTCAGTGCTGATGCCAAATGCAAAAAGGGGGGAAGAAGAAAAGAAAG	Matches 85
Ор	637 TGTCCAGGAATGTCAGTGCTGATGCCAAATGCGAAGAAGGAGGAAGAAAAAAGGAAAA 696	Qy 363
ò	904 TGACCAACATAATCTCATTTGATGAGAAGAAGAGGAGCAGAACTCTGGGGACGTGTTTA 963	Db 1381
Op	697 IGACCAACATAATCTCATTTGATGAGGAAGATGAGCAGAACTTCTGGGGACGTGTTTA 756	Qy 422
ò	964 AAAAGACACCTGGGGCAGGGAGAGCTCAGAGGACAACTCCGACGCCTCCTCTGTCAATA 1023	Db 1441
ф	757 AAAGACACCTGGGGCAGGGGGGGGGCCCCCACCCCCCCCC	Qy 482
ò	1024 TCATGTCCGCCTTTGAAAGCCCCTTCGGGCCTAACTCCAATGGAA-TCAGAGCAGCAACT 1082	Db 1501
ΩP	817 TCATGICCGCCTITGAAAGCCCCTICGGGCCTAACTCCCAATGGAAGTCAGAGCAGCAACT 876	Qy 542
ò	1083 CATGGAAATTGATTCCCTGTCTTTGAACGGGAGTTTGGGTACCAGAAGCTTGATGTGA 1142	1561
QQ	877 CAFGGAAAATTGATTCCCTGTCTTTGAACGGGGAGTTTGGGTACCAGAAGCTTGATGTGA 936	Qy 602
ò	1143 AAAGCATCGATGATGAAGATGGGATGAAAACGAAGATGACGTGTATGGAAACTCATCAG 1202	Db 1621
QQ	937 AAAGCATCGATGAAGAAGATGTGGATGAAAACGAAGATGACGTGTATGGAAACTCATCAG 996	Qy 662
ò	1203 GAAGGAAGCAAGGGGCCACTCGGAGTCGCCCGAGAA 1239	Db 1681
QQ	997 GAAGGAAGCACAGGGCCACTCGGAGTCGCCCGAGAA 1033	Qy 722
		Db 1741

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Pred. No. 1e-185;
0; Mismatches 21; Indels 6;
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Local Similarity 96.9%;
es 853; Conservative (
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Homo sapiens mRNA; cDNA DKFZp686E09125 (from clone DKFZp686E09125).
BX648280
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840

Homo sapiens (human) Homo sapiens

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 9 HSM808428 LOCUS

781

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1052 CCTCAACGAACACTCCCTGGAGCGCTACCTGCACTGCTCCTGGCCGACCGCTGCAGGC 1111
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                         1469 AAGTGACCAACATTATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGACATGT
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                                                  CCCTCAACGAACACTCCCTGGAGCGCTACCTGCACATGCTCCTGGCCGACCGCTGCAGGC
                                                                                                                TGAGCACTTTTTATGAAGACTGGTCTTTTGTGATGAAGAAAGGTCCAGTATGCTTC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 6045)
Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 15070 09-JUL-2002;
                                                                                                                                                                                                                                                   TGAAAAGCATCGATGATGAAGATGTGGATGAAAACGAAGATGACGTGTATGGAAACTCAT 1199
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Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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KEIICHI NAGAI, TETSUJI OTSUKI
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OS Homo sapiens (human)
PN JP 2002191363-A/15070
PD 09-JUL-2002
PF 28-JUL-2000 JP 200280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATS
PI JUNICHI NAGAI, TETSUJI OTSUKI
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                 1978 TIARAAAAGACACCTGGGGCAGGGGAGAGCTCAGAGGACAACTCCGACCACTCCTCTGTCA
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AAGTGACCAACATAATCTCATTTGATGATGAGGAAGATGAGCAGAACTCTGGGGACGTGT
                                                          TTAAAAAAGACACCTGGGGGAGGGGGAGAGGTCAGAGGACAACTCCGACCGCTCCTGTCA
                                                                                                                        ATATCATGTCCGCCTTTGAAAGCCCCTTCGGGCCTAACTCCAATGGAA-TCAGAGCAGCA
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Primer for synthesizing full-length cDNA and use thereof.
BD160227
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                                                                                                                                                                                                                                                                                                                                (364). (954).
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002191363-A/15070.
Homo sapiens (human)
Homo sapiens
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Matches 852; Conservative
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Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sakamatsu,A., Hayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishiah,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Yatakai,T., Iwayanagi,T., Wagatsuma,M., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sudo,H., Hosoiri,T., Kaku,Y., Rodaira,H., Kondo,H., Kukawa,E., Cmura,Y., Abe,K., Kamhara,K., Katsuta,M., Sato,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,N., Hara,H., Tanase,T., Nomura,Y., Toqiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Wasashino,K., Yuuki,H., Cohima,A., Sasaki,M., Aotsuka,S., Yoshikawa,S., Komai,F., Hara,R., Sasaki,M., Sano,S., Moriya,S., Momiyama,H., Xiuki,H., Takami,S., Todiya,S., Momiyama,H., Xiuki,H., Takami,S., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Rukawami,Y., Fujimori,H., Tanigami,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,T., Goto,Y., Shimizu,F., Rukura,S., Fuvuxan,B., Yamazaki,M., Tagashi,T., Rusaki,A., Itakura,S., Fuvuxan,B., Yamazaki,M., Watanabe,T., Nakabata,A., Itakiji,T., Kobatake,N., Tashiro,H., Tanagami,A., Puliwara,T., Matsumura,K., Nakakami,T., Nagashi,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakabati,A., Itakan,Y., Sangaki,M., Toqashi,T., Nagase,T., Nagase,T., Nawashi,A., Yawashi,A., Y
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                                       1709 TGAAAAGCATCGATGATGAGATGTGGATGAAAACGAAGATGACGTGTATGGAAACTCAT 1768
                                                                                                                                                                                                                                                                                                                                                                                        PRI 30-JAN-2004
weakly similar
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                    AKO23827 6045 bp mRNA linear Homo sapiens cDNA FLJ13765 fis, clone PLACE4000128, to Mus musculus putative transcription factor mRNA.
                                                                                                                      1200 CAGGAAGGAAGCACAGGGGCCACTCGGAGTCGCCCGAGAA 1239
                                                                                                                                                                      oligo capping; fis (full insert sequence)
Homo sapiens (human)
Homo sapiens
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sogai, T. and Otsuki, T.
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/db_xref="G1:40038171"
/db_xref="G1:4003817
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                                                                                                               __type="unassigned DNA"
_xref="taxon:9606"
                                                                           organism="Homo sapiens"
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Matches 852; Conservative
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JP 2002191363-A/1808
09-JUL-2002
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Homo sapiens (human)
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DGQVQVIPQGHLHIAKVPQGEQVQITQDSESPCSGTT"
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etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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                                  1..6645
/organism="Homo sapiens"
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/mol_type="mRNA"
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/tissue_type="placenta"
/clone_lib="pLACE400128"
/clone_lib="pLACE4"
/clone_lib="placenta"
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/clone="unnamed protein product"
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/protein_id="BAB14692.1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 730)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 1808 09-JUL-2002;
HELIX RESEARCH INSTITUTE
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KEIICHI NAGAI, TETSUJI OTSUKI
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TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
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1080 ACTCATGGAAAATTGATTCCCTGTCTTTGAACGGGGAGTTTGGGTACCAGAAGCTTGATG
                                                                                                            TGAAAAGCATCGATGAAGATGTGGATGAAAACGAAGATGACGTGTATGGAAACTCAT
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Location/Qualiflers
1. .730
/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
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Eukaryotta; Buteleostomi; Bukaryotta; Buteleostomi; Bukaryotta; Butleria; Primates; Catarrhin; Hominidae; Homo.

CE I (bases It o. 1229)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Ugdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, K.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Mocken, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Hellon, B., Garcia, A.M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Ketteman, M., Madan, A., Young, A.C., Schwutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnutz, J., Worle, J.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnutz, J., Schein, J.E., Schnutz, J., Schein, J.E., Schnutz, J., Schein, J.E., Schnutz, J., and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC041583 1229 bp' mRNA linear PRI 07-0CT-2003
Homo sapiens hypothetical protein FLJ12363, mRNA (cDNA clone
MGC:52410 IMAGE:4765274), complete cds.
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                                                            202 CCCAGTTTGAAGCCGTCCTGCATGCTTGAAGAGAGTCGAGGATTGGCACTCACAG
                                                                                                                           317 CGGCAGCGATCAAGCAGCAGCGGGCTTTGCCAGCAAAACCGAAACAGAGCCCGTGTTCT
                                                                                                                                                                                                                                                      GGTACTACGTGAAGGAGGTCCTCAACAAGCACGAGCTGCAGCGCTTCTACTCCCTGCGCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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963 AAAAAGACACCTGGGGCAGGGGAGGGTCAGAGGACAACTCCGACCGCTCCTCTGTCAAT 1022
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                                                                                                                                                  GTGACCAACATAATCTCATTTGATGAGGAAGATGAGCAGAACTCTGGGGACGTGTTT
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland,
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
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Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.B. Consortium/LiNL at: http://image.llnl.gov
Series: IRAL plate: 44 Row: e Column: 20.
Location/Qualifiers
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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Sequence 7, Appli
Sequence 14, Appl
Sequence 1471, Ap
Sequence 14226, A
Sequence 183, App
Sequence 1644, Ap
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10799, A
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Copyright (c) 1993 - 2005 Compugen Ltd
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1 MAVMEMACPGAPGSAVGQQKELPKPKEKTPPLGKKQSSVYKLEAVEKSPVFCGKWEILND 61 VITKGTAKEGSEAGPALSIIAQAECENSQEFSPTFSERIFIAGSKQYSQSESLDQIPNN

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1 MAVMEMACPGAPGSAVGQQKELPKPKEKTPPLGKKQSSVYKLEAVEKSPVFCGKWEILND

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121 VAHATEGKMARVCWKGKRRSKARKKRKKKSSKSLAHAGVALAKPLPRTPEQESCTIPVQE

Sequence 9386, Ap Sequence 16140, A Sequence 16140, A Sequence 11304, A Sequence 4, Appli Sequence 1116, A Sequence 10142, Ap Sequence 1014, App Sequence 11014, A Sequence 1508, App Sequence 1508, App Sequence 1608, App Sequence 1608, App Sequence 1608, App Sequence 1608, App Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1857, Appl Sequence 1854, Appl Sequence	ATED FACTOR (TRAF), THEIR	Length 947; Indels 0; Gaps 0;
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26 325 6.4 1478 28 324.5 6.4 1478 29 324.5 6.4 1478 31 318.5 6.4 1315 31 315.5 6.2 1315 31 315.5 6.2 1423 31 315.5 6.0 1490 315.5 6.0 1490 315.5 6.0 1490 315.5 6.0 1490 315.5 6.0 1490 315.5 6.0 2139 42 301.5 6.0 2139 44 301.5 6.0 968	RESULT 1 US-09-155-676B-7 SEQUENCE 7, Application US/09155676B GENERAL INFORMATION: APPLICANT: WALLACH, David APPLICANT: WALLACH, David APPLICANT: WALLACH, David APPLICANT: WALLACH, DAVID APPLICANT: ROYALENKO, Andrei APPLICANT: KOVALENKO, Andrei APPLICANT: KOVALENKO, Andrei APPLICANT: WALLACH-21 TITLE OF INVENTION: REPRARATION AND USE TITLE OF INVENTION: REPRARATION AND USE FILE REFERENCE: WALLACH-21 CURRENT FILING DATE: 1999-01-04 PRIOR PILING DATE: 1997-04-01 PRIOR PILING DATE: 1997-04-01 PRIOR PILING DATE: 1996-08-26 NUMBER OF SEQ ID NOS: 22 SOFTWARE: PATENTIN VETSION 3:3 SEQ ID NO 7 LENGTH: 947 TYPE: PRT TYPE: P	Query Match Best Local Similarity 100 Matches 947; Conservative

180 240 300 480 61 VITKGTAKEGSEAGPAAISIIAQAECENSQEFSPTFSERIFIAGSKQYSQSESLDQIPNN 120 61 VITKGTAKEGSEAGPAAISIIAQAECENSQEFSPTFSERIFIAGSKQYSQSESLDQIPNN 120 121 VAHATEGKMARVCWKGKRRSKARKKRKKSSKSLAHAGVALAKPLPRTPEQESCTIFVOE 180 240 КІННРОООСЕРГРІРІНРЕРУЅЯГЕРНРЕРЕНРІОРЖКРИРІВЅЕГСКІЛАСУОЅОКРІРОРН 300 LSKLACVDSPKPLPGPHLEPSCLSRGAHEKFSVEEYLVHALQGSVSSSQAHSLTSLAKTW 360 360 AARGSRSREPSPKTEDNEGVLLTEKLKPVDYEYREEVHWATHQLRLGRGSFGEVHRMEDK 420 420 480 540 540 9 600 9 9 720 720 780 780 840 840 900 900 9 DESPLGAPYVRNTPQFTKPLKEPGLGQLCFKQLGEGLRPALPRSELHKLISPLQCLNHVW DESPLGAPYVRNTPQFTKPLKEPGLGQLCFKQLGEGLRPALPRSELHKLISPLQCLNHVW VKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVC 1 MAVMEMACPGAPGSAVGQQKELPKPKEKTPPLGKKQSSVYKLEAVEKSPVFCGKWEILND 1 MAVMEMACPGAPGSAVGQQKELPKPKEKTPPLGKKQSSVYKLEAVEKSPVFCGKWEILND KLHHPQDGGPLPLPTHPFPYSRLPHPFPFHPLQPWKPHPLESFLGKLACVDSQKPLPDPH AARGSRSREPSPKTEDNEGVLLTEKLKPVDYEYREEVHWATHQLRLGRGSFGEVHRMEDK LQPDGLGKSLLTGDY1PGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF RGPLCLKIASEPPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGG RGPLCLKIASEPPPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGG LKSPWRGEYKEPRHPPPNQANYHQTLHAQPRELSPRAPGPRPAEETTGRAPKLQPPLPPE 721 PPEPNKSPPLTLSKEESGGMEPLPLSSLEPAPARNPSSPERKATVPEQELQQLEIELFLN SLSQPFSLEEQEQILGCLSIDSLSLSDDSEKNPSKASQSSRDTLSSGVHSWSSQAEARSS SWNWVLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS VAHATEGKMARVCWKGKRRSKARKKKKKSSKSLAHAGVALAKPLPRTPEQESCTIPVQE QTGFQCAVKKVRLEVFRAEELMACAGLTSPRIVPLYGAVREGPWVNIFMELLEGGSLGQL LOPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF PPEPNKSPPLTLSKEESGMWEPLPLSSLEPAPARNPSSPERKATVPEQELQQLEIELFLN SLSOPFSLEEQEQILSCLSIDSLSLSDDSEKNPSKASQSSRDTLSSGVHSWSSQAEARSS SWNWVLARGRPIDIPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS ö 947;

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APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: VERSPONSE TO INTERFERON TREATMENT IN HEPA
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION OF THEREOF
CURRENT APPLICATION NUMBER: US/60/659,397
CURRENT FILING DATE: 2005-03-09
NUMBER OF SEQ ID NOS: 47869
SOCTWARE: FEALESC for Windows Version 4.0
                                                                                                                                                                                                   LVTKDGQPVRYDMEVPDSGIDLQCTLAPDGSFAWSWRVKHGQLENRP
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Pred. No. 2.6e-230;
0; Mismatches 2;
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; ORGANISM: Homo sapiens
US-60-659-397-1472
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                                                    APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: CRANG, Sheng-Yung
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ASSPONSE TO INTERFERON TREATMENT IN HEPATITIS (
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION I
TITLE OF INVENTION: THEREOF
FILE REFERNCE: CL001470
CURRENT APPLICATION NUMBER: US/60/659,397
CURRENT FILING DATE: 2005-03-09
NUMBER OF SEQ ID NOS: 47859
SSOFTWARE: PASESQ for Windows Version 4.0
SEQ ID NO 1471
LENGTH: 947
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llarity 99.8%; Pred. No. 2.6e-230;
Conservative 0; Mismatches 2;
                           Sequence 1471, Application US/60659397 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-60-659-397-1471
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Best Local Similarity
Matches 945; Conserv
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                                                                                       338 VHA-LQGSVSSQAHSLTSLAKTWAARGSRSREPSPKTEDNEGVLLTEKLKPVDYEYREE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                  VLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFFRGPLCLKIASEPPVREIPPSCAPLTA 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAIQEGLRKEPIHRVSAAELGGKVNRALQQVGGLKSPWRGEYKEPRH-PPPNQANYHQTL 686
                                              -----SRSRFDSEIGS
                                                                                                                                                                       397 VHWATHQLR--LGRGSFGEVHRMEDKQTGFQCAVKKVRLEVFRABELMACAG-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: ||:| | || | :: :: DLIMQCFNKDPAKRPSAEML--FEHEWMQQV-----WGG-HKDLRELRPQDSVPFLRRI
                                                                                                                                                                                                                                                            448 TSPRIVPLYGAVREGPWVNIFMELLEGGSLGQLVKEQGCLPEDRALYYLGQALEGLEYLH
                                                                                                                                                                                                                                                                                                                                                 508 SRRILHGDVKADNVLLSSDGSHAALCDFGHAVCLQPDGLGKSLLTGDYIPGTETHMAPEV
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APPLICANT: Gangolli et al.

TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-225

CURRENT APPLICATION NUMBER: US/11/113,424

CURRENT APPLICATION NUMBER: 60/256,704

PRIOR APPLICATION NUMBER: 60/311,590

PRIOR FILING DATE: 2000-12-19

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-20

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: 60/315,617

PRIOR FILING DATE: 2001-09-14

PRIOR SPELING DATE: 2001-09-14

PRIOR FILING DATE: 2001-09-14

PRIOR SPELING DATE: 2001-09-14

PRIOR FILING DATE: 2001-09-14

PRIOR PRIOR DATE: 2001-09-14

PRIOR FILING DATE: 2001-09-14

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PRIOR PRIOR PRIOR DATE: 2001-09-14

PRIOR PRIOR PRIOR DATE: 2001-09-14

PRIOR PRIOR PRIOR DATE: 2001-09-14

PRIOR PRIOR PRIOR DATE: 2001-09-14
                                                                                                             ; Sequence 183, Application US/11113424; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              790 RESLLNIGSQANGESDALASSRVPFPRGANDSPGARRMARHLSMNAGVSDTISTASGPST 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 850 AIATNGSSSSKVSSRPHFRH---MRYSSD---LHLPSMSRPTS------- 887
                          LKSPWRGEYKEPRHPPPNQANYHQTLHAQPRELSPRAPGPRPAEETTGRAPKLQPPLPPE
                                                                                                                                                                                                                                                                                                                                                                 SWNMVLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS
                                                                                                                                                                                                                                                                                     SLSQPFSLEEQEQILSCLSIDSLSLSDDSEKNPSKASQSSRDTLSSGVHSWSSQAEARSS
                                                                                LQPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF
                                                                                                                                                                   RGPLCLKIASEPPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGG
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GENERAL INFORMATION:
APPLICANT: Abad, Mark S.

TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53629)A

CURRENT APPLICATION NUMBER: US/60/643,717

CURRENT FILING DATE: 2005-01-12

NUMBER OF SEQ ID NOS: 19247

LENGTH: 1673
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7.7%; Score 391.5; up o;
Best Local Similarity 24.3%; Pred. No. 1.2e-10;
Matches 205; Conservative 115; Mismatches 357;
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US-60-643-717-14226
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US-60-643-717-14226
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GTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF----RGPLCLKIA-SEPP
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CURRENT APPLICATION NUMBER: US/10/940,774A
CURRENT FILING DATE: 2004-09-15
PRIOR PAPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                   ; Sequence 10456, Application US/10940774A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 27.2%
Matches 116; Conservative
                                                                                                                                                                                                               734 KEESGM 739
                                                                                                                                                                                                                                                432 TEESEM 437
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US-10-940-774A-10456
                                                                                                                                                                                                                                                                                                                      US-10-940-774A-10456
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ORGANISM: Human
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APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENETIC FOLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERPERON TREATMENT IN HEBATITIS C
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOO1470
CURRENT APPLICATION NUMBER: US/60/659,397
CURRENT FILING DATE: 2005-03-09
SUFFMENT FILING DATE: 2005-03-09
SUFFMENT FILE SESTING DATE: 2005-03-09
SUFFMENT FILE SESTING DATE: 2005-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 LGRGSFGEVHRMEDKQTGFQCAVKKVRLEVFRAE-----ELMACAGLTSPRIVPLYGA 458
                                                                                                                                                                                                                                                                  459 VREGPWVNIFMELLEGGSLGOLVKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKA 518
                                                                                                                                                                                                                                                                                       67 FEDDDXLYLVMEYCEGGDLFDLLKKRGRLSEDEARFYARQILSALEYLHSQCIIHRDLKF 126
                                                                                                                                                                                                                                                                                                                                                           VWSSCCMMLHMLNGCHPWTQFFRG----PLCLKIASEPPPVREIPP---SCAPLTAQAI 630
                                                                                                                                                                                                                                                                                                                                                                                                                                   332 SVEEYLVHALQGSVSSSQAHSLTSLAKTWAARGSRSREPSPKTEDNEGVLLTEKLKPVDY 391
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                                                OTHER INFORMATION: Description of Artificial Sequence: consensus; OTHER INFORMATION: sequence
US-11-113-424-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
                                                                                                                                                           28;
                                                                                                                          Length 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.1%; Score 360; DB 8; Length 467
Best Local Similarity 27.2%; Pred. No. 9e-10;
Matches 116; Conservative 69; Mismatches 155; Indels
                                                                                                                                                         94; Indels
                                                                                                                      7.3%; Score 367; DB 7;
larity 37.9%; Pred. No. 2.2e-10;
Conservative 37; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1644, Application US/60659397; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: | |:| |:| |
234 KKLLVKDPEKRLTAEE 249
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                ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
                                                                                                                      Query Match
Best Local Similarity
Matches 97; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: HOMO
US-60-659-397-1644
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                          7.1%; Score 360; DB 6; Length 475
27.2%; Pred. No. 9.2e-10;
tive 69; Mismatches 155; Indels
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RESULT 11
US-10-941-635-157
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                                                                                                                                                        APPLICANT: WALLACH, David

APPLICANT: WALLACH, David

APPLICANT: WALLACH, David

APPLICANT: WALLACH, Mark

APPLICANT: WALLENNC, Andrei

APPLICANT: KOVALENNC, Andrei

APPLICANT: KOVALENNC, Andrei

APPLICANT: KONALENNC, MODULATORS OF THE RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR

TITLE OF INVENTION: PREPARATION AND USE

FILE REFERENCE: WALLACH=21

CURRENT APPLICATION NUMBER: US/09/155,676B

PRIOR APPLICATION NUMBER: PCT/1197/00117

PRIOR PLING DATE: 1999-01-04

PRIOR FILING DATE: 1996-04-02

PRIOR PLING DATE: 1996-04-02

PRIOR FILING DATE: 1996-04-02

PRIOR FILING DATE: 1996-04-02

PRIOR FILING DATE: 1996-04-02

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin version 3.3
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                                                                                                                             Sequence 13, Application US/09155676B GENERAL INFORMATION:
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734 KEESGM 739
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RESULT 10
PCT-US04-30360-157

Sequence 157, Application PC/TUS0430360

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350 AHSLTSLAKTWAARGSRSREPSPKTEDNEGVLLTEKLKPVDYEYREE-----VHWATHQL 404
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GENERAL INFORMATION:
APPLICANT ARTIS, DEAN R.
APPLICANT BREMER, RYAN E.
APPLICANT GILLETTE, SAMUEL J.
APPLICANT HURT, CLARENCE R.
APPLICANT: LARAHHA, PRABHA L.
APPLICANT: SUCKERMAN, REBECCA L.
TITLE OF INVENTION MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE REFERENCE: 039363-1702
CURRENT APPLICATION NUMBER: US/10/941,635
CURRENT APPLICATION NUMBER: 60/503,277
PRIOR FILING DATE: 2004-09-15
NUMBER OF SEQ ID NOS: 167
SOFTWARE PATENTIN Ver. 3.2
SEQ ID NO 157
LENGTH: 351
LENGTH: 351
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APPLICANT: PLEXXIKON, INC.
TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LICAND DEVELOPMENT
FILE REFERENCE: 039363-1703
CURRENT APPLICATION NUMBER: PCT/US04/30360
CURRENT FILING DATE: 2004-09-15
PRIOR APPLICATION NUMBER: 60/503,277
PRIOR FILING DATE: 2003-09-15
NUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
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                                                                                                                                                                                                                                                                                                                                                 FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Mammalian

OTHER INFORMATION: protein sequence

PCT-USO4-30360-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 358; DB 1; Length 35; Pred. No. 8.2e-10; 68; Mismatches 151; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 27.7%;
Matches 113; Conservative 68
                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Unknown Organism
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APPLICANT: MALININ, Nikolai
APPLICANT: MALININ, Nikolai
APPLICANT: MALININ, Nikolai
APPLICANT: BOLDIN, Mark
APPLICANT: BOLDIN, Mark
APPLICANT: MCVALENCO, Andrei
APPLICANT: MCVALENCO, TOOR
TITLE OF INVENTION: PREPARATION AND USE
TITLE OF INVENTION: PREPARATION AND USE
TITLE OF INVENTION: PREPARATION AND USE
FILE REFERENCE: MALLACH=21
CURRENT APPLICATION NUMBER: US/09/155,676B
CURRENT FILING DATE: 1999-01-04
PRIOR PAPLICATION NUMBER: IL 117800
PRIOR PLING DATE: 1996-00-01
PRIOR PLING DATE: 1996-08-26
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VEX SION 3.3
SEQ ID NO 19
LENGTH: 672
  107 GILLNMVISPQNGRYQIDSDVLLVPWKLTYRSIGSGFVPRGAFGKVYLAQDMKTKKRMAC 166
                                                                      EDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVCLQPDGLGK 548
                                                                                                                                                                                                                         549 SLLTGDYIP----GTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF---R 601
                                                                                                                                                                                                                                              602 GPLCLKIA-SEPPPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SB SLQAVAPTSCLENSSLEHTVHREKTGKGLSATRLSASSEDISDRLAGVSVGLPSSTTTEQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 PQFTKPLKEPGLGQLCFKQLGGGLRPALPRSELHKLISPLQ--CLNHVWKLHHPQDGGPL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 PQAFVPCKIPS------RDSDQL-RKFSLQFQRNCSEH------RDSDQL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SPVFTQSRPPPSSNIHRPKPSRPVP-----GSTSKLGDATKSSMTLDLGSA 248
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                                                                                                                                                          | :: |:||:|||:|| |: | EFEIIWVIKGLDFLHSKKVIHHDIKPSNIVFMS--TKAVLVDFGLSVQMTED----
                                               KKVRLEVFRAEELMACAGLTSPRIVPLYGAVREGPWVNIFMELLEGGSLGQLVKEQGCLP
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                                                                                                                                                                                                                                                                                                                                      336 YPSYLYIIHKQAPPLEDIAGDCSPGMRELIEAALERNPNHRPKAADL---
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; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SENERAL INFORMATION:
APPLICANT: WALLACH, David
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APPLICANT: WALLACH, David
APPLICANT: WALLACH, David
APPLICANT: WALLACH, David
APPLICANT: BOLDIN, Mark
APPLICANT: BOLDIN, Mark
APPLICANT: ROYLENKO, Andrei
APPLICANT: NOTATION: MODILATORS OF THE RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR
TITLE OF INVENTION: PREPARATION AND USE
TITLE OF INVENTION: PREPARATION AND USE
TITLE OF INVENTION: PREPARATION AND USE
CURRENT APPLICATION NUMBER: US/09/155,676B
CURRENT PILING DATE: 1999-01-04
PRIOR FILING DATE: 1999-01-04
PRIOR APPLICATION NUMBER: IL 117800
PRIOR PILING DATE: 1996-04-02
PRIOR PILING DATE: 1996-04-02
PRIOR PILING DATE: 1996-08-26
SOFTWARE: PAGENTIN VERSION 3.3
SEQ ID NOS: 22
SOFTWARE: PAGENTIN VERSION 3.3
                                                                                                                                                                              13;
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                                                                                                                                                                                                                                                                                                                                      NVLLSSDGSHAALCDFGHAVCLQPDGLGKSLLTGDYIP----GTETHMAPEVVLGRSCDA 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVDVWSSCCMMLHMLNGCHPWTQFF---RGPLCLKIA-SEPPVREIPPSCAPLTAQAIQ 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         379 GVLLTEKLKPVDYEYREE-----VHWATHQLRLG-----RGSFGEVHRMEDKQTGFQCAV 428
                                                                                                                                                                                                                                                405 RLG-----RGSFGEVHRMEDKQTGFQCAVKKVRLEVFRAEELMACAGLTSPRIVPLYGAV
                                                                                                                                                                                                                                                                                                                                                                                               REGPWVNI FMELLEGGSLGQLVKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKAD
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                                      OTHER INFORMATION: Description of Unknown Organism: Mammalian; OTHER INFORMATION: protein sequence US-10-941-635-157
                                                                                                                                 Length 351;
                                                                                                                               Query Match
7.1%; Score 358; DB 6; Length 35
Best Local Similarity 27.7%; Pred. No. 8.2e-10;
Matches 113; Conservative 68; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/09155676B GENERAL INFORMATION:
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98; Conservative
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US-09-155-676B-12
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Best Local Si
Matches 98;
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            ----ASPQTQ-RKFSLQFQRNCSEH-----RDSDQL 202
                                                                                                             ---GSTSKLGDATKSSMTLDLGSA 248
                                                                                                                                                                                           249 SRCDDSFGGGGNSGNAVIPSDETVFTPVEDKCRLDVNTELNSSIEDLLEASMPSSDTTVT 308
                                                                                                                                                                                                                                                           -SQAHSLTSLAKTWAARGSRSR---EPSP 372
                                                                                                                                                                                                                                                                                                   PKSEVAVLSPEKAENDDTYKDDVNHNQKCKEKMEAEEEEALAIAMAMSASQDALPIVPQL 368
                                                                                                                                                                                                                                                                                                                                                           424
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                                                            PLPTHPFPYSRLPHPFPFHPLQPWKPHPLESFLGKLACVDSQKPLPDPHLSKLA-----
                                                                                                                                                                                                                                                                                                                                                                                    GGSLGQLVKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             594 HPWTQFFRG---PLCLKIASE-----PPPVREIPPSCAPLTAQ--AIQEGLRKEP
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                                                                                                                                                        --CVDS-----PKPLPGPH----LEPSC-LSRGAHEKFSVEEYLVHALQGSVSS--
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                                                                                                          203 ---SPVFTQSRPPSSNIHRPKPSRPVP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 4, Application US/09608890A; GENERAL INFORMATION:
               166 PQAFVPCKIPS-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus
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HERENERAL LINCKMALIOUS:

TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness TO TITLE OF INVENTION: External Signals
FILE REFERENCE: CPI-004DVCP3CN
CURRENT FILING DATE: 2000-06-30
CURRENT FILING DATE: 2000-06-30
FRIOR APPLICATION NUMBER: 08/440,421
FRIOR FILING DATE: 1995-05-15
FRIOR FILING DATE: 1995-05-15
FRIOR FILING DATE: 1995-05-15
FRIOR FILING DATE: 1995-06-15
FRIOR FILING DATE: 1995-06-15
FRIOR FILING DATE: 1995-06-06
FRIOR FILING DATE: 1995-03-24
FRIOR FILING DATE: 1995-03-24
FRIOR FILING DATE: 1995-06-06
FRIOR FILING DATE: 1995-06-06
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FRIOR FILING DATE: 1995-06-06
FRIOR FILING DATE: 1995-06-06
FRIOR PLING DATE: 1995-06-06
FRIOR APPLICATION NUMBER: 08/472,934
FRIOR FILING DATE: 1995-06-06
FRIOR PLING DATE: 1995-06-06
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FRIOR APPLICATION NUMBER: 08/472,934
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SRCDDSFGGGGNSGNAVIPSDETVFTPVEDKCRLDVNTELNSSIEDLLEASMPSSDTTVT 308
                                                       SQAHSLTSLAKTWAARGSRSR---EPSP 372
                                                                                                                                                                                 QCAVKKV------RLEVFRA--EELMACAGLTSPRIVPLYGAVREGPWVNIFMELLE 473
                                                                                                                                                                                                                                                                                      428 LMAVKQVTYVRNTSSEQEEVVEALREBIRMMGHLNHPNIIRMLGATCEKSNYNLFIEWMA 487
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                                                                                                                                                                                                                                                                                                                                              GGSLGQLVKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALC 533
                                                                                                                                                                                                                                                                                                                                                                                                                                            DEGHAVCLOPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGC 593
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                                                                                             309 FKSEVAVLSPEKAENDDTYKDDVNHNOKCKEKMEÅEBEBEALÅIAMAMSASODALPIVPOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPWTQFFRG---PLCLKIASE------PPPVREIPPSCAPLTAQ--AIQEGLRKEP
                                                                                                                                                KTEDNEGVLLTEKLKP-------VDYEYREEVHWATHQLRLGRGSFGEVHRMEDKQTGF
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7.0%; Score 355.5; DB 5;
Best Local Similarity 23.6%; Pred. No. 2.2e-09;
Matches 157; Conservative 81; Mismatches 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09608890A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Mus musculus
US-09-608-890A-2
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979 SLQAVAPTSCLENSSLEHTVHREKTGKGLSATRLSASSEDISDRLAGVSVGLPSSTTTEQ 1038	137 KRRSKARKKKKKSSKSLAHAGVALAKPLPRTPEQESCTIPVQEDESPLGAPYVRNT 193	PKPAVQTKGRPHSQCLNSSPLSHAQLMFPAPSAPCSSAPSVPDISKHR 1086	PQFTKFPGKEPGGLCFKQLGEGLRPALPRSELHKLISPLQCLNHVWKLHHPQDGGFL	' PQAFVPCKIPSRDSDQL 1123	PLPTHPFPYSRLPHPFPPHPLQPWKPHPLESFLGKLACVDSQKPLPDPHLSKLA		CVDSPKPLPGPHLEPSC-LSRGAHEKFSVEEYLVHALQGSVSS	SKCDDSFGGGGNGGNAVIPSDETVFTPVEDKCKLDVNTELNSSIEDLEASMPSSDITVT 1229	EPSP 372	1230 FKSEVAVLSPEKAENDDTYKDDVNHNQKCKEKMEÅEEEBALAIAMAMSAŠQDALPIVPQL 1289	KTEDNEGVLITEKLKPVDYEYREEVHWATHQLRLGRGSFGEVHRMEDKQTGF 424	VVENGEDIIIIQQDIPETLPGHTKAKQPYREDAEWLKGQ-QIGLGAFSSCYQAQDVGTGT 1348	QCAVKKVRLEVFRAEELMACAGLISPRIVPLYGAVREGPWVNIFMELLE 473		474 GGSLGQLVKEQGCLPEDRALYYLGQALBGLEYLHSRRILHGDVKADNVILSSDGSHAALC 533	GGSVAHLLSKYGAFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQRLRIA 1468	DFGHAVCLQPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGC 593		HPWTQFFRGPLCLKIASEPPPPVREIPPSCAPLTAQAIQEGLRKEP 638	PPWNAEKHSNHLALIFKIASATTAPSIPSHLSPGLRDVAVRCLELQPQDRPPSRELLKHP 1587	IHRVS 643	. FRTT 1592	
979	137	1039	194	1087	252	1124	306	7170	348	230	373	1290	425	349	474	409	534	1469	594	1528	639	1588	
Ор	È	Db 1		Op 1		DP 1		qn	ò	Db 1	ò	Db 1	ò	Db 1	۵	Db 1	ò	Db 1.	ò	Op 1	č	Db 1	

Search completed: June 7, 2005, 12:21:21 Job time : 50.1575 secs

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Description

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APPLICANT: WALLACH, David
APPLICANT: WALLININ, Nikolai
APPLICANT: MALININ, Mark
APPLICANT: KOVALEND, Mark
APPLICANT: KOVALEND, Andrei
APPLICANT: METT, Igor
TITLE OF INVENTION: MODULATORS OF TWF RECEPTOR ASSOCIATED
TITLE OF INVENTION: FACTOR (TRAF), THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                           S US-09-155-676-14
S US-09-155-676-14
S US-09-155-676-14
S US-09-155-676-14
S US-09-155-676-17
S US-09-151-1606
4 US-09-949-003C-2282
4 US-09-949-003C-2282
4 US-09-949-003C-2282
4 US-09-949-003C-2282
6 US-01-394-322A-44
US-09-949-003C-2282
6 US-10-36-36-3904
7 US-60-443-566-2591
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7 US-60-456-412-13078
7 US-60-456-412-13078
7 US-60-456-412-13078
7 US-60-456-412-13078
8 US-10-087-192-885-758
8 US-10-192-925-758
8 US-01-219-925-758
8 US-01-213-847-1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 624 Ninth Street, N.W., Suite 300 CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09155676
GENERAL INFORMATION:
           B
           Length
 Query
Match ]
                            4196.5
3439.5
2439.5
2301
2301
1572.5
1028
992
586
Result
No.
                                                                                                                              7, 2005, 11:52:21 ; Search time 422.493 Seconds (without alignments) 2618.037 Million cell updates/sec
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                                                                                            US-09-155-676B-7
5052
1 MAVMEMACPGAPGSAVGQQK.......PDGSFAWSWRVKHGQLENRP 947
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ptodata/1/paa/US107_COMB.pep:*
ptodata/1/paa/US108_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                 6959266 segs, 1168006243 residues
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/cgn2_6/ptodata/1/paa/US110_
/cgn2_6/ptodata/1/paa/US60_7
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Maximum Match 100%
Listing first 45 summaries
                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                      seq length: 0
seq length: 200000000
                                                       June
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Sequence 493, App Sequence 8184, App Sequence 9184, App Sequence 2590, Ap Sequence 13077, A Sequence 13078, A Sequence 13077, A Sequence 13077, A Sequence 13077, A Sequence 13077, A Sequence 13070, A Sequence 1471, Ap Sequence 2326, Ap Sequence 2326, Ap Sequence 2326, Ap Sequence 2326, Ap Sequence 1471, Ap Sequence 2326, Ap Sequence 1471, Ap Sequence 1307, Ap Sequence 1326, Ap Sequence 1471, Ap Sequence 1326, Ap Sequence 1326, Ap Sequence 1316, Ap Sequence 1471, Ap

Sequence 1 Sequence 4 Sequence 4

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

Run on:

Sequence

Sequence

Sequence

Sequence 4878, Sequence 758, A Sequence 758, A

Sequence Seguence

SUMMARIES

099

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PPEPNKSPPLTLSKEESGMMEPLPLSSLEPAPARNPSSPERKATVPEQELQQLEIELFLN 780
                                                                                                                                                                                                                           781 SLSQPFSLEEGEQILSCLSIDSLSLSDDSEKNPSKASQSSRDTLSSGVHSWSSQAEARSS
                                                                                                                                                                                                                                                                                                                                           SWNMVLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS
                                                                                                                                                                                                                                                                                              541 LOPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF
                     LKSPWRGEYKEPRHPPPNQANYHQTLHAQPRELSPRAPGPRPAEETTGRAPKLQPPLPPE
                                                                    RGPLCLKIASEPPPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WALLIAIN, Nikolai
APPLICANT: WALLININ, Nikolai
APPLICANT: MALININ, Nikolai
APPLICANT: ROLDIN, Mark
APPLICANT: ROYALENKO, Andrei
APPLICANT: KOVALENKO, Andrei
TITLE OF INVENTION: MODULATORS OF THE RECEPTOR ASSOCIATED
TITLE OF INVENTION: PACTOR (TRAF), THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE AND NEIMAR, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                              901 LVTKDGQPVRYDMEVPDSGIDLQCTLAPDGSFAWSWRVKHGQLENRP 947
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPREX: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,676
FILING DATE: 04-JAN-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/IL97/00117
FILING DATE: 01-APR-1997
PRICK APPLICATION DATA:
APPLICATION NUMBER: IL 117800
FILING DATE: 02-APR-1966
PRICK APPLICATION NUMBER: IL 119133
FILING DATE: CA-AGG-1966
ATTONEY/AGENT INPORMATION:
ANDONEY AGENTALING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C. STREET: 624 Ninth Street, N.W., Suite 300 CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REPERENCE/DOCKET NUMBER: WALLACH=21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 14, Application US/09155676
; GENERAL INFORMATION:
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US-09-155-676-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               КІННРОДССРІРІРТИРЕРУЅВІРНРЕРЕНРІОРИКРИРІЕЅFІСКІАСУДЅСКРІРДЕН 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 KLHHPQDGGFLFLPTFTFPFFYSRLPHPFPFFHPLQPWKPHFLESFLGKLACVDSQKPLFDFH 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VITKGTAKEGSEAGPAAISIIAQAECENSQEFSPTFSERIFIAGSKQYSQSESLDOIPNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAVMEMACPGAPGSAVGQQKELPKPKEKTPPLGKKQSSVYKLBAVEKSPVFCGKWEILND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAVWEMACPGAPGAVGQQKELPKPKEKTPPLGKKQSSVYKLEAVEKSPVFCGKWEILND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VITKGTAKEGSEAGPAAISIIAQAECENSQEFSPTFSERIFIAGSKQYSQSESLDQIPNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
     COMPUTER READABLE FUARM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/15,676
FILING DATE: 04-JAN-1999
CLASS!FICATION DATA:
APPLICATION NUMBER: PCT/IL97/00117
FILING DATE: 01-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117800
FILING DATE: 01-APR-1966
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 119133
FILING DATE: 22-APR-1966
PRIOR APPLICATION NUMBER: IL 119133
FILING DATE: 25-40G-1996
ATTORNEY/AGRAY INFORMATION:
NAME: BROWDY, ROGET L.
REFERENCE/DOCKET NUMBER: WALLACH=21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 202-737-3528
INFORMATION FOR EQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
TEMETHAL 947 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e-306;
Matches 947; Conservative 0; Mismatches 0; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
   COMPUTER READABLE FORM
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US-09-155-676-7
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                                                                                                                                                                                   APPLICANT: WALLACH, David
APPLICANT: MALININ, Nikolai
APPLICANT: MALININ, Mark
APPLICANT: KOVALENKO, Andrei
APPLICANT: METT, Igor
TITLE OF INVENTION: MODULATORS OF THE RECEPTOR ASSOCIATED
TITLE OF INVENTION: FACTOR (TRAF), THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 20
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                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,676A
FILING DATE: 04-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 5052; DB 15;
; Pred. No. 5.5e-306;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C.
STREET: 624 Ninth Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IL97/00117
FILING DATE: 01-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117800
FILING DATE: 02-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 119133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WALLACH=21
                                                                                                                                                  ; Sequence 7, Application US/09155676A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618 REPERENCE/DOCKET NUMBER: WAL TELECOMMUNICATION: 10FORMATION: 202-628-5197
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-AUG-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                     100.0%; Score 5052; DB 15; Length 947; 100.0%; Pred. No. 5.5e-306; ive 0; Mismatches 0; Indels 0;
TELEPAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 947 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 947; Conservative
                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                US-09-155-676-14
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COMPUTER RELATED TO THE MEDIUM TYPE: FIDEDY disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPATIONS SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: PATENTON DATA:
APPLICATION NUMBER: US/09/155,676A FILING DATE: 04-JAN-1999
PILING APPLICATION DATE: PCT/IL97/00117
APPLICATION NUMBER: PCT/IL97/00117
APPLICATION NUMBER: IL 117800
FILING DATE: 02-APR-1996
PRIOR APPLICATION DATE: 11 119133
FILING DATE: 26-AUG-1996
ATTONNEY/AGENT INFORMATION:
NAME: BROWNY, ROGER L.
REGISTRATION NUMBER: 15 618 ARTONNEY/ACCOUNT NUMBER: 25,618 ARTONNEY/ACCOUNT NUMBER: 26,618 ARTONNEY/ACCOUNT NUMBER: 25,618 ARTONNEY/ACCOUNT NUMBER: 26,618 ARTONNEY/ACCOUNT NUMBER: 26,618 ARTONNEY/ACCOUNT NUMBER: 26,618 ARTONNEY/ACCOUNT NUMBER: 26,618 ARTONNEY/ACCOUNT NUMBER: 25,618 ARTO
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                         КДННРООССРЕРГРТНРЕРУЅКЕРНРЕРЕНРЕОРИКРИРЕЕЅГЕСКТАСУОЅОКРЕРОРН 300
VAHATEGKWARVCWKGKRRSKARKKRKKKSSKSLAHAGVALAKPLPRTPEQESCTIPVQE 180
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                                                                                                                                                              241 KLHHPQDGGPLPLPTHPFPYSRLPHPFPFHPLQPWKPHPLESFLGKLACVDSQKPLPDPH
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Sequence 14, Application US/09155676A

Sequence 14, Application US/09155676A

Sequence 14, Application

GENERAL INFORMATION:

APPLICANT: WALLION:

APPLICANT: WALLION: Mark

APPLICANT: WOVLENKO, Andrei

APPLICANT: WOVLENKO, Andrei

APPLICANT: METT, IGOT

ITTLE OF INVENTION: MODULATORS OF THE RECEPTOR ASSOCIATED

ITTLE OF INVENTION: FACTOR (TRAF), THEIR PREPARATION AND USE

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                     Length 947;
                                                                                                                                                                                            Indels
                                                                                                                                                                  100.0%; Score 5052; DB 15;
100.0%; Pred. No. 5.5e-306;
iive 0; Mismatches 0;
  WALLACH=21
REFERENCE/DOCKET NUMBER: WAI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                  INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                             LENGTH: 947 amino acids
                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 947; Conservative
                                                                                                     ss: single
linear
                                       202-737-3528
                                                                                                                                MOLECULE TYPE: peptide
                                                                                             amino acid
                                                                                                      STRANDEDNESS:
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US-09-155-676A-14
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E: BROWDY AND NEIMAR, P.L.L.C. 624 Ninth Street, N.W., Suite 300

STREET: 624 Ninter CITY: Washington CITY: Washing STATE: D.C. COUNTRY: USA

ADDRESSEE:

Db 241 KLHHPQDGGPLPLPTHPFPYSRLPHPFPFHPLQPWKPHPLESFLGKLACVDSQKPLPDPH Qy 301 LSKLACVDSPKPLPGPHLEPSCLSRGAHEKFSVEEYLVHALQGSVSSSQAHSLTSLAKTW	Db 301 LSKLACVDSPKPLPGFHILIFIH	Db 361 AARGSRSREPSPKTEDNEGVLLTEKLKPVDYEYREEVHWATHQLRLGRGSFGEVHRMEDK	QY 421 QTGFQCAVKKVRLEVFRAEELMACAGLTSPRIVPLYGAVREGPWVNIFMELLEGGSLGQL 	Qy 481 VKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVC	Qy 541 LQPDGLGKSLLTGDYIPGTETHWAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF	Qy 601 RGPLCLKIASEPPPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGG	Qy 661 LKSBWRGEYKEPRHPPPNQANYHQTLHAQPRELSPRAEGPRPAEETTGRAPKLQPPLPPE 	721 PPEPNKSPPLTLSKEESGAWEPLPLSSLEPAPARNPSSPERKATVPEOELOQ 721 PPEPNKSPPLTLSKEESGAWEPLPLSSLEPAPARNPSSPERKATVPEOELOQ 732 PPEPNKSPPLTLSKEESGAWEPLPLSSLEPAPARNPSSPERKATVPEOELOQ 733 SLSQPFSLEEGEQILSCLSIDSLSLSDDSEKNPSKASQSSRDTLSSGVHSWS 743 SLSQPFSLEEGEQILSCLSIDSLSLSDDSEKNPSKASQSSRDTLSSGVHSWS 844 SWMWLARGRPTDTPSYFNGVKVQIOSLNGEHLHIREFHKVKVGDIATGISS 841 SWMWLARGRPTDTPSYFNGVKVQIOSLNGEHLHIREFHKVKVGDIATGISS 841 SWMWLARGRPTDTPSYFNGVKVQIOSLNGEHLHIREFHKVKVGDIATGISS 841 SWMWLARGRPTDTPSYFNGVKVQIOSLNGEHLHIREFHKVKVGDIATGISS 842 SWMWLARGRPTDTPSYFNGVKVQIOSLNGEHLHIREFHKVKVGDIATGISS 843 SWMWLARGRPTDTPSYFNGVKVQIOSLNGEHLHIREFHKVKVGDIATGISS 844 SWMWLARGRPTDTPSYFNGVKVQIOSLNGEHLHIREFHKVKVGDIATGISS 845 SWMWLARGRPTDTPSYFNGVKVQIOSLNGEHLHIREFHKVKVGDIATGISS 846 SWMWLARGRPTDTPSYFNGVKVQIOSLNGEHLHIREFHKVKVGDIATGISS 847 INFORMATION: 846 ON STANDAR S	Query Match Best Local Similarity 100.0%; Pred. No. 5.5e-306; Matches 947; Conservative 0; Mismatches 0; Indels 0; Gaps	QY 1 MAVMEMACPGAPGSAVGQQKELPKPKEKTPPLGKKQSSVYKLEAVEKSPVFCGKWEILND
Db 481 VKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVC 540 Qy 541 LQPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF 600	Db 541 LQPDGLGKSLLTGDYIPCTETHWAPEVVLGRSCDAKUDUWSSCCMILHMLNGCHPWTQFF 600 Qy 601 RGPLCLKIASEPPPVREIPPSCAPLTAQAIQEGRRKEPIHRVSAAELGGRVNRALQQVGG 660	Db 601 RGPLCLKIASEPPPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAABLGGVVRALQQVGG 660	Qy 661 LKSPWRGEYKEPRHPPPNQANYHQTLHAQPRELSPRAPGPRPAEETTGRAPKLQPPLPPE 720	Qy 721 PPEPNKSPPLTLSKEESGWWEPLPLSSLEPAPARNPSSPERKATVPEGELQQLEIELFLM 780	QY 781 SLSQPPSLEEQEQILSCLSIDSLSLSDSEKNPSKASQSSRDTLSSGVHSWSSQAEARSS 840	Qy 841 SWNWVLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS 900 Db 841 SWNMVLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS 900	Oy 901 LVTKDGQPVRYDWEVPDSGIDLQCTLAPDGSFAWSWRVKHGQLENRP 947 Db 901 LVTKDGQPVRYDWEVPDSGIDLQCTLAPDGSFAWSWRVKHGQLENRP 947	SULT 5 Sequence 1606, Application US/09791537 GENERAL INFORMATION: APPLICANT: Bionomix, Inc. APPLICANT: Bionomix, Inc. APPLICANT: Debc, Derek APPLICANT: Debc, Derek APPLICANT: Debc, Derek APPLICANT: Debc, Derek APPLICANT: Debc, Derek APPLICANT: Debc, Derek APPLICANT: Debc, Derek APPLICANT: Debc, Derek APPLICANT: Debc, Derek APPLICANT: Debc, Derek APPLICANT: Debc, Derek APPLICANT: Debc, Derek APPLICANT: Debc, Derek APPLICANT: Debc, Derek APPLICANT: Debc, Derek TITLE OF INVENTION: METHED DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND TITLE OF INVENTION METHED STRUCTURES. US/09/791,537 CURRENT FILLING DATE: 261/210 CURRENT FILLING DATE: 261/20 CURRENT FILLING DATE: 261/20 CURRENT FILLING DATE: 261/20 CURRENT FILLING DATE: DOS: 153055 SEQ ID NO 1606 LENGTH: 947 TYPE: PAT TYPE: PAT TYPE: DE 22; Length 947; DEGANISM: Homo sapiens -09-791-537-1606 COUETY MATCh Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity 100.0%; Score 5052; DB 22; Length 947; Beet Local Similarity	OY 181 DESPICARYYRNTPOFTKPIKEPGEGGCKROLGEGERRALFRSEHKLISPLOCLNHVW 240	ОУ 241 КІННРОДССРІРІРІРТИРРРУЅВІРНРГРЕНРІОРМКРНРІЕЅГІСКІАСУДЅОКРІРДЯ 300

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240
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                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                       Length 947;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                       Score 5052; DB 25;
Pred. No. 5.5e-306;
Mismatches 0;
; TITLE OF INVENTION: Inhibition
; FILE REFERENCE: AXM-004.1 US
; CURRENT APPLICATION NUMBER: US/09/981,397A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/240,750
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PATENTIN VERSION 3.1
; SEQ ID NO 18
                                                                                                                                                                                       100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 947; Conservative
                                                                                                                                                   sapiens
                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo
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APPLICANT: Schubart, Daniel
APPLICANT: Habenberger, Feter
APPLICANT: Stein-Gerlach, Matthias
APPLICANT: Bevec, Dorian
TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
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US-60-366-892-44
; Sequence 44, Application US/60366892
; GENERAL INFORMATION:
; APPLICANT: Prescott, John C.
; TITLE OF INNENTION: IDENTIFICATION OF KINASE INHIBITORS;
; FILE REFERENCE: SUNESTS. 006FR;
; CURRENT APPLICATION NUMBER: US/60/366,892
; CURRENT FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
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Matches 947; Conservative
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ORGANISM: Homo sapiens
US-60-366-892-44
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                                                                             RESULT 8

US-10-394-322A-44

Sequence 44, Application US/10394322A

GENERAL INFORMATION:
APPLICANT: SUNESIS PHARMACEUTICALS, INC.
TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REFERENCE: 39750-0006 US
CURRENT PRELICATION NUMBER: US/10/394,322A

CURRENT PILING DATE: 2002-03-20

PRIOR PILING DATE: 2002-03-21

NUMBER OF SEQ ID NOS: 70

SEQ ID NO 44

LENGTH: 947
                                                              LVTKDGQPVRYDMEVPDSGIDLQCTLAPDGSFAWSWRVKHGQLENRP
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100.0%; Pred. No. 5.5e-306;
iive 0; Mismatches 0;
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ORGANISM: Homo
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Best Local Simi
Matches 947;
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                                       DESPLGAPYVRNTPQFTKPLKEPGLGQLCFKQLGEGLRPALPRSELHKLISPLQCLNHVW
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 5.29452000122
CURRENT FILING DATE: 2002-03-01
PRIOR PAPLICATION NUMBER: US 09/747,377
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR PELING DATE: 2000-10-30
PRIOR PELING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-087-192-888
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APPLICANT: Ly, Ngoc
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APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
TITLE OF INVENTION: RENAL TRANSPLANT REJECTION
FILE REFERENCE: 5064300700
CURRENT APPLICATION NUMBER: US/60/474,850
CURRENT FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 552
SOFTWARE: Patentin version 3.1
ERGTH: 947
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AARGSRSREPSPKTEDNEGVLLTEKLKPVDYEYREEVHWATHQLRLGRGSFGEVHRMEDK 420
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                                                       RGPLCLKIASEPPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGG
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                                  QTGFQCAVKKVRLEVFRAEELMACAGLTSPRIVPLYGAVREGPWVNIFMELLEGGSLGQL
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Pred. No. 5.5e-306;
0; Mismatches 0;
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100.0%;
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Best Local Similarity 100.
Matches 947; Conservative
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US-60-474-850-493
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GENERAL INFORMATION:
TITLE OF INVENTION:
FITLE OF INVENTION:
FITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT APPLICATION NUMBER: US/10/170,205E
NUMBER OF SEQ ID NOS: 40312
SEQ ID NO 8384
LENGTH: 947 Length Indels 9 Score 5040; DB 27; Pred. No. 3.1e-305; 0; Mismatches 2; ; 0 99.8%; Query Match
Best Local Similarity 99.8
Matches 945; Conservative sapiens

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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES:
CURRENT APPLICATION NUMBER: US/60/443,566
CURRENT FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 25102
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2590
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CORGANISM: Homo sapiens
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US-60-443-566-2590
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                                   SLSQPFSLEEQEQILSCLSIDSLSLSDDSEKNPSKASQSSRDTLSSGVHSWSSQAEARSS
                                                        SWNMVLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS
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TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: PALENTIN VERSION 3.2
SEQ ID NO 9184
LENGTH: 947
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Pred. No. 3.1e-305;
0; Mismatches 2;
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Local Similarity 99.8%;
les 945; Conservative
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US-10-170-205E-9184
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Best Local S:
Matches 945
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                                                                                                                       КІННРОДОССРІРІРТИРРРУЅКІРНРРРУНРГОРИКРИРІЕЅРІСКІАСУДЗОКРІРДРИ
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GENERAL INFORMATION:
APPLICANT: CARCILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1447
CURRENT APPLICATION NUMBER: US/60/443, S66
CURRENT FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 25102
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2591
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                                                  AARGSRSREPSPXTEDNEGVLLTEKLKPVDYEYREEVHWATHQLRLGRGSFGEVHRMEDK
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Pred. No. 3.1e-305;
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Best Local Similarity 99.8%;
Matches 945; Conservative 0
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ORGANISM: Homo sapiens
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US-60-443-566-2591
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US-60-443-566-2591
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/cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
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- 2005 Compugen Ltd.
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APPLICANT: Greene, Warner C.
APPLICANT: Lin, Xin
APPLICANT: Lin, Xin
APPLICANT: Lin, Xin
APPLICANT: Glecuinas, Romas
TITLE OF INVENTION: A NOVEL INHIBITOR OF THE INFAMMATORY RESPONSE INDUCED
TITLE OF INVENTION: BY TNF-ALPHA AND IL-1
FILE REFERENCE: 30448.61915
CURRENT APPLICATION NUMBER: US09/257,703
CURRENT FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: 60/076,299
EARLIER FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PALENTIN VET. 2.0
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ORGANISM: NF-KAPPA B INDUCING KINASE (NIK)
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Patent No. 5843721
GENERAL INFORMATION:
APPLICANT: No. Lin
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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APPLICANT: Greene, Karner C.
APPLICANT: Greene, Rarner C.
APPLICANT: Greene, Romas
APPLICANT: Gleetuinas, Romas
TITLE OF INVENTION: A NOVEL INHIBITOR OF THE INFLAMMATORY RESPONSE INDUCED BY TINF-ALF
TITLE OF INVENTION: 1L-1
TITLE OF INVENTION: 1L-1
CURRENT PLICATION NUMBER: US/09/871,889A
CURRENT FILING DATE: 2001-06-01
PRIOR PLILNG DATE: 2001-06-01
PRIOR PLILNG DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-27
RIOR FILING DATE: 1998-02-27
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                                             VKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVC
                                                                                                                                                                                LQPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCNMLHMLNGCHPWTQFF
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                                                                                           QTGFQCAVKKVRLEVFRAEELMACAGLTSPRIVPLYGAVREGPWVNI FMELLEGGSLGQL
                                                                                                             RGPLCLKIASEPPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGG
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Patent No. 6645728
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Best Local S
Matches 947
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720 780

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841 SWNWYLARGRPIDIPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS 900
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                                                                                                            541 LOPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF
                                                                                                                                                                                                661 LKSPWRGEYKEPRHPPPNQANYHQTLHAQPRELSPRAPGPRPAEETTGRAPKLQPPLPPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
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Pred. No. 0;
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CLASSIFICATION: 435
PULD BATCH APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
TITLE OF INVENTION: NIK Proteins,
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY
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IBM PC compatible
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
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CLIENCE & TECHNOLOGY LAW GROUP EET: 268 BUSH STREET, SUITE 3200 C: SAN FRANCISCO E: CALIFORNIA Y: USA 941.
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Pred. No. 0;
0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: OSWAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-(
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 947 main acids
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STRANDEDNESS: single
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                                                                                                                                                                CITY: SAN
STATE: CA
COUNTRY:
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                     and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 947;
                                                                                                                                              MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-008
TELECOMMUNICATION INFORMATION:
                   Proteins, Nucleic Acids
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    APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GRG
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                             (415) 343-4341
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 947 amino acids
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Matches 946; Conservative
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                                                                                                                       ZIP: 94104
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Sequence 2, Application US/09032475 Patent No. SB54003 GENERAL INFORMATION: APPLICANT: Rothe, Mike

US-09-032-475-2

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Patent No. 6660906
GENERAL INFORMATION:
APPLICANT: TBIOLIS, Philip N.
TILE OF INVENTION: Linhibition of Tpl2 To Treat inflammatory Diseases
FILE REFERENCE: OTT-3202
CURRENT APPLICATION NUMBER: US/09/522,775A
CURRENT FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
GENERAL INFORMATION:
APPLICANT: Tsichlis, Philip N.
TITLE OF INVENTION: Inhibition of Tpl2 To Treat inflammatory Diseases
FILE REFERENCE: OTT-3202
CURRENT APPLICATION NUMBER: US/09/522,775A
CURRENT FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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US-09-522-775A-2
                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.1%; Score 360.5; DB 4; Best Local Similarity 27.9%; Pred. No. 5.3e-19; Matches 107; Conservative 66; Mismatches 127;
                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Rat Tpl2 polypeptide sequence US-09-522-775A-4
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Best Local Similarity 27.2*
Matches 116; Conservative
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US-09-522-775A-2
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                              481 VKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVC
                                                                                                                    LQPDGLGKSLLTGDY1PGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF
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                                                                                            LQPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REPERENCE: 59.US2.REG
CURRENT APPLICATION WHBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-26
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98.9%; Pred. No. 6.4e-29;
iive 0; Mismatches 1
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; Patent No. 6783961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6660
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Matches 93; Conservative
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ORGANISM: Homo sapiens
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US-09-513-999C-6660
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US-09-513-999C-6660
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US-09-522-775A-4
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                                                                                                                                                                                                                                                                            PVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGGLKSPWRGEYKEPR 673
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                                                      GLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVCLQPDGLGKSLLTGDYIP----
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APPLICANT: CADUS PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREFOR
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: CPL-085CPC
CURRENT APPLICATION NUMBER: US/09/423,890
CURRENT APPLICATION NUMBER: US/09/163
PRIOR APPLICATION NUMBER: USSN 60/078,153
PRIOR FILING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: USSN 60/099,165
PRIOR SED ID NOS: 38
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN VET. 2.0
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                                                                                         248 GLDFLHSKKVIHHDIKPSNIVFMS--TKAVLVDFGLSVQMTED-
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Pred. No. 3.1e-18;
2; Mismatches 276;
                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09423890 Patent No. 6312934
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Similarity 23.8%;
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ORGANISM: Homo sapiens
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Best Local Simil
Matches 158; (
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Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FEBSESEQ for Windows Version 4.0

SEQ ID NO 10456
                                                               TVEDLL--AFANHISNTAKHFY------GORPOR-----SGILLNMVITPONG 119
                                                                                                                                                           442 MACAGLISPRIVPLYGAVREGPWVNIFMELLEGGSLGQLVKEQGCLPEDRALYYLGQALE 501
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           SVEEYLVHALQGSVSSSQAHSLTSLAKTWAARGSRSREPSPKTEDNEGVLLTEKLKPVDY 391
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27.2%; Pred. No. 5.9e-19;
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Best Local Similarity 27.23
Matches 116; Conservative
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58 SLQAVAPTSCLENSSLEHTVHREKTGKGLSATRLSASSEDISDRLAGVSVGLPSSTTTEQ 117
                                                          118 PKPAVQTKGRPHSQCLNSSPLSHA--QLMFPAPSAPCSSAPSVP---DIS-----KHR 165
                                                                                                               PQFTKPLKEPGLGQLCFKQLGEGLRPALPRSELHKLISPLQ--CLNHVWKLHHPQDGGPL 251
                                                                                                                                                                                                                            ---SPVFTQSRPPSSNIHRPKPSRPVP-----GSTSKLGDATKSSMTLDLGSA 248
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APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield
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APPLICATION NUMBER: US/08/472,934
FILING DATE: 06-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release ***
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60 State Street
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CITY: Boston
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US-08-472-934-2
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                                                                                                                                                                                          24;
                                                                                                                                                                     GGSLGQLVXEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVXADNVLLSSDGSHAALC 533
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                 KTEDNEGVLLTEKLKP-----VDYEYREEVHWATHQLRLGRGSFGEVHRMEDKQTGF
                                                                                          QCAVKKV------RLEVFRA--EELMACAGLTSPRIVPLYGAVREGPWVNIFMELLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Johnson Ph.D., Gary L.
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS & MCINTOSH, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.25
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1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Ve CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,254
FILING DATE: 19930415
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOVATIK ESQ., JOSEPH E.
REGISTRATION NUMBER: 2879-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5405941
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amino acid
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Best Local Similarity 23.63
Matches 157; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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1297 VFRTT 1301
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STREET: 1,0
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US-08-049-254-2
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77 AISIIAQAECENSQEFSPTFSERIFIAGSKQYSQSESLDQIPNNVAHATEGKWARVCWKG 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 PKPAVQTKGRPHSQCLNSSPLSHA--QLMFPAPSAPCSSAPSVP---DIS-----KHR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 PQAFVPCKIPS-----RDSDQL 202
                                                                 594 HPWTQFFRG---PLCLKIASE------PPPVREIPPSCAPLTAQ--AIQEGLRKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 PQFTKPLKEPGLGQLCFKQLGEGLRPALPRSELHKLISPLQ--CLNHVWKLHHPQDGGPL
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                                                                                                                                                                                                                                                                                                                                                               GARY L. METHOD AND PRODUCT FOR REGULATING CELL
                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08323460A
Patent No. 5854043
GENERAL INFORMATION:
APPLICANT JOHNSON, GARY L.
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING C
TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS & MCINTOSH
STREET: 1700 LINCOLN STREET, SUITE 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/323,460A
FILING DATE: 14-OCT-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.0%; Score 355.5; DB 2; Best Local Similarity 23.6%; Pred. No. 2.1e-18; Matches 157; Conservative 81; Mismatches 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 14-APR-1993
ATTONNEY/AGENT INFORMATION:
NAME: KOVARIK, JOSEPH E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-1-1
TELEPHONE: 303/863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          672 amino acids
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MEDIUM TYPE: Floppy
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US-08-323-460A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 ---SPVFTOSRPPPSSNIHRPKPSRPVP------GSTSKLGDATKSSMTLDLGSA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 FKSEVAVLSPEKAENDDTYKDDVNHNQKCKEKMEAEEEEALAIAMAMSASQDALPIVPQL 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KHR 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 149;
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                                                                                                                                                                                                                                                                                                                              FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GAULIO A. DeCORLI, Jr. ESQ.
RELISTRATION NUMBER: 31,503
REPERENCE/DOCKET NUMBER: CPI-004DVCP2
TELECOMMUNICATION INFORMATION:
             FILING DATE: 15-May-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/354,516
FILING DATE: 21-FEB-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5,405,941
FILING DATE: 15-Apr-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,460
FILING DATE: 14-Occ-1994
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
FILLING DATE: 14-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
US 08/440,421
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID 0. 2.
SEQUENCE CHARACTERISTICS:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                    Query Match
7.0%; Score 355.5; DB 2;
Best Local Similarity 23.6%; Pred. No. 2.1e-18;
Matches 157; Conservative 81; Mismatches 278;
                            NAME: KARA, Catherine ...

REGISTRATION NUMBER: P41,106
REGISTRATION NUMBER: CPI-004CN3
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08461145C; Patent No. 6074861
                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-461-146C-2
                                                                                                                                                                                                                    amino acid
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TOPOLOGY:
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US-08-461-145C-2
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---GSTSKLGDATKSSMTLDLGSA 248
                                     -----PKPLPGPH-----LEPSC-LSRGAHEKFSVEEYLVHALQGSVSS-- 347
                                                                                                                   --SQAHSLTSLAKTWAARGSRSR---EPSP 372
                                                                                                                                                         309 FKSEVAVLSPEKAENDDTYKDDVNHNQKCKEKMEAEEEEALAIAMAMSASQDALPIVPQL 368
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                                                                                                                                                                                                                                                                                                     GGSLGQLVKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALC 533
                                                                                                                                                                                                                                                                                                                                                                                    DEGHAVCLOPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGC 593
                                                                                                                                                                                              KTEDNEGVLLTEKLKP-----VDYBYREEVHWATHQLRLGRGSFGEVHRMEDKQTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    594 HPWTQFFRG---PLCLKIASE------PPPVREIPPSCAPLTAQ--AIQEGLRKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOR REGULATING MEKK PROTEIN ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,146C
FILING DATE: 05-JUN-1995
CLASSIFFORMATON
---SPVFTQSRPPSSNIHRPKPSRPVP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/354,516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08461146C
Patent No. 5981265
GENERAL INFORMATION:
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METHODS
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 00
FILING DATE: 14-0CT-1994
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COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: JOHNSON,
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  639 IHRVS 643
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VFRTT 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 PKPAVQTKGRPHSQCLNSSPLSHA--QLMFPAPSAPCSSAPSVP---DIS------KHR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 KR---RSKARKKRKKKSSKSLAHAGVALAKPLPRTPEQESCTIPVQEDESPLGAPYVRNT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --CVDS----PKPLPGPH----LEPSC-LSRGAHEKFSVEEYLVHALQGSVSS-- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 POFTKPLKEPGLGQLCFKQLGEGLRPALPRSELHKLISPLQ--CLNHVWKLHHPQDGGPL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SPVFTQSRPPPSSNIHRPKPSRPVP------GSTSKLGDATKSSMTLDLGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 672;
                                                                                                                       STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenting Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.0%; Score 355.5; DB 3; Best Local Similarity 23.6%; Pred. No. 2.1e-18; Matches 157; Conservative 81; Mismatches 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kara, Catherine J.
REGISTRATION NUMBER: P-41,106
REFERENCE/DOCKET NUMBER: CPI-004CN1
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
ITELEPHONE: (617) 227-7401
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: NOVEL MEKK PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield, LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 5-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 11-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,460
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 15-APR-1994
PRIOR APPLICATION DATA:
FILING DATE: 15-APR-1994
PRIOR APPLICATION DATA:
FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: KATA: CATCHING J.
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,145C
FILING DATE: 5-JUNE-1995
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amino acid
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MOLECULE TYPE: protein
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SQAHSLTSLAKTWAARGSRSR---EPSP 372
                                            309 FKSEVAVLSPEKAENDDTYKDDVNHNOKCKEKMEAEEEEALAIAMAMSASQDALPIVPQL 368
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                                                                                                                                                                                                                       428 LMAVKQVTYVRNTSSEQEEVVEALREEIRMMGHLNHPNIIRMLGATCEKSNYNLFIEWMA 487
                                                                                                                                                                                                                                                                                                                488 GGSVAHLLSKYGAFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQRLRIA 547
                                                                                                                                                                                                                                                                                                                                                                                                           594 HPWTQFFRG---PLCLKIASE-----PPPVREIPPSCAPLTAQ--AIQEGLRKEP 638
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                                                                                                                              DFGHAVCLQPDGLGKSLLTGDYIPGTETHWAPEVVLGRSCDAKVDVWSSCCMMLHMLNGC
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Sequence Sequence

Sequence 83, Appl Sequence 856, Appl Sequence 876, Appl Sequence 876, Appl Sequence 183, Appl Sequence 18, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 22, Appl Sequence 24, Appl Sequence 24, Appl Sequence 25, Appl Sequence 27, Appl Sequence 28, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 199, Appli Sequence 199, Appli Sequence 199, Appli Sequence 199, Appli

US-10-218-779-98
US-00-964-956-72
US-00-054-956-72
US-10-042-865-83-99
US-00-072-012-856
US-10-072-012-856
US-10-072-012-856
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US-10-287-226-230
US-10-287-226-330
US-10-287-226-330
US-10-287-226-330
US-10-287-226-330

Sequence Sequence Sequence Sequence

ALIGNMENTS

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APPLICANT: Greene, Warner C.
APPLICANT: Greene, Warner C.
APPLICANT: Greene, Warner C.
APPLICANT: Greene, Marner C.
TITLE OF INVENTION: BY TNF-ALPHA AND IL-1
FILE REFERENCE: 30448-610510
CURRENT APPLICATION NUMBER: 05/209/871,889
CURRENT APPLICATION NUMBER: 05/257,703
PRIOR APPLICATION NUMBER: 06/256,703
PRIOR APPLICATION NUMBER: 06/256,29
PRIOR APPLICATION NUMBER: 60/076,299
PRIOR PILING DATE: 1999-02-25
PRIOR PILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2:0
SEC ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VITKGTAKEGSEAGPAAISIIAQAECENSQEFSPTFSERIFIAGSKQYSQSESLDQIPNN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAVMEMACPGAPGSAVGQQKELPKPKEKTPPLGKKQSSVYKLEAVEKSPVFCGKWEILND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: NF-KAPPA B INDUCING KINASE (NIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09871889; Patent No. US20020042499A1; GENERAL INFORMATION:
LENGTH: 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-871-889-1
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Sequence 44, Appl
Sequence 888, App
Sequence 8758, Appl
Sequence 31, Appl
Sequence 102, Appl
Sequence 102, Appl
Sequence 160, Appl
Sequence 160, Appl
Sequence 160, Appl
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Sequence 150, App
Sequence 98, Appl
                                                                                                                                             June .7, 2005, 12:02:31; Search time 119.819 Seconds (without alignments) 2846.907 Million cell updates/sec
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                                                                                                                                                                                                                                                                                    1 MAVMEMACPGAPGSAVGQQK......PDGSFAWSWRVKHGQLENRP 947
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1: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{Pubcomb} \text{Pubcomb} \( 1\) \\( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{Pubcada} \( 1\) \text{Pubcada} \( 1\) \text{Pubcomb} \( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\( 1\) \\
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-394-322A-44
US-10-087-192-888
US-10-087-192-8885
US-10-087-192-885
US-09-976-782-31
US-10-042-865-102
US-10-052-648A-41
US-10-074-978A-150
US-10-074-978A-150
US-10-087-684-98
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Pred. No. 1.8e-286;
Mismatches 0;
  CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION WUMBER: 60/240,750
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 947
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APPLICANT: Schubart, Daniel
APPLICANT: Schubart, Daniel
APPLICANT: Stein-Gerlach, Matthias
APPLICANT: Bevec, Dorian
TITLE OF INVENTION: Cellular Kinases Involved
TITLE OF INVENTION: Inhibition
FILE REFERENCE: AXM-004.1 US
CURRENT APPLICATION NUMBER: US/09/981,397A
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Publication No. US20030082519A1
GENERAL INFORMATION:
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT PLILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: EastSEQ for Windows Version 4.0
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99.8%; Pred. No. 9.2e-286;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 888, Application US/10087192; Publication No. US20020182586A1; GENERAL INFORMATION:
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Best Local Similarity 99.8°
Matches 945; Conservative
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; ORGANISM: Homo sapiens
US-10-087-192-888
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                                               RESULT 3
US-10-394-322A-44

Sequence 44, Application US/10394322A

Publication No. US20030232391A1

GENERAL INFORMATION:
APPLICANT: SUNESIS PHARMACEUTICALS, INC.
TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REFERENCE: 39750-0006 US
CURRENT APPLICATION NUMBER: US 60/366,892
PRIOR PILLIATION NUMBER: US 60/366,892

PRIOR PILLIATION NUMBER: 2003-03-21

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PASTESQ for Windows Version 4.0

LENGTH: 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 947; Conservative
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US-10-394-322A-44
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Sequence 57758, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
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ORGANISM: Glycine max
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361 AARGSRSREPSPKTEDNEGVL/LIEKL/KPVDYEYREEVHWATHQLRLGRGSFGEVHRMEDK
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| Publication No. US20020182586A1
| GENERAL INFORMATION:
| APPLICANT: MOTATION:
| APPLICANT: Engelhard, Eric K. |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR |
| TITLE OF INVENTION: ACACER |
| FILE REFERENCE: 52945200122 |
| CURRENT FILING DATE: 2002-03-01 |
| PRIOR FILING DATE: 2000-12-22 |
| PRIOR FILING DATE: 2001-13-02 |
| PRIOR FILING DATE: 2001-03-01 |
| PRIOR FILING DATE: 2001-03-02 |
| PRIOR FILING DATE: 2001-03-05 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 885 |
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Best Local Similarity 86.1%
Matches 466; Conservative
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US-10-087-192-885
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Sourid K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 57758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.3%; Score 369; DB 15; Length 891; 23.4%; Pred. No. 4.5e-13; artive 107; Mismatches 353; Indels 27;
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US-10-425-114-57758
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GRGSFGEVHRMEDKQTGFQCAVKKVRLEVFRAEELMACAGLTSPRIVPLYGAVREGPWVN 466

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OTHER INFORMATION: Description of Artificial Sequence:Consensus; OTHER INFORMATION: sequence
US-09-976-782-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.3%; Score 367; DB 10; Best Local Similarity 37.9%; Pred. No. 1.3e-13; Matches 97; Conservative 37; Mismatches 94;
PRIOR APPLICATION NUMBER: 60/240,662
PRIOR FILING DATE: 2000-10-16
PRIOR PELLING DATE: 2001-01-18
PRIOR PELLING DATE: 2001-01-18
PRIOR PELLING DATE: 2001-01-16
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APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
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234 KKLLVKDPEKRLTAEE 249
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Shenoy, Suresh G
Spytek, Kimberly
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APPLICANT:
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APPLICANT:
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                                             80 SFIDRPHAQPLPLPGLHPSSVGRVDSEISISSKSRLEKVSKPLSFLTLPTPGCIRCRPNP 139
                                                                                                                                                                             140 ADLIGOMVTASVFSDCSADSDEPADSHNRSPLAIDCETGTRTAAGSPSSLMLKDQPPAVS 199
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                                                                                                                                                                                                                                                                                                                      200 QLNSTGVKKPG-----NILSNHMSSTSPKRR-----PLR--NHVPNLQVPPHGA---- 241
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                                                                                                                                                                                                                                                        PL----KEPGLGQLCFKQLGEGLRPALPRSELHKLISPLQCLNHVWKLHHPQDGGPLPL
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Sequence 31, Application US/09976782

Publication No. US20030190715A1

GENERAL INFORMATION:
      135 KGKRRSKAR-----
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67 FEDDDXLYLVWEYCEGGDLFDLLKKRGRLSEDEARFYARQILSALEYLHSQGIIHRDLKP 126
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                                                                                                       459 VREGPWVNIFWELLEGGSLGQLVKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKA
                                                                                                                                                                                                                                               DNVLLSSDGSHAALCDFGHAVCLQPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVD
                                                                                                                                                                                                                                                                                                                               VWSSCCMMLHMLNGCHPWTQFFRG-----PLCLKIASEPPVREIPP---SCAPLTAQAI
                                      28;
Length 250;
                                    Indels
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Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
Taylor, Velizar T
Miller, Charles E
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APPLICANT:
APPLICANT:
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MacDougall, John R
Mehraban, Fuad
Ellerman, Karen
Gerlach, Valerie
Gunther, Erik
Kekuda, Ramesh
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Matches 97; Conserva
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                                                                                                                                                                                                                                                                                                                               ## APPLICANT: Peyman, Jounna | APPLICANT: Seyman, Jounna | APPLICANT: Smithson, Glennda | APPLICANT: Gunther, Erik | APPLICANT: Gunther, Erik | APPLICANT: Gunther, Brid | APPLICANT: Stone, David | TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of TITLE OF INVENTION: Using the Same | FILE REFERENCE: 21402-537 | CURRENT APPLICATION NUMBER: 60/260,417 | PRIOR APPLICATION NUMBER: 60/260,417 | PRIOR APPLICATION NUMBER: 60/260,831 | PRIOR FILING DATE: 2001-01-00 | PRIOR PRIOR DATE: 2001-01-00 | PRIOR PRIOR DATE: 2001-03-09 | PRIOR PRIOR DATE: 2001-03-09 | PRIOR PRIOR DATE: 2001-03-09 | PRIOR PRIOR DATE: 2001-03-09 | PRIOR PRIOR DATE: 2001-04-18 | PRIOR PRIOR DATE: 2001-04-18 | PRIOR PRIOR DATE: 2001-04-18 | NUMBER OF SEQ ID NOS: 264 | SEQ ID NO 102 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH: 250 | LENGTH
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Pred. No. 1.3e-13;
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US-10-052-648A-41
i Sequence 41, Application US/10052648A
j Publication No. US20040005558A1
i GENERAL INFORMATION:
APPLICANT: Anderson, David
j APPLICANT: Casman, Stacie
j APPLICANT: Colman, Steven
j APPLICANT: Edinger, Shlomit R.
               Boldog, Ference L
Grosse, William M
Alsobrook II, John P
Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
Bllerman, Karen
MacDougall, John
Malyankar, Uriel M
Millet, Isabelle
Peyman, John
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US-10-042-865-102
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Suches, Daylul U.
APPLICANT: Serbusen, Bryan D.
TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: UNBER: 00/210-05.0
CURRENT PILING DATE: 2001-01-20
PRIOR APPLICATION NUMBER: 60/220,454
PRIOR APPLICATION NUMBER: 60/220,20
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR PELIOR OFFE: 2001-03-02
PRIOR PELIOR OFFE: 2001-03-03
PRIOR PELIOR OFFE: 2001-03-03
PRIOR PELIOR OFFE: 2001-03-03
PRIOR PELIOR OFFE: 2001-03-03
PRIOR PELIOR DATE: 2001-03-03
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PRIOR PELIOR DATE: 2001-03-03
PRIOR PELIOR OFFE: 2001-03-03
PRIOR PELIOR DATE: 2001-03-03
PRIOR PELIOR PELIOR NUMBER: 60/265,517
PRIOR PELIOR DATE: 2001-03-03
PRIOR PELIOR DATE: 2001-03-03
PRIOR PELIOR PELIOR NUMBER: 60/265,517
PRIOR PELIOR DATE: 2001-03-03
PRIOR PELIOR DATE: 2001-03-03
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SOFTWARE: PatentIn Ver. 2.1
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Patturajan, Meera
Rothenberg, Mark
Shimkets, Richard
Smithson, Glennda
Spytek, Kimberly A.
Stone, David J.
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ORGANISM: Artificial Sequence
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406 LGRGSFGEVHRMEDKQTGFQCAVKKVRLEVFRAE-----ELMACAGLTSPRIVPLYGA 458
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                                                                                                                                                                                                                             459 VREGPWVNIFMELLEGGSLGOLVKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKA
                                                                                                                                                                                                                                                                                                                                                                                                 519 DNVLLSSDGSHAALCDFGHAVCLQPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVD
                                                                                                                                         Indels 28; Gaps
; OTHER INFORMATION: Serine/Threonine protein kinases domain sequence US-10-074-978A-160
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-269
                                                                                       Length 252;
                                                                                       Query Match 7.3%; Score 367; DB 15; Best Local Similarity 37.9%; Pred. No. 1.3e-13; Matches 97; Conservative 37; Mismatches 94;
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Shimkets, Richard A
Lupier Jr, Raymond J
Moore, No. US20040010119Allle
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5. US20040010119A1
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Guo, Xiaojia (Sasha)
Fernandes, Elma
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234 KKLLVKDPEKRLTAEE 249
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Malyankar, Uriel M
Gusev, Vladimir
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Millet, Isabelle
Peyman, John
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Gunther, Erik
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Rastelli, Luca
Mezes, Peter S
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Heyes, Melvin P
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Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Casman, Stacie
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Publication No. US20
GENERAL INFORMATION:
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERBNCE: 21402-269
CURRENT APPLICATION NUMBER: US/10/074,978A
CURRENT PILING DATE: 2003-01-07
FRIOR APPLICATION NUMBER: 60/286,221
FRIOR APPLICATION NUMBER: 60/312,284
FRIOR APPLICATION NUMBER: 60/312,284
FRIOR APPLICATION NUMBER: 60/312,284
FRIOR APPLICATION NUMBER: 60/212,284
FRIOR APPLICATION NUMBER: 60/268,496
FRIOR FILING DATE: 2001-02-13
FRIOR APPLICATION NUMBER: 60/26,703
FRIOR FILING DATE: 2001-10-11
FRIOR PILING DATE: 2001-10-13
FRIOR PILING DATE: 2001-10-14
FRIOR FILING DATE: 2001-10-16
FRIOR FILING DATE: 2001-11-21
FRIOR APPLICATION NUMBER: 60/212,127
FRIOR PILING DATE: 2001-11-21
FRIOR APPLICATION NUMBER: 60/280,899
FRIOR FILING DATE: 2001-04-02
FRIOR FILING DATE: 2001-04-02
FRIOR FILING DATE: 2001-04-02
FRIOR FILING DATE: 2001-08-08
FRIOR FILING DATE: 2001-08-08
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NUMBER OF SEQ ID NOS: 547
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 160
LENGTH: 252
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: S_TKC,
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Pena, Carol B A
Shimkets, Richard A
Taupier Jr. Raymond J
Moore, No. US20040010119Allle
Schengy, Suresh
Edinger, Shomit
Gunther, Erik
                                                                                                                                         Sequence 160, Application US/10074978A
Publication No. US20040010119A1
                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Leite, Mario
APPLICANT: Spytek, Kimberly A
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Fernandes, Elma
             229 KKLLVKDPEKRLTAEE 244
                                                                                                                                                                                                                                                                                                                       Li, Li
Kekuda, Ramesh
Liu, Xiahong
Casman, Stacie
Boldog, Ferenc
Patturajan, Meera
Blalock, Angela
Ballinger, Robert
Vernet, Corine
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Malyankar, Uriel M
Gusev, Vladimir
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Millet, Isabelle
Peyman, John
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Heyes, Melvin P
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APPLICANT: Zerhusen, Bryan D.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Guo, Xiaojia
APPLICANT: Miller, Charles E.
APPLICANT: Gangolii, Esha A.
TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                    Rastelli, Luca
Tchernev, Velizar T.
Vernet, Corine A.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 ENILLDSDG-HVKLADFGLAKQLDSGG---TLLT--TFVGTPEYMAPEVLLGKGYGKAVD 180
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PRIOR PILING DATE: 2001-08-41

PRIOR APPLICATION NUMBER: 60/268,496

PRIOR PILING DATE: 2001-08-13

PRIOR PELING DATE: 2001-02-13

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2001-03-16

PRIOR PILING DATE: 2001-10-18

PRIOR PILING DATE: 2001-10-18

PRIOR APPLICATION NUMBER: 60/320,127

PRIOR APPLICATION NUMBER: 60/280,899

PRIOR PILING DATE: 2001-04-02

PRIOR PILING DATE: 2001-08-08

PRIOR PILING DATE: 2001-08-08

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PRIOR PILING DATE: 2001-08-08

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Publication No. US20040029116A1
GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit R.
APPLICANT: MacDougall, John R.
APPLICANT: Millet, Isabelle
APPLICANT: Ellerman, Karen
APPLICANT: Stone, David J.
APPLICANT: Grosse, William M.
APPLICANT: Lepley, Denise M.
APPLICANT: Lepley, Denise M.
60/312,284
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Casman, Stacie, J.
Spytek, Kimberly A.
Boldog, Ferenc L.
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Padigaru, Muralidhara
Mishra, Vishnu
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234 KKLLVKDPEKRLTAEE 249
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 37.9*
Matches 97; Conservative
APPLICATION NUMBER:
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US-10-087-684-98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artifical Sequence: US-10-087-684-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.3%; Score 367; DB 15;
37.9%; Pred. No. 1.4e-13;
tive 37; Mismatches 94;
THE REPERENCE: 21402-214 CIP
CURRENT APPLICATION NUMBER: US/10/087,684
CURRENT FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: 60/253,834
PRIOR PILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/264,180
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2001-01-25
PRIOR PELING DATE: 2001-01-25
PRIOR PELING DATE: 2001-01-25
PRIOR PELING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/244,194
PRIOR PILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/313,656
PRIOR APPLICATION NUMBER: 60/313,656
PRIOR PELING DATE: 2001-08-20
PRIOR PLING DATE: 2001-08-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stone, David
Gerlach, Valerie
Grosse, William
Alsobrook II, John
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KKLLVKDPEKRLTAEE 248
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ORGANISM: Artificial Sequence
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Best Local Similarity 37.9*
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Verner, Colling
APPLICANT: Zerhusen, Bryan
APPLICANT: Malyankar, Uriel
APPLICANT: Malyankar, Uriel
APPLICANT: Malyankar, Uriel
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Baha
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REPREBRENCE: 21402-214
CURRENT APPLICATION NUMBER: US/10/218,779
CURRENT PILING DATE: 2000-11-29
FRIOR FILING DATE: 2000-11-29
FRIOR FILING DATE: 2000-11-30
FRIOR PRLICATION NUMBER: 60/250,-926
FRIOR FILING DATE: 2001-01-25
FRIOR FILING DATE: 2001-01-25
FRIOR FILING DATE: 2001-01-25
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                                                                                                                                                                                                           Padigaru, Muralidhara
Mishra, Vishnu
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233 KKLLVKDPEKRLTAEE 248
                                                            Catherine
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Rastelli, Luca
Tchernev, Velizar
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Shenoy, Suresh
                                                     Burgess, Catherin
Casman, Stacie
Spytek, Kimberly
Boldog, Ferenc
Denise
Daniel
                                                                                                                                                                                                                                       Vishnu
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ORGANISM: Homo sapiens
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US-09-964-956-72
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APPLICANT:
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Sequence 72, Application US/09964956
Publication No. US20040041926A1
GENERAL INFORMATION:
APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R

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APPLICANT: Spytek, Kimberly A
APPLICANT: Leach, Martin D
APPLICANT: Shimkers, Richard A
TITLE OF INVENTION: No. US20040043926Alel Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 FEDDDKLYLVMEYCEGGDLFDLLKKRGRLSEDEARFYARQILSALEYLHSGGIIHRDLKP 126
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OTHER INFORMATION: Serine/Threoniune protein kinase Consensus

OTHER INFORMATION: Sequence
US-09-964-956-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.3%; Score 367; DB 11; Length 256; Best Local Similarity 37.9%; Pred. No. 1.4e-13; Matches 97; Conservative 37; Mismatches 94; Indels 26
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CURRENT PEDLICATION NUMBER: 05/9564,956

CURRENT FILING DATE: 2001-09-26

PRIOR FLILING DATE: 2001-09-27

PRIOR FLILING DATE: 2000-09-27

PRIOR FLILING DATE: 2000-09-27

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                                                                                                             Lepley, Denise M
Burgess, Catherine E
Padigaru, Muralidhara
Kekuda, Ramesh
Spytek, Kimberly A
Leach, Martin D
Ellerman, Karen
Grosse, William M
Alsobrook II, John P
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ORGANISM: Artificial Sequence
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APPLICANT:
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519 DNVLLSSDGSHAALCDFGHAVCLQPDGLGKSLLIGDYIPGTETHMAPEVVLGRSCDAKVD 578
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---ELMACAGLTSPRIVPLYGA 458
                               406 LGRGSFGEVHRMEDKOTGFOCAVKKVRLEVFRAE--
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Job time : 121.819 secs
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TITLE OF INVENTION: No. US20040024181Alel Human Proteins, Polymucleotides Encoding Tit
TITLE OF INVENTION: No. US20040024181Alel Human Proteins, Polymucleotides Encoding Tit
TITLE OF INVENTION: Methods of Using the Same
FILE REFRENCE: 21402-191
CURRENT APPLICATION NUMBER: US/10/055,569A
CURRENT FILING DATE: 2000-10-26
PRIOR PAPLICATION NUMBER: 60/243,520
PRIOR PELING DATE: 2000-10-26
PRIOR PELING DATE: 2000-10-26
PRIOR PELING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/243,681
PRIOR APPLICATION NUMBER: 60/243,681
PRIOR APPLICATION NUMBER: 60/243,681
PRIOR APPLICATION NUMBER: 60/244,443
PRIOR PILING DATE: 2000-10-31
PRIOR PELING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: 60/244,443
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-02
PRIOR PILING DATE: 2000-11-02
PRIOR PILING DATE: 2000-11-02
PRIOR PILING DATE: 2000-11-02
PRIOR PILING DATE: 2000-11-02
PRIOR PILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: 60/245,335
PRIOR PILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: 60/245,335
PRIOR PILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: 60/245,335
PRIOR PILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: 60/245,335
PRIOR PILING DATE: 2000-11-02
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           630
                                                       181 IWSLGVILYELLTGKPP----PPGDDQLLALFKKIGKPPPP----PPPFEWKISPEAKDLI 233
              579 VWSSCCMMLHMLNGCHPWTQFFRG----PLCLKIASEPPPVREIPP---SCAPLTAQAI
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                                                                                                                                                                                                                                                                                                                   Sequence 99, Application US/10055569A Publication No. US20040024181A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ellerman, Karen
Padigaru, Muralidhara
Taupier Jr., Raymond J
Anderson, David W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shenoy, Suresh
Mishra, Vishnu S
Furtak, Katezyna
Gerlach, Valerie L
Edinger, Shlomit
Malyanker, Uriel
Stone, David
                                                                                                                                                               :: | |:| |:| |
234 KKLLVKDPEKRLTAEE 249
                                                                                                                            631 QEGLRKEPIHRVSAAE 646
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gangolli, Esha A
APPLICANT: Spytek, Kimberly A
APPLICANT: Gilbert, Jennifer
APPLICANT: Casman, Stacie
APPLICANT: Blalock, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Millet, Isabelle
Smithson, Glennda
Gunther, Erik
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SEQ ID NO 99
LENGTH: 256
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Best Local Similarity 37.9
Matches 97; Conservative
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Vernet, (
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US-10-055-569A-99
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APPLICANT:
APPLICANT:
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APPLICANT:
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Sequence 6464, Ap Sequence 20, Appl Sequence 4731, Ap Sequence 1232, Ap Sequence 11, Appl Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 27184, A Sequence 27184, A Sequence 27184,

Sequence 182401, Sequence 12212,

Sequence Sequence Sequence

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CCCCTCTCACAGCCCAGGCCATCCAAGAGGGGCTGAGGAAAGAGCCCATCCACCGCGTGT 1927
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08887518
Fatent No. 5843721
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 3156;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                        US-09-902-540-1232
US-09-499-884-11
US-08-703-809-9
US-08-703-808-9
US-08-7703-808-9
US-08-777-108A-9
US-09-211-9
US-09-532-803-3
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US-09-949-016-12212
                             -09-902-540-4731 ·
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94.8%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3156 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 94.8
Matches 1241, Conservative
                               1521
28462
38462
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3299
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6019
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STRANDEDNESS: double
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요
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Sequence 8, Appli
Sequence 1655, A
Sequence 14, Appl
Sequence 14, Appl
Sequence 1
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Sequence 2, Appli
Sequence 2, Appli
Sequence 9023, Ap
Sequence 9108, Ap
Sequence 9108, Ap
Sequence 8985, Ap
Patent No. 5223425
Patent No. 5223425
Patent No. 5223425
Sequence 2, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3456, Ap
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8976, Ap
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14842.245 Million cell updates/sec
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Sequence 6
Sequence 6
                                                                                                          June 8, 2005, 23:21:54 ; Search time 290.053 Seconds
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/RECOMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
              5.1.6
Compugen Ltd
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US-09-023-475-1
US-09-032-475-1
US-09-257-703-2
US-09-257-703-2
US-09-252-991A-9108
US-09-252-991A-8985
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US-08-459-701-8
US-08-460-298-8
US-08-459-174-8
US-09-621-976-16656
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US-09-343-733A-1
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US-09-252-991A-6166
US-10-101-464A-422
US-09-252-991A-6010
US-09-252-991A-629
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US-09-103-840A-1
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              GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                          nucleic search, using sw model
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5223425-7
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5223425-3
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Score

Result o N 9,2,6,6,6 3399.

Post-processing:

Database

seq seq

Minimum DB Maximum DB

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

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ACCAGACCTCCATGCCCAGCGAGAGCTTTCGCCAAGGGCCCCAGGGCCCCGGCCAG 240
2999 GCAAGCAGAATGCCTCCCAGGATTTCACACCTGAGCCCTGCCCCAC-----CCTGCTGA 3052
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                                            AAACAYTNCCGCCACGTGAAGAGACAGAAGGAGGATGGNCAGGAGTTNNACCTYGGGGAA
                                                                 CCCCTCTCACAGCCCAGGCCATCCAAGAGGGGCTGAGGAAAGAGCCCCATCCACCGCGTGT
                                                                                                                       Length 3156
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Roche, Mike
APPLICANT: Roche, Mike
APPLICANT: Roche, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1133.4;
Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIPTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSNAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFRENCE/DOCKET NUMBER: 197-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS: 1
                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/09023321; Patent No. 5844073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDDESS:
STRANDEDDESS: double
TOPOLOGY: linear
MOLECTUR TYPE: CDNA
US-09-023-321-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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94.8%;
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Best Local Similarity 94.8
Matches 1241; Conservative
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            CCAAAGACGGGCAGCCTGTTCGCTACGACATGGAGGTGCCAGACTCGGGCATCGACCTGC
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                              Sequence 1, Application US/09032475
Patent No. 5854003
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESSE:
ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
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94.8%; Pred. No. 0;
iive 4; Mismatches
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APPLICATION NUMBER: US/09/032,475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-008
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPANE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3156 base pairs
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Best Local Similarity 94.8
Matches 1241; Conservative
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CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
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STRANDEDNESS: double
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APPLICANT: Gelezuinas, Romas
TITLE OF INVENTION: A NOVEL INHIBITOR OF THE INFAMMATORY RESPONSE INDUCED
TITLE OF INVENTION: BY THE ALBHA AND IL-1
FILE REFERENCE: 30448 LUSJU
CURRENT APPLICATION NUMBER: US/09/257,703
CURRENT FILING DATE: 1999-02-25
BARLIER PAPLICATION NUMBER: 60/076,299
EARLIER FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 2.2
LENGTH: 2844
                                                                                                                                                                                                                                                                                                                                                                    1928 CTGCAGCGGAGCTGGGAAGGTGAAGCCGGCCACTACAGAGAAGTGGGAGGTCTGAAGA
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tive 0; Mismatches 0;
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US-09-257-703-2
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Best Local S:
Matches 977
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Sequence 2, Application US/09257703
Patent No. 6255538
GENERAL INFORMATION.
APPLICANT: Greene, Warner C.
APPLICANT: Lin, Xin

RESULT 4 US-09-257-703-2

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Sequence 9023, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Fubenfield et al.
APPLICANT: Marc J. Fubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PLING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PLING DATE: 1998-07-27
SEQ ID NOS: 33142
SEQ ID NOS: 33142
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Pred. No. 0.099;
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Best Local Similarity 54.5%;
Matches 85; Conservative
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TITLE OF INVENTION: A NOVEL INHIBITOR OF THE INFLAMMATORY RESPONSE INDUCED BY THF-ALE
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ORGANISM: NF-KAPPA B INDUCING KINASE (NIK)
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;BARRY M.;WHITE, TYLER R.
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
;D ACTIVITY
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Pred. No. 0.43;
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Pred. No. 0.43;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/277,963
FILING DATE: 30-NOV-1988
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 34,203
FILING DATE: 02-APR-1987
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/277,963
FILING DATE: 30-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,203
FILING DATE: 02-APR-1987
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;Patent No. 5223425
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9108
LENGTH: 1359
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Sequence 8985, Application US/09252991A

Sequence 8985, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27
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Pred. No. 0.15;
0; Mismatches 71; Indels 0;
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1.6%; Score 42.4; DB 4;
Best Local Similarity 54.5%; Pred. No. 0.13;
Matches 85; Conservative 0; Mismatches 71;
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Patent No. 6551795
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9108
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US-09-252-991A-8985
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Best Local Similarity 54.5%;
Matches 85; Conservative
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SEQ ID NO 8985
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744 GAACACCTGCACATCCGGGAGTTCCACCGGGTCAAAGTGGGAGACATCGCCACTGGCATC 803

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CACCTGCACATCCGGGAGTTCCACCGGGTCAAAGTGGGAGACATCGCCACTGGCATCAGC 806
                                                                                                                                                                                                                                                          614 GACAGCTGCAAGGGTGACTCCGGGGGCCCGCTGGTGTGCGGGGGGCGTCCTCGAGGGCGTG 673
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;PACEDI NO. 5223425
PARDICANT: FLIER, JEFFREY S.;SPIEGELMAN, BRUCE M.;ROSEN,
;BARRY M.;WHITE, TYLER R.
TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; APPLICANT: FLIER, JEFFREY S.;SPIEGELMAN, BRUCE M.;ROSEN,
;BARRY M.;WHITE, TYLER R.
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
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1.5%; Score 40.2; DB 6; Length 1093;
Best Local Similarity 48.1%; Pred. No. 0.5;
Matches 114; Conservative 0; Mismatches 123; Indels 0
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; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; FILING DATE: 30-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 34,203
; FILING DATE: 02-APR-1987
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APPLICATION NUMBER: US/07/277,963
FILING DATE: 30-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,203
FILING DATE: 02-APR-1987
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;Patent No. 5223425
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; LENGTH: 1093
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LENGTH: 1093
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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    Length 1093;
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47.9%; Pred. No. 59;
tive 0; Mismatches 125; Indels
                                               Indels
Score 40.2; DB 6;
Pred. No. 0.5;
0; Mismatches 123;
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APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, John C.
TITLE OF INVENTION: DIA SEQUENCES FOR STRAIN J.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UNMERR: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
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1.5%;
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Best Local Similarity 47.9%
Matches 115; Conservative
                                               Conservative
                      Similarity
Query Match
Best Local Simi
Matches 114;
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US-09-103-840A-2
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                                  APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, Owen R.
APPLICANT: VENTER, Owen R.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFRENCE: 24366-22007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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59;
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47.9%; Pred. No. 59;
tive 0; Mismatches 125; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lam, Stephen T.
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Stein, Jeffrey I.
APPLICANT: Howell, Charles R.
APPLICANT: Becker, J. Ole
TILE OF INVENTION: Gene Activating Element
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/087,636
FILING DATE: 01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHEN TORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08287442
Patent No. 5670350
GEMERAL INFORMATION:
APPLICANT: Gaffney, Thomas D.
APPLICANT: Lam, Stephen T.
               APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, OWEN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: CIBA-GEIGY Co
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 47.9
Matches 115, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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GENERAL INFORMATION:
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US-08-287-442-8
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1.5%; Score 39.6; DB 1; Length 1005;
Best Local Similarity 46.5%; Pred. No. 0.72;
Matches 126; Conservative 0; Mismatches 145; Indels 0
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ne : 303.303 secs
APPLICATION NUMBER: US 07/908,284
FILING DATE: 02-UUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/570,184
FILING DATE: 08-AUG-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 15
TELECOMMULICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1005 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                         NAME: Elmer, James Scott REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..1005
OTHER INFORMATION:
OTHER INFORMATION:
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Sequence 17, Appl
Sequence 975, App
Sequence 975, App
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                                                                                                                                                                 June 10, 2005, 14:23:14 ; Search time 999.861 Seconds
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3: (cgn2_6/ptodata/2/pubpna/USO7 PUBCOMB. seq:*

3: (cgn2_6/ptodata/2/pubpna/USO6_PUBGOMB. seq:*

4: (cgn2_6/ptodata/2/pubpna/USO7_NEW PUB. seq:*

5: (cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB. seq:*

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-172-118-975

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3 US-10-283-975A-294

3 US-10-087-192-887

US-09-871-889-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Sequence 294, App Sequence 887, App Sequence 2, Appli Sequence 886, App

US-10-087-192-886

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APPLICANT: Axxima Pharmaceuticals AG
APPLICANT: Axxima Pharmaceuticals AG
APPLICANT: Schubart, Daniel
APPLICANT: Schubart, Daniel
APPLICANT: Habenberger, Peter
APPLICANT: Stein-Gerlach, Matthias
APPLICANT: Bevec, Dorian
TITLE OF INVENTION: Callular Kinases Involved in Cytomegalovirus Infection and their
TITLE OF INVENTION: Inhibition
FILE REFERENCE: AXM-004.1 US
CURRENT FILING DATE: 2002-06-28
PRIOR PILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 22
           Sequence 884, App
Sequence 1754, Ap
Sequence 2585, Ap
Sequence 11852, A
Sequence 883, App
Sequence 2052, A
                                            Sequence 22052, A Sequence 22052, A Sequence 22052, A Sequence 12325, A Sequence 31496, A Sequence 3156, Ap Sequence 25736, Ap Sequence 25736, Ap
                                                                                                                     Sequence 2583, Ap
Sequence 3841, Ap
Sequence 19657, A
Sequence 153036,
Sequence 11, Appl
Sequence 20, Appl
Sequence 20, Appl
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Sequence 214, App
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Sequence 1, Appl
Sequence 3, App
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15 US-10-156-761-1
17 US-10-282-122A-14856
9 US-09-821-255-1
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US-10-202-676-1
US-10-044-090-214
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Best Local Similarity 90.55
Matches 2334; Conservative
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ORGANISM: Homo sapiens
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Pred. No. 0;
4; Mismatches 159; Indels
                               SQUENCE 294, Application US/10283975A
Publication No. US20040110792A1
GENERAL INFORMATION:
TITLE OF INVENTION: Methods For Assessing and
FILE REFERENCE: CDS 293 FOT
CURRENT APPLICATION NUMBER: US/10/283,975A
CURRENT FILING DATE: 2002-10-30
PRIOR PILING DATE: 2001-10-30
PRIOR FILING DATE: 2001-10-30
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NUMBER OF SEQ ID NOS: 900
SOFTWARE: Patentin version 3:1
SEQ ID NO 294
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Best Local Similarity 90.5
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ORGANISM: HUMAN
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Publication No. US20020182586A1

GENERAL INCORMATION:
APPLICANT: Board W.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US/10/147,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR PILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/747,377
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                                                                                                                                                                   Length 4684;
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                                                                                                                                                                                    Pred. No. 0;
5; Mismatches 183; Indels
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                                                                                                                                                                   Score 1783.4;
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 887
LENGTH: 4684
TYPE: DATE: Homo sapiens
                                                                                                                                                                 67.8%;
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Best Local Similarity 89.3
Matches 2297; Conservative
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US-10-087-192-887
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                                                                                                            GCAGGGNCAGGGNCAGTGACANCTGTAGGNAGCATANGCAANGCCAGGAGATGG
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100.0%; Pred. No. 1.7e-290;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09871889;
Sequence 2, Application US/09871889;
Patent No. US20020042499A1
GENERAL INFORMATION:
APPLICANT: Greene, Warner C.
APPLICANT: Greene, Warner C.
APPLICANT: Gelezuinas, Romas, Romas, TITLE OF INVENTION: A NOVEL INHIBITOR OF THE ITTLE OF INVENTION: BY TRY-ALPHA AND IL-1;
FILE REPERENCE: 30448.61USU1
CURRENT APPLICATION NUMBER: US/09/871,889
CURRENT FILING DATE: 2001-06-01
PRIOR FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: 60/076,299
PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: NF-KAPPA B INDUCING KINASE (NIK)
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US-09-871-889-2
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Pred. No. 7.6e-289;
5; Mismatches 183;
 FILE OF INVENTION: CANCER
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 886
LENGTH: 73967
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ilarity 84.4%;
Conservative
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Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
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Pred. No. 8.6e-222;
4; Mismatches 159;
APPLICANT: Hyseq Inc
TITLE OF INVENTION: No. US20040053248A1el Nuc
FILE REFERENCE: 784PCT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR PILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
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Sequence 97, Application US/10296115 Publication No. US20040053248A1 GENERAL INFORMATION:

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                                                                                                CACCCCTCACACGCCCAGGCCATCCAAGAGGGGCTGAGGAAAGAGCCCGTCCACCGAGCAT
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Matches 798; Conservative
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Sequence 884, Application US/10087192
| Publication No. US20020182586A1
| GENERAL INFORMATION:
| APPLICANT: Morris, David W. |
| APPLICANT: Engelhard, Eric K. |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: UNDUBER: US/10/087,192 |
| CURRENT FILIG DATE: 2002-03-01 |
| PRIOR PILING DATE: 2000-12-2 |
| PRIOR APPLICATION NUMBER: US 09/747,377 |
| PRIOR FILING DATE: 2001-03-02 |
| NUMBER OF SEQ ID NOS: 2059 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 884 |
| LENTING DATE: 2001-03-02 |
| WINDER OF SEQ ID NOS: 2059 |
| LENTING DATE: 2001-03-02 |
| SEQ ID NOS 882 |
| LENTING DATE: 2001-03-02 |
| LENTING DATE: 2001-03-02 |
| SEQ ID NOS 882 |
| LENTING DATE: 2001-03-02 |
| LENTING DATE: 2001-03-02 |
| CANTANTE: PASTSEQ FOR WINDOWS VERSION 4.0 |
| SEQ ID NOS 882 |
| LENTING DATE: 2008-04 |
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Matches 288; Conservative
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                                                                                                                                                                                                                                                                           DB 17; Length 2475;
        Sequence 1754, Application US/10108260A
; Bodlication No. USZO0040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELLIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. USZO040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Parentin Ver. 2.1
; SEQ ID NO 1754
LENGTH: 2475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES CURRENT ENTLE REPERENCE: 2011-756 CURRENT APPLICATION NUMBER: US/09/235,076 PRIOR PILING DATE: 1999-01-20 NUMBER OF SEQ ID NOS: 38054 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2885 LENGTH: 499
                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                           Score 349.4; DB 1
Pred. No. 1.2e-96;
0; Mismatches 1
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Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1) - (499)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2585
                                                                                                                                                                                                                                                                            Query Match 13.3%;
Best Local Similarity 99.7%;
Matches 350; Conservative
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LOCATION: (1)...(499)
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                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo sapiens
US-10-108-260A-1754
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          US-10-108-260A-1754/c
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Sequence 11852, Application US/09783590

Sequence 11862, Application US/09783590

Sequence 11862, Application US/09783590

GENERAL INFORMATION:

APPLICANT: Dillon, Patrick J.

APPLICANT: Haseltine, William A.

APPLICANT: Haseltine, William A.

APPLICANT: Rosen, Craig A.

APPLICANT: Roben, Steven M.

TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2

TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2

FILE REFERENCE: PO-16.21

CURRENT FILING DATE: 12995-04-12

PRIOR PILING DATE: 1995-04-12

PRIOR FILING DATE: 1994-11-21

NUMBER OF SEQ ID NOS: 12485

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 11852

LENGTH: 296
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                                                                                           811 AGATCCCAGCTGCAGCCTTCAGCTTGGTCACCAAAGACGGGCAGCCTGTTCGCTACGACA
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     Indels
     23;
          1; Mismatches
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
(5)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (100)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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21; Gaps

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APPLICANT: Schlegel.
APPLICANT: Schlegel.
APPLICANT: Schlegel.
APPLICANT: Schlegel.
APPLICANT: Schlegel.
APPLICANT: Brdege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: DENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMBER: US/10/357,930
CURRENT APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-04
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
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PRIOR FILING DATE: 2000-07-18
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PRIOR FILING DATE: 2000-07-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 CCCACCAGAGCCCCCAGAGCCAAACAAGTCTCCTCCTTGACTTTGAGCAAGGAGGAGTC 343
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                                                                                                                                                                                                                                   Query Match 7.2%; Score 188.8; DB 13; Length 42566; Best Local Similarity 73.9%; Pred. No. 1.4e-46; Matches 263; Conservative 0; Mismatches 72; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 22052, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
                                                                          FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(4256)

OTHER INFORMATION: n = A,T,C or G
US-10-087-192-883
                           TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-357-930-22052/c
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; ORGANISM: Homo E
US-10-357-930-22052
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LENGTH: 455
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     LENGTH:
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APPLICANT: BRIGHAID, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: OANCER
FILE REFERENCE: $29452000122
CURRENT FELLING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 20001-03-02
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.3%; Score 193; DB 9;
88.2%; Pred. No. 1.1e-48;
tive 0; Mismatches 28
                                                                                                                                                                         LOCATION: (228)
OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature
LOCATION: (247)
OTHER INFORMATION: n equals a,t,g, or c LOCATION: (250)
OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (293)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-11852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (287)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                     LOCATION: (130)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (268)
OTHER INFORMATION: n equals a,t,g,
                                                                                                  LOCATION: (195)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similaricy ....
Matches 224; Conservative
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (277)
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---- Local Similarity
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                                      458 AGAATTATTCCTCAACAGCCTGTCCCAGCCATTTTCTCTGGAGGAGCAGGAAGTTCT 517
                                                227 AGAATTATTCCTCAACAGCCTGTCCCAGCCATTTCTCTGGAGGAGCAGAAGCAAATTCT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458 AGAATTATTCCTCAACAGCCTGTCCCAGCCATTTTCTCTGGAGGAGCAGGAATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
3.4%; Score 88.4; DB 20; Length 455;
Best Local Similarity 98.9%; Pred. No. 2.6e-16;
Matches 89; Conservative 0; Mismatches 1; Indels 0
Query Match
Best Local Similarity 98.9%; Pred. No. 2.6e-16;
Matches 89; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        518 CTCGTGCCTCAGCATCGACAGCCTCTCCCT 547
                                                                              518 CTCGTGCCTCAGCATCGACAGCCTCTCCCT 547
                                                                                          167 CTCGTGCCTCAGCATCGACAGCCTCTCCTT 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-10-357-930-27909
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(without alignments)
16321.674 Million cell updates/sec
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                                                                    June 10, 2005, 06:13:19 ; Search time 6580.54 Seconds
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//pna/US097C_COMB.seq:*
//pna/US098A_COMB.seq:*
//pna/US098B_COMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/pna/US099c_comp.ecq.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                  45554873 seqs, 20411521753 residues
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                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           nucleic search, using sw model
                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
                                                                                                               US-09-155-676B-3
2631
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                                                                                                                 Title:
Perfect score:
                                             OM nucleic
                                                                                                                                         Sequence:
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                                                                    Run on:
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45: cgn2 6/ptodata/1/pna/U8099F COMB. seq; 46: cgn2 6/ptodata/1/pna/U8109A COMB. seq; 46: cgn2 6/ptodata/1/pna/U8109A COMB. seq; 46: cgn2 6/ptodata/1/pna/U8109A COMB. seq; 46: cgn2 6/ptodata/1/pna/U8109A COMB. seq; 47: cgn2 6/ptodata/1/pna/U8101A COMB. seq; 6/ptodata/1/pna/U8101A COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U8101B COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U86012 COMB. seq; 6/ptodata/1/pna/U860
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	ednence	equence 3,	Sequence 6, Appli	sequence o, emience 152	75.	equence 975,	Sequence 123	equence 437,	17,	equence 975,	equence 29	9/5	sequence 14	equence 6881,	1000	equence 10109,	1727	equence 4	equence 887,	quence 9152,	equence 3284	equence 227, A	equence 5385	equence 5385,	equence 2733,	ednence	equence 5385,	equence 567,	equence 913,	Sequence 307, App	emience 226.	Sequence 5384, Ap	equence 5384,	e 2732,	e 2732,	e 5384,	e 566,	equence 91	e 566,	ce 912,	, 4040	6 45/1, 6 4571	17/C# 1
DB ID	7 US-09-155-676-3	7 US-09-155-676A	7 US-09-155-676-6	0-40/0-1001-EO4 9-1-100-1001-EO4	.USU1-U8631-1323 .TISU2-18947-975	PCT-US04-01100-97	6 US-09-053-375B-1	US-09-949-003C-43	US-09-981-397A	US-10-172-118-97	1 US-10-283-975A-	US-10-342-887-975	17 US-60-474-850-144	2 US-09-496-914A-688	6 US-U9-56U-8/5A-688	9 US-10-1/0-235-101	1 US-U9-949-003C-129	7 US-60-278-258-448	-10-087-192-887	US-10-170-235-9152	2 US-60-324-185-32	4 US-60-443-566-227	5 US-60-453-050-538	5 US-60-453-135-538	5 US-60-455-444-273	6 US-60-465-241-27	6 US-60-466-412-538	8 US-60-485-450-56	8 US-60-487-610-91	126 US-60-563-440-567	4 TIS-60-443-566-22	US-60-453-050-53	US-60-453-135-53	-60-455-444-273	US-60-465-241-27	6 US-60-466-412-53	8 US-60-485-450-56	8 US-60-487-610-91	US-60-563-440-56	28 US-60-582-609-91	6 US-60-1/2-3/3-349	10-760	Z US-10-/60-620A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GCCCTTGGAGGGAGAATATAAAGAACCAACATCCACCGCCAAATCAAGCCAATTACC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ACCAGACCCTCCATGCCCAGCCGAGAGCTTTCGCCAAGGGCCCCAGGGCCCCGGCCAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CTGCAGCGGAGCTGGAGGGGAAGGTGAACCGGGCACTACAGCAAGTGGGAGGTCTGAAGA 120
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0
  Sequence 3, Application US/09155676

GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: WALLNIN, NIKolai
APPLICANT: MALININ, NIKolai
APPLICANT: KOVALENKO, Andrei
APPLICANT: METT, Igor
TITLE OF INVENTION: MODULATORS OF THE RECEPTOR ASSOCIATED
TITLE OF INVENTION: PACTOR (TRAF), THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/155,676
FILING DATE: 04-JAN-1999
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C. STREET: 624 Ninth Street, N.W., Suite 300 CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.1%; Score 2553.8;
100.0%; Pred. No. 0;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: >>>
PRIOR APPLICATION DATA:
APPLICATION UNMER: PCT/LL97/00117
FILING DATE: 01-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117800
FILING DATE: 02-APR-196
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 119133
FILING DATE: 26-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
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REFERENCE/DOCKET NUMBER: 35,618
REFERENCE/DOCKET NUMBER: 36,917
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
REGIONAL SOCIETATION OF 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2631 base pairs
"VODE: nucleic acid
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Best Local Similarity 100.0
Matches 2631; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
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MOLECULE TYPE: cDNA
US-09-155-676-3
US-09-155-676-3
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Qy 2461 GGGGAGAGAGAGCCCCGAGCCCTAAAGAACTGCAGCCTTGGTACTGCAGAGTCTG DD 2461 GGGGAGAGAGAGCCCCCGAGCACATAAAGAACTGCAGCCTTGGTACTGCAGAGTCTG	2520 25 2 2520 Qy 61 2520 Dh 61	120
Qy 2521 GGTTGTAGAGAACTCTTTGTAAGCAATAAAGTTTGGGGTGATGACAAATGTTAAAAAAG 	2580 QY 121 2580 Db 121	180
Oy 2581 GCCTTCGTGGCCTCGAATCAAGCTTATCGATACCGTCGACCTCGAGGGGG 2631	181	240
RESULT 2 US-09-155-676A-3 ; Sequence 3, Application US/09155676A	Qy 241 CTGAGGAGACAAGAGGAGAGCCCTAAGCTCCAGCCTCCTCCCACCAGGGCCCCCAGG	300
GENEKAL INFORMATION: APPLICANT: WALLACH, David APPLICANT: MALLINI, Nikolai APPLICANT: BOLDIN, Mark	Qy 301 AGCCAAAGTCTCCTCCTTGACTTTGAGCAAGGAGGAGTCTGGGATATGGGAACCTT	360
APPLICANT: KOVALENKO, Andrei, APPLICANT: METT, 1gor 1TILE OF INVENTION: MODULATORS OF TWF RECEPTOR ASSOCIATED 1TILE OF INVENTION: PACTOR (TRAF), THEIR PREPARATION AND USE	Qy 361 TACCTCTGTCCTCCTGGAGCCAGCCCCTGCCAGAAACCCCAGGTCACCAGAGAGAG	420
NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESSS: ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C. STREET: 624 Ninth Street, N.W., Suite 300	Oy 421 CAACCGTCCCGGAGCAGCAGCAGCAGCAGCAGAATATTCCTCAACAGCTGT	480
) CITY: Mashington ; STATE: D.C. ; COUNTRY: USA ; ZIP: 20001	Qy 481 CCCAGCCATTITCTCTGGAGGAGCAAATTCTCTCTGTGCCTCAGCATCGACAGCC Do 481 CCCAGCCATTITCTCTGGAGGAGCAAATTCTCTCGTGCCTCAGCATCGACAGCC	540
COMPUTER READABLE FORM: MEDULUM TYPE: Floppy disk; COMPUTER: IBM PC compatible; OPERATING SYSTEM: PC-DOS/MS-DOS	Qy 541 TCTCCCTGTCGGATGACAGTGAGAAGACCCCATCAAAGGCTCTCAAAGGTCGGGGACA	009
SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PELLING DATE: 04-JAN-1999	Qy 601 CCCTGAGCTCAGGCGTACACTCCTGGAGCCCGAGGCCCGAGGCTCGAAGGTCCAGGTGGA	099
; CLASSIFICATION: 530 PRIOR APPLICATION DATA: ; APPLICATION NUMBER: PCT/IL97/00117 ; FILING DATE: 01-APR-1997	Qy 661 ACATGGTGCTGGCCCGGGGCGGCCCACCGACCCCAAGCTATTCAATGGTGAAAG	720
; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 1L 117800 ; FILING DATE: 02-APR-1996 ; PRIOR APPLICATION DATA:	Qy 721 TCCAAATACAGTCTCTTAATGGTGAACACTGGACATCGGGAGTTCCACGGGTCAAAG 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	780
	Qy 781 TGGGAGACATCGCCACTGGCATCAGCAGCTCCCAGTGCAGCTTTCAGTTGGTCA 1	840
; REGISTRATION NUMBER: 25,618 REGISTRATION NUMBER: WALLACH=21 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 202-628-5197	Qy 841 CCAAAGACGGCAGCCTGTTCGCTACGACATGGAGGTGCCAGACTCGGGGATCGACCTGC	006
; TELBFAX: 202-737-3528 ; INFORMATION FOR SEQ ID NO: 3: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 2631 base pairs	QY 901 AGTGCACACTGGCCCTGATGGCAGCTTCGCCTGGAGGGTGGAGGGTCAAGCATGGCCAGC Db 901 AGTGCACACTGGCCCCTGATGGCAGCTTCGCCTGGAGGTCAAGGTCAAGCCAGC	096
TYPE: mucleic acid TYPE: mucleic acid STRANDEDNESS: single JOPOLOGY: linear MOLECULE TYPE: CDNA	Oy 961 TGGAGAACAGGCCCTAACCCTGCCCTCCACGGCGGCTCCACACTGCCGGAAAGCAGCCTTAACCTTGCCCTCCACCGGCTCCACACACTGCCGGAAAGCAGCCTTAACCCTGCCCTCCACCGCGCTCCACACACTGCCGGAAAGCAGCCTTAACCTTGCCGGCTCCACACACTGCCGGGAAAGCAGCCTTAACCTTAACCTTCCACCGCGGCTCCACACACTGCCGGGAAAGCAAGC	1020
3 97.1%; Score 2553.8; DB 17; Length 2 milarity 100.0%; Pred. No. 0;	Qy 1021 TCCTGCTCGGTGCACGATGCTGCCCTGAAAACACAGGCTCAGCCGTTCCCAGGGGATYTG	1080
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Oy 2221 NCCAGNATTCTCTAAGAATAGCANCCCCCTTNCCCCATTGCCCCAGCTTAGCCTCTCT 2	2401 TCCCACATCTTGCCCAGCACAGCCTTTNGTCCAGCTGTCCACATTGAGTCAGAGAGAGAGAGAGACAGCTTTNGTCCAGCTGTCCACATTGAGTCAGAGACAGCCTTTNGTCCAGCTGTCCACATTGAGTCAGAGACAGCCCCCAGCACTTTNGTCCAGCTGTCCACATTGAGTACTGCAGAGAGAGAGAGAG	RESULT 3 CENERAL INFORMATION: RESULT 3 US-09-155-676-6 SCHECANT: WALLININ, Nikolai APPLICANT: WALLININ, Nikolai APPLICANT: WONDEN, Andrei APPLICANT: MARTKO, Andrei APPLICANT: MATK, 1900	TITLE OF INVENTION: MODULATORS OF TWF RECEPTOR ASSOCIATED TITLE OF INVENTION: FACTOR (TRAF), THEIR PREPARATION AND USE NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSE: BROWDY AND NEIMAR, P.L.L.C. STREET: 624 Ninth Street, N.W., Suite 300 CITY: Washington STREET: 0.0 COUNTRY: USA ZIP: 20001 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IEM PC compatible COMPUTER: IEM PC Compatible COMPUTER: DAFFMING SYSTEM: PC-DOS/MS-DOS SOFTWARR: PAFFMING SYSTEM: PC-DOS/MS-DOS SOFTWARR: PAFFMING SYSTEM: PC-DOS/MS-DOS	
1081 NCCAGCCCCCGGCTCARCAGNTGGGAACCAGGGCCTCGNCAGCNAGCNAAGGTNGGGGG	ANTCACTGACCATTTGTTGGCAGANCAGGGAGAGCTTCCAGCCTGGACCCGGTCAGAAGGG	1501 GGTTAANNGGGGCCCTCTNAAACCCCTTGCCTNGGCCTNCACCTNGGCCAGCTCANCCC 1500		1921 TCCGGCGCCCCAGNCCCACTNATCAGTGTNCCAGCTNGGTTNCCCCAGNAGCACA 1980 1921 TCCGGCGCCCCAGNACCCACTNATCAGTGTNCCAGCTNGGTTNCCCCAGNAGCACA 1980 1921 TCCGGCGCCCCAGNACCCACTNATCAGTGTNCCCAGNAGCTACA 1980 1981 GCTNCAGNCATCANCACTGACATNCACCTNGCCTGCCCTNGGCCANGAGGGTACTG 2040 1981 GCTNCAGNCATCANCACTGACATNCACCTNGCCTNGGCCANGAGGGTACTG 2040 1981 GCTNCAGNCATCANCACTGACACTNCACCTNGCCCTNGGCCANGAGGGTACTG 2040 2041 CCGNACGGCACTTTGCACNTCTGATGNACCTCAAAGCACTTTCATGGCTNGCCCTCTNNG 2100 2101 GCAGGGNCAGGGNCAGTGACANCTGTAGGNAGCACTTTCATGGCTNGCCCTCTNNG 2100 2101 GCAGGGNCAGGGNCAGTGACANCTGTAGGNAGCATANGCAANGCCAGGAGATGG 2160 2101 GCAGGGNCAGGGNCAGTGACANCTGTAGGNAGCATANGCAANGCCAGGAGATGG 2160 2101 GCAGGGNCAGGGNCAGTGACANCTGTAGGNAGCATANGCAANGCCAGGAGATGG 2160 2101 GGTGNAAGGGANCAGTGACANCTGTAGGNAGCATANGCAANGCCAGGAGATGG 2160 2161 GGTGNAAGGGANCACAGTCTTGAGCTTCCANCATGACTNCCTCCAAACCTCTTN 2220 2161 GGTGNAAGGGANCACAGTCTTCAAGCTTCCACAAACCTCTTN 2220 2161 GGTGNAAGGGANCACAGTCTTCAAGCTTCCACAAACCTCTTN 2220

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                                                                                   Length 4596
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                                                                                                     159; Indels
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                                                                                   Score 1851.2; 1; Pred. No. 0; 4; Mismatches
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: 1.ENGTH: 4596 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA US-09-155-676-6
                                                                                     Query Match
Best Local Similarity 90.5%;
Matches 2335; Conservative
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                                                                        CCGNACGGCACTITGCACNICIGAIGNACCICAAAGCACTITCAIGGCINGCCCTCINNG 2100
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GCTINCAGNCATCANCACTGACACTNCACCCTNGCCCTTGCCCCTNGGCCANGAGGGTACTG
                                   4083 ccg-accicriticcacr--crgardaccrcaaaccacriticardecrecccrcrccca
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APPLICANT: MALLACH, David
APPLICANT: MALININ, Nikolai
APPLICANT: BOLDIN, Mark
APPLICANT: BOLDIN, Mark
APPLICANT: METT, 1gor
TITLE OF INVENTION: MODULATORS OF THE RECEPTOR ASSOCIATED
TITLE OF INVENTION: FACTOR (TRAF), THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/155,676A

FILING DATE: 04-07N-1999

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IL97/00117

FILING DATE: 01-APR.1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C.
STREET: 624 Ninth Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
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US-09-155-676A-6
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4; Mismatches
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APPLICATION NUMBER: IL 117800
FILING DATE: 02-APR-1996
PRIOR APPLICATION DATA:
APPLICATION DATA: 119133
FILING DATE: 26-AUG-1996
ATTORNEY/AGENT INPORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH
TELECOMUTUNICATION INPORMATION:
TELEPANOR: 202-628-5197
FELEPHONE: 202-628-5197
FELEPANOR: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4596 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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Matches 2335; Conserv
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US-09-155-676A-6
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1861 CAGGARACATCAGTTCCCTCATCAGTAAAGGGTGATGCAGGATATCCCTGA 3918 1861 CAGGARACAGTCTGGATGGACATCAGTGAAGGATGATGCAGGAGAAGACCAGAGAGACCAGAGAGACCAGAGAGACCAGAGAGACCAGAGAGACCAGAGAGACCAGAGAGACCAGAGAGACCAGAGACCAGAGACCAGAGACCAGAGACCAGAGACCAGAGACCAGAGACCAGAGACCACAGAGACCACAGAGACCACAGAGACCACAGAGACCACAGAGACCACAGAGACCACAGAGACCACAGAGACCACACACACACACACACACACACACACACACACACACA	RESULT 5 PGT-USO1-08631-15294 FGT-USO1-08631 GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES FILE REFERENCE: 21272-049 CURRENT APPLICATION NUMBER: PCT/USO1/08631 CURRENT APPLICATION NUMBER: DO1-03-30 FRIOR FILING DATE: 2000-03-31 FRIOR FILING DATE: 2000-03-31 FRIOR FILING DATE: 2000-08-23 NUMBER OF SEQ ID NOS: 60736 SOFTWARE CUSTOM SEQ ID NO 15294 LENGTH: 4596 TYPE: DNA COGANESM: Homo sapiens FRAUTHE: NAME/KEY: SIMILAR
	1501 GGTTAANNGGGGGCCCTCTNAAACCCCTTGCCTNGGCCTNGGCCAGCTCANCCC 1560 1

----CAGCAGCAAGGTGGGG

1320 3396 1380 1440

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AGGONCCCAAANCTCAGGNTTCAGTGCAGAACCAGGTNCAGCAGGTATGCCCGCCGGNTA 1500
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                                    GATCAGTGACCATTIGITIGITIGGAGA-CAGGGAGAGAGCTTCCAGCCTGGGTCAGAGGG
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                                                                          NCCAGCCCCCGGGTCARCAGNTGGGAACCAGGGCCTCGNCAGCNAGGNAAGGTNGGGGG
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                                                                                             CCCCTCTCACAGCCCAGGCCATCCAAGAGGGGCTGAGGAAAGAGCCCATCCACCGCGTGT
                                                                                                                                                          GCCCTTGGAGGGGAGAATATAAAGAACCAAGACATCCACCGCCAAATCAAGCCAATTACC
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                                                                                 CCCCTCTCACAGCCCAGGCCATCCAAGAGGGGCTGAGGAAAGAGCCCCATCCACCGCGTGT
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                                                                Gaps
           protein
                                                                81;
                                              Length 4596
           Score=809
                                                                159; Indels
i DOCATION: (1117)..(1581)
OTHER INFORMATION: 100% homologous to Homo sapiens
OTHER INFORMATION: number M82968, Smith-Waterman Sco
PCT-US01-08631-15294
                                              1;
                                              DB
                                           Query Match
70.3%; Score 1850.2;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 2334; Conservative 4; Mismatches
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APPLICANT: Rosetta Impharmatics
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CURRENT APPLICANTON NUMBER: CT/USO2/18947
CURRENT APPLICANTON NUMBER: 60/380,770
FRIOR PILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 975
IENGTH: 4596
TYPE: DNA
ORGANISM: HOMO Sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM_003954
PCT-USO2-18947-975
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                                                                                              Score 1850.2;
Pred. No. 0;
4; Mismatches
1998-08-31
1543
Windows Version 4.0
                                                                                              70.3%;
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Best Local Similarity 90.5
Matches 2334; Conservative
 CURRENT FILING DATE: 1990;
NUMBER OF SEQ ID NOS: 154,
SOFTWARE: FastSEQ for Winc;
SEQ ID NO 1234
LENGTH: 4596
TYPE: DNA
ORGANISM: Homo sapiens
US-09-053-3758-1234
CURRENT FILING DATE: 1
NUMBER OF SEQ ID NOS: 1
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	TENGTH: 4596 TYPE: DNA TO:3%; Score 1850.2; DB 41; Length 4596; ORGANISM: Homo sapiens US-09-949-003C-437 TO:3%; Score 1850.2; DB 41; Length 4596; Dest Local Similarity 90.5%; Pred. No. 0; Matches 2334; Conservative 4; Mismatches 159; Indels 81; Gaps 34; Matches 2334; Conservative 4; Mismatches 159; Indels 81; Gaps 34; Option of the conservation of the con

ACADAMCATCCGCCACGTGAAGAGACGAGGAGGGCAGGAGTTACCTGGGGAA 3340 ACADAMCAGGGATCTTTNTTCTGCCCCTGCTCCAGTTGGCTGACCTGAC	SCCTCAACCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTC
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                                                                                                      APPLICANT: Discontinual APPLICANT: Discontinual APPLICANT: Linsley, Peter APPLICANT: Linsley, Peter APPLICANT: Linsley, Peter APPLICANT: Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, Maco, M
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM 003954
DATABASE ENTRY DATE: 2001-06-18
                                                      Sequence 975, Application US/10172118 GENERAL INFORMATION:
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Best Local Similarity
Matches 2334; Conserv
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                                                                                                  CAGGAACAGTCTGTGGATGGACATGATCAGTGCTNAAGGNAAAGCAGCAGAGAGAGACGY 1920
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                     GCTACCACTCTTCCCCAGAGCAGCCCCCGAGCCCCTTCAGGCCCCAGCACTGCCCCAG
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GENERAL INFORMATION:
APPLICANT: Ortho-Clinical Diagnostics, Inc.
TILLE OF INVENTION: Methods For Assessing and Treating Leukemia FILE REFERENCE: CDS 293 PCT
CURRENT APPLICATION NUMBER: US/10/283,975A
CURRENT FILING DATE: 2002-10-30
PRIOR PILING DATE: 2001-10-30
PRIOR PILING DATE: 2001-10-30
PRIOR PILING DATE: 2001-10-30
PRIOR FILING DATE: 2001-10-30
PRIOR FILING DATE: 60/38,997
PRIOR APPLICATION NUMBER: 60/340,081
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Pred. No. 0;
4; Mismatches
PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION WUMBER: 60/341,012
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 900
SOFTWARE: Patentin version 3.1
SEQ ID NO 294
LENGTH: 4596
                                                                                                                                                                  70.3%;
                                                                                                                                                                    Query Match
Best Local Similarity 90.5
Matches 2334; Conservative
                                                                                                       TYPE: DNA
ORGANISM: HUMAN
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APPLICANT: Ho, Yudong
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
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APPLICANT: Van ce Vijver, Marc J.
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APPLICANT: Bernards, Rene
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APPLICANT: He, Yudong
APPLICANT: Linaley, Peter S.
APPLICANT: Mao, Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
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; ORGANISM: Homo sapiens
US-10-342-887-975
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                                                              CCAAAGACGGGCAGCCTGTTCGCTACGACATGGAGGTGCCAGACTCGGGCATCGACCTGC
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ò	CTGAGGGGACAACAGGCAGAGGCCCCTAAGCTCCAGCCTCCTCCCCACCAGAGCCCCCAG	ු අ	
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ACTINCACCTINGCCTGCCCTNGGCCANGAGGGTACTG 2040 rctgatgnaccrcaaagcactttcatggctngcccrctnng 2100 |||||||||||||||||--crgatgaccrcaaagcacttcatggctgcccrcaggca 4140 CAGTGACANCTGTAGGNAGCATANGCAANGCCAGGAGATGG 2160 AGAATGCCTGACCTGGGAAGGCTWCCCTGGTAGAATACAC 1620 TACACAGGTCCTGAGTTGACCTCTGGTTCAGCCAAGGACC 1680 AGTGGTTCTCAGINCCCCAGACATGTGCCCCTTTGCTGCTG 1740 3859 CTCATCTGTAAAGGTGAAGGGTGATGCCAGATATGCCTGA 1860 ACATGATCAGTGCTNAAGGNAAAGCAGCAGAGAGACGY 1920 CCTCACCTNCCAGGCTGCTGTGNAGAGTGTCAAGTGTGTA 1440 CAGCAGGCCCCGAGCCCCTTCAGGCCCCAGCACTGCCCCAG 1800 1140 Agriedelakicaledecercie----caecaecaageredee 1200 3284 1260 CCTGCCCTGCTCCAGTNCGAGTTGGCCTGNACCCGCTTGG 1320 1380 TCAGTGCAGAACCAGGTNCAGCAGGTATGCCCGCCGNTA 1500 TCAGTGCAGAACCAGGT-CAGCAGGTATGCCCGCCCGTAG 3569 AAACCCTTGCCTNGGCTNCACCTNGGCCAGCTCANCCC 1560 GATTTCACANCCTGAGCCONTGCCCANCCCTGCTGAADA GATTTCACACCTGAGCCCTGCCCCAC----CCTGCTGA CAGANCAGGGGAGGAGCTTCCAGCCTGGGTCAGAAGGG GAGACAGAAGGAGGATGGNCAGGAGTTNNACCTYGGGGAA GNTGGGAACCAGGGCCTCGNCAGCNAGCNAAGGTNGGGGG

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Oy 2221 N Db 4246 -	NCCAGNATTICTCTAAGAATAGCANCCCCTINCCCCATIGCCCCAGCTTAGCCTCTTCT 2280 	ço d	361 TACCTCTGTCCTGGAGCCAGCCCTGCCAGAAACCCCAGCTCACCAGAGCGGAAAG 420
Oy 2281 C Db 4302 C	CCCAGGGGAGCTANCTICAGGACTCACGTAGCATTAAATCAGCTGTGNAATCGTCAGGGGG 2340	ò a	421 CAACCGTCCCGGAGCAGGAACTGCAGCAGCTGGAAATAGAATTATTCCTCAACAGCCTGT 480
Qy 2341 T Db 4360 T	TGTCTGCTAGCCTCAACCTCCTGGGGGACGCCGAGACTCCGTGGGAGAGACTCAT 2400	ò a	481 CCCAGCCATTTTCTCTGGAGGAGCAGAAATTCTCTCGTGCCTCAGCATCGACAGCC 540
Oy 2401 T Db 4420 T	TCCCACATCTTGCCAAGACAGCCTTTNGTCCAGCTGTCCACATTGAGTCAGACTGCTCCC 2460	& 8	541 TCTCCCTGTCGGATGACAGAGAACCCATCAAAGGCCTCTCAAAGCTCGCGGGACA 600
Qy 2461 G Db 4479 G	GGGGAGAGACCCCCGGCCCCCAGCACATAAAGAACTGCAGCCTTGGTACTGCAGAGTCTG 2520	& a	601 CCCTGAGCTCAGGCGTACACTCCTGGAGCAGCCGAGGCTCGAGGCTCCAGCTGGA 660
Qy 2521 G	GGTTGTAGAGAACTCTTTGTAAGCAATAAAGTTTGGGGTGATGACAAATGTTAAAAAA 2578 	ò a	661 ACATGGTGCTGGCGGGGGGCGCCCACCGACCCCAAGCTATTTCAATGGTGTGAAAG 720
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., 0	Sequence 144, Application US/60474850 GENERAL INFORMATION: APPLICANT: Wohlgemuth, Jay APPLICANT: Ly, Ngoc	<i>&</i> 40	781 TGGGAGACATGGCCACTGGCATCAGCAGATCCCAGCTGCAGCTTCAGCTTGAGTCA 840
; TITLE OF INV; TITLE OF INV; FILE REFEREN	VERTICE: James VERTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING VENTION: RENAL TRANSPLANT REJECTION VCE: 56613000700	& g	841 CCAAAGACGGCAGCCTGTTCGCTACGACATGGAGGTGCCAGACTCGGGCATCGACCTGC 900
•	CURRENT FILING DATE: 2003-05-30 NUMBER OF SEQ ID NOS: 552 SOFTWARE: Patentin version 3.1	<u>ک</u> م	901 AGTGCACACTGGCCCCTGATGGCAGCTTCGCCTGGAGCTGGAGGGTCAAGCATGGCCAGC 960
" "	96 Homo sapiens	oy Oy	961 TGGAGAACAGGCCCTAACCCTGCCCTCCACCGCCGGCTCCACACTGCCGGAAAGCAGCCT 1020
Query Match Best Local Si	70.3%; Score 1850.2; DB 117; Length 4596; 90.5%; Pred. No. 0;	ò qa	1021 TCCTGCTCGGTGCACGATGCTGCCCTGAAACACAGGCTCAGCCGTTCCCAGGGGATYTG 1080
Oy 1 0	8 - 8	ò a	1081 NCCAGCCCCCGGCTCARCAGNTGGGAACCAGGGCCTCGNCAGCNAAGGTNGGGGG 1140
61 61	AAGA 120	oy Oy	1141 CAAGCNAGAATGCCTCCCAGGATTTCACANCCTGAGCCCNTGCCCANCCTGCTGAADA 1200
Oy 121 G	CIGCAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	& g	1201 AAACAYTNCCGCCACGTGAAGAQACAGAAGGAGGATGGNCAGGAGTTNNACCTYGGGGAA 1260
181	CCAG 240	ò a	1261 ACAAACAGGGAICTITNITCTGCCCTGCTCCAGINCGAGITGGCCTGNACCCGCTTGG 1320
241	300	ò a	1321 ANTCACTGACCATTTGTTGGCACANCACGGGAGCACCTTCCACCTGGCTCAGAGGG 1380
2340	CTGAGGAGACAGAGGCCCCTAAGCTCCAGCCTCCTCTCCCACCAGAGCCCCCAG 2399	ò	1381 GIGGGCGAGCCCTTCGGCCCCTCACCCTNCCAGGCTGCTGTGNAGAGTGTCAAGTGTGTA 1440

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4479 GGGGAGAGACCCCCGGCCCCCAGCACATAAGAACTGCAGCCTTGGTACTGCAGAGTCTG 4538
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2.09-496-914A-6881
; Sequence 6881, Application US/09496914A
; GENERAL INFORMATION:
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SOFTWARE: pt_T_genes Version 1.02
SEQ ID NO 6881
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                                          AGGGNCCCAAANCTCAGGNTTCAGTGCAGAACCAGGTNCAGCAGGTATGCCCGCCGGNTA 1500
                                                        4141 GGCAGGGCAGGCAGTGACT-----GTAGGAGCATAGCAAGCCAGGAGATGG
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                                      PAPLICANT: Tangy Yuanhua T.
APPLICANT: Tangy Yuanhua T.
APPLICANT: Tillinghast, John
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: From Various Libraries
FILER REFREENCE: 787
TITLE OF INVENTION: From Various Libraries
FILER PEPLICATION NUMBER: US/09/496,914A
CURRENT FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: US 09/355,690
PRIOR APPLICATION NUMBER: US 09/353,690
PRIOR PILING DATE: 1998-07-13
PRIOR PLILNG DATE: 1998-00-13
PRIOR PLILNG DATE: 1998-00-13
PRIOR PLILNG DATE: 1998-00-13
PRIOR PLILNG DATE: 1999-00-20
PRIOR APPLICATION NUMBER: US 09/312,14
PRIOR PLILNG DATE: 1999-00-10
PRIOR APPLICATION NUMBER: US 09/312,14
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PRIOR APPLICATION NUMBER: US 09/313,58
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CRATURE:
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OTHER INPORMATION: similar to gil841434 in
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Db 1921 TCCGGCGCCCCAGNCCCCACTNATCAGTGCTNAAGGNAAAGCAGAGAGAGAGAGGCY 1920 Qy 1921 TCCGGCGCCCCAGNCCCCACTNATCAGTGTNCCAGCGTGCTNGGTTNCCCCAGNAGCACA 1980 Db 1921 TCCGGCGCCCCAGNCCCCACTNATCAGTGTNCCAGCGTGCTNGGTTNCCCCAGNAGCACA 1980 Qy 1981 GCTNCAGNCATCANCACTGACACTNCACCCTNGCCCTGCCCT	210	OY 2101 GCAGGGNCAGGGNCAGTGACANCTGTAGGNAGCATANGCAANGCCAGGAGATGG 2160	Qy 2161 GGTGNAAGGGANCACAGTCTTGAGCTGTCCANCATGCATGTGACTNCCTCAAACCTCTTN 2220	OY 2221 NCCAGNATITCICIAAGAAIAGCANCCCCCTINCCCCATGCCCCGAGCTGAGCTCTTCT 2280	Qy 2281 CCCAGGGGAGCTANCTCAGGACTCACGTAGCATTAAATCAGCTGTGNAATGGTCAGGGGG 2340	Qy 2341 TGTCTGCTAGCCTCAACCTCCTGGGGCAGGGACGCCGAGACTCCGTGGGAGAAGCTCAT 2400 Db 2341 TGTCTGCTAGCTCAACCTCCTGGGGCAGGGGACGCCGAGACTCCGTGGGAGAAGCTCAT 2400		Qy 2461 GGGGAGAGAGCCCGGGCCCCCAGCACATAAAGAACTGCAGCCTTGGTACTGCAGAGTCTG 2520 Db 2461 GGGGAGAGAGCCCCGGGCCCCCAGCACATAAGAACTGCAGCCTTGGTACTGCAGAGTCTG 2520	Oy 2521 GCTTGTAGAACTCTTTGTAAGCAATAAAGTTTGGGGTGATGACAAATGTTAAAAAAG 2580 		RESULT 2 11S-09-155-676B-6	; Sequence 6, Application US/09155676B ; GENERAL INFORMATION: ; APPLICANT: WALLACH, David ; APPLICANT: MALININ, Nikolai) APPLICANT: BOLDIN, Mark ; APPLICANT: KOVALENKO, Andrei ; APPLICANT: METT, Igor : TITE OF INVENTION: MODILATORS OF THE RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR		; PRIOR APPLICATION NUMBER: PCT/IL97/00117; PRIOR FILING DATE: 1997-04-01; PRIOR PILING DATE: 1997-04-01; PRIOR APPLICATION NUMBER: IL 117800; PRIOR PILING DATE: 1996-04-02	; PRIOR APPLICATION NUMBER: IL 119133 ; PRIOR FILING DATE: 1996-08-26 ; NUMBER OF SEQ ID NOS: 22 ; SOFTWARE: Patentin version 3.3

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                             Sequence 566, Application US/60659397

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPA
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
MUMBER OF SEQ ID NOS: 47859
NUMBER OF SEQ ID NOS: 47859
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RESULT 7
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Sequence 560, Application US/11060756
Sequence 560, Application US/11060756
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: US/11/060,756
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
SOFTWARE: PatentIn version 3.2
SEQ ID NO 560
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                                               Gaps
                        Length 65967;
                                              87;
                                              Indels
                        DB 15;
                     Score 971.8; DB 15;
Pred. No. 1.6e-222;
9; Mismatches 183;
                     36.9%;
Similarity 84.2%;
33; Conservative
US-60-659-397-12129
                                            Matches 1483;
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                       Query Match
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Drug

59438 59896 AGAACTGCAGCCTTGGTACTGCAGAGTCTGGGTTGTAGAGAACTCTTTGTAAGCAATAAA -CCAGCGTGCTGCTTCCC-----CAGAGCACAGCTCAGCATCACACTGACACTCACC 59384 CTGCCCTGCCCCTGG--CCAGAGGTACTGCCG-ACGGCACTTTGCAC-TCTGATG-ACC TCAAAGCACTTTCATGGCTNGCCCTCTNNGGCAGGGNCAGGGNCAGGGNCAGTGACANCT ---GTAGGAGCATAGCAAGCCAGGAGATGGGGTGAA--GGGACACAGTCTTGAGCTGTCC CATTAAATCGGCGGTGAGGGGGGGTGTCTGCTAGCCTCAACCTCCTGGGGCAGG caectriccacatricaetraeacrecteceeeeaaaaaaaacceeeceeecaaaaaa TGCTNAAGGNAAAGCAGCAGAGAGAGACGYTCCGGCGCCCCAGNCCCCACTNATCAGTGT NCCAGCGTGCTNGGTTNCCCCCAGNAGCACAGCTNCAGNCATCANCACTGACACTNCACCC TNGCCCTGCCCCTNGGCCANGAGGGTACTGCCGNACGGCACTTTGCACNTCTGATGNACC 59439 TCAAAGCACTTTCATGGCTGCCCTCTGGCAGGGCAGGGYAGGGCAGTGACACT----GTAGGNAGCATANGCAANGCCAGGAGATGGGGTGNAAAGGGANCACAGTCTTGAGCTGTCC ANCATGCATGTGACTNCCTCAAACCTCTTNNCCAGNATTTCTCTAAAGAATAGCANCCCCC TINCCCCATTGCCCCAGCTTAGCCTCTTCTCCCAGGGGAGCTANCTCAGGACTCACGTAG CATTAAATCAGCTGTGNAATCGTCAGGGGGGTGTCTGCTAGCCTCAACCTCCTGGGGCAGG GGACGCCGAGACTCCGTGGGAGAAGCTCATTCCCACATCTTGCCAAGACAGCCTTTNGTC CAGCTGTCCACATTGAGTCAGACTGCTCCCGGGGAGAGAGCCCCCGGCCCCCAGCACATAA

Db 966 TGTAGGAGCATA Qy 2183 AGCTGTCCANCATGCATGTGAC Qy 2243 CANCCCCTTNCCCCATTGTGAC Qy 2243 CANCCCCTTNCCCCATTGCCC Db 1069 CACCCCCTTCCCCATTGCCC	2303	Oy 2423 CTTINGTCAGCTGTCCACATT Db 1245 CTTT-GTCCAGCTGTCCACATT Qy 2483 GCACATAAAGAACTGCAGCCTT Db 1304 GCACATAAAGAACTGCAGCCTT Oy 2543 GCAATAAAGAACTGGGGTGATGA Db 1364 GCAATAAAGTTTGGGGTGATGA	RESULT 8 US-11-060-756-4832 Sequence 4832, Application US/1106 GENERAL INFORMATION: APPLICANT: Myeth APPLICANT: Myeth TITLE OF INVENTION: Nacleic Acid TITLE OF INVENTION: Target Genes FILE REFERENCE: AM101083 (031896-1) CURRENT APPLICATION NUMBER: US/11. MINDERSO OF COLINIORS	0 10 OHZ	Oy 1103 TGGGAACCAGGGCTTCGNCAGC Db 3 TGGGAACCAGGGCTTGG Oy 1163 TTTCACANCTGGGCTTGC- Db 58 TTTCACANCTGAGGCCTTGC Oy 1223 GACAGAGGAGGATGGNCAGGA Oy 1283 GACAGAAGGAGGATGGNCAGGA Oy 1283 GACAGAAGGAGGATGGNCAGTTG Oy 1283 GACAGAAGGAGGATGGNCAGTTG Oy 1283 GACAGAAGGAGGATGGNTGA Oy 1283 GACAGAAGGAGATGGNTGA Oy 1283 GACAGAAGGAGATTGA Oy 1283 GACAGAAGGAGATTGA Oy 1283 GACAGAAGGAGATTGA Oy 1283 GACAGAAGGAGAATTGA OY 1284 GANCAGAGAAGCAGATTGA OY 1343 GANCAGAGAAGCAGATTGA
Query Match 29.2%; Score 769.2; DB 13; Length 1400; Best Local Similarity 82.9%; Pred. No. 2.6e-174; Accession of the conservative and the con	Qy 1223 GACAGAAGGAGGATTNNACCTYGGGGAACAAACAGGGATCTTINTTCT 1282 Db	1343 GANCAGGGAGAGCTTCCAGCTCAGAGGGGTGGGGCGAGCCCTTCGGCCCT 1402	Oy 1523 ACCCCTTGCCTNGGCCTNCGCCTNGGCCAGCTCANCCCCTTTTGGGTGTAGGGGAAAAGA 1582 Db 390 ACCCCTTGCCTGGCCAGCTCACCTGGCCAGCTCA-CCCCTTTTGGGTGTAGGGGAAAAGA 445 Oy 1583 ATGCCTGACCCTGGGAAGGCTWCCCTGGTAGAATACACCACACTTTTCAGGTTGTTGCAA 1642 Db 446 ATGCCTGACCTGGGAAGGCTCCCTGGTAGAATACACCACACTTTTCAGGTTGTTGCAA 504 Oy 1643 CACAGGTCCTGAGTTGACCTCTGGTTAGAATACACCAAAGAAGGTGTTAAAGTGAAGT Db 505 CACAGGTCCTGAGTTGACCTCTGGTTCAGCCAAAGAACGTGTTAAGTGAAGT 505 CACAGGTCCTGAGTTGACCTCTGGTTCAGCCAAAGAACGACCAAAGAAGGTGTTAAGTGAAGT 506 CACAGGTCCTGAGTTGACCTCTGGTTCAGCCAAAGAAGAACGTGTTAAGTGAAGT 507 CACAGGTCCTGAGTTGACCTCTGGTTCAGCCAAAGAACGATGAAGTAGTAAGTGAAGT 507 CACAGGTCCTGAGTTGACCTCTGGTTCAGCCAAAGAACGATGAAGAAGTGTGTAAAGTAGAAGT 507 CACAGGTCCTGAGTTGACCTCTGGTTCAGCCAAAGAAGATGTGTAAAGTGAAGTAGAAGT 508 CACAGGTCCTGAGTTGACCTCTGGTTCAGCTCAAAGAAGATGTGTAAAGTAGAAGTTGAAAGTAGAAGTAGAAGA	Oy 1703 GGTTCTCAGTNCCCCACACATGGCCCCTTTGCTGCTGGCTACCACTTTCCCCAGAGCA 1762	1883 ATGATCAGGCTNAAGGNAAAGCAGAGAGAGAGAGACGYTCCGGCGCCCCAGNCCCACTN 1943 ATGATCAGGCTNAAGGNAAAGCAGCAGAGAGAGAGCGTCCGGCGCCCCAGNCCCCACTN 1943 ATGATCAGTGCTNAA-GGAAAGCAGCAGAGAGCACCCCAGCCCCACTAT 1943 ATGATGTNCCAGCTGCTNCCCCAGNAGCACAGCTNCAGCTACTA 1943 ATCAGTGTNCCAGCTNCCCCAGNAGCACAGCTNCAGCACTAT 1943 ATCAGTGTNCCAGCTGCTNCCCAGNAGCAGCTNCAGCACATACACTAC 1943 ATCAGTGTNCCCCTGCCCTNGGCCANGAGGACACACGCACACACACACACACACACACA

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in
Arrays for Monitoring Expression Profiles of Drug
                                                                                                                                                                                                          ACTNCCTCAAACCTCTTNNCCAGNATTTCTCTAAGAATAG 2242
                                                             CCCAGCTTAGCCTCTTCTCCCAGGGAGCTANCTCAGGAC 2302
                                                                                                 TGTGNAATCGTCAGGGGTGTCTGCTAGCCTCAACCTCCT 2362
                                                                                                                                    CCGTGGGAGAAGCTCATTCCCACATCTTGCCAAGACAGC 2422
                                                                                                                                                                       31;
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red. No. 2.6e-174;
Mismatches 166; Indels 79; Gaps
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11/060,756
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APPLICANT: Kinch, Deborah
APPLICANT: Rosenberg, Michael
APPLICANT: Rosenberg, Michael
APPLICANT: Stak, Suzanne
APPLICANT: Stak, Suzanne
APPLICANT: Li, Huo
APPLICANT: Li, Huo
APPLICANT: Derbel, Maher
TITLE OF INVENTION: Pragments of, Cynomolgus Monkey Genes and the Use Thereof
TITLE OF INVENTION: Pragments of, Cynomolgus Monkey Genes and the Use Thereof
TITLE OF INVENTION: 12/60/680,544
CURRENT APPLICATION NUMBER: 2005-05-13
NUMBER OF SEQ ID NOS: 48714
SOFTWARE: Patent Sequence Analysis Tool Version 1.0
                                                                                                                                               1005
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                                                                                                425 CGGCCATCGACCTGCAGTGCACACTGGCCCCTGATGGCAGCTTCGCCTGGAGGGG
                                                                                                                                               946 TCAAGCATGGCCAGCTGGAGAACAGGCCCTAACCCTGCCCTCCACCGCCGGCTCCACACT
                                                                                                                                                                    485 TCAAGCATGGCCAGCTGGAGAACAGGCCCTAACCCTGCCCTCCACGCGGCGGCTCCACACT
                                                                                                                                                                                                                                            545 TGCCGGAAGCCTTCCTGCTTCGGTGCACGATGCTTGCCCTTGAAACACAGGCTCAGC
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                                                                           CGGGCATCGACCTGCAGTGCACACTGGCCCCTGATGGCAGCTTCGCCTGGAGCTGGAGGG
                                                                                                                                                                                                                       1006 GCCGGAAAGCAGCCTTCCTGC-TCGGTGCACGATGC-TGCCCTGAAAACACAGGCTCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.2%; Score 295.6; DB 15; Length 3658;
28.7%; Pred. No. 1.4e-60;
tive 1; Mismatches 1491; Indels 107; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cooper, Matthew
APPLICANT: Kinch, Deborah
APPLICANT: Rosenberg, Michael
APPLICANT: Subramaniam, S. Sai
APPLICANT: Szak, Suzanne
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OTHER INFORMATION: n = A,T,C
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LOCATION: (1)...(3658)
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Best Local Similarity
Matches 645; Conservat
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COTHER INFORMATION: 68% homologous to Mus musculus Pro-Pol-dUTPase
COTHER INFORMATION: polyprotein, accession number Y12713, Smith-Waterman Score=354.
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CACCTGCACATCCGGGAGTTCCACCGGGTCAAGTGGGAGACATCGCCACTGGCATCAGC 806
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                                                                                            AGCCAGATCCCAGCTGCAGCCTTCAGCTTGGTCACCAAAAAAGACGGGCAGCCTGTTCGCTAC 112
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                                                                       AGCCAGATCCCAGCTGCAGCCTTCAGCTTGGTCACCAAAGACGGGCAGCCTGTTCGCTAC
                                                                                                                                           GACATGGAGGTGCCAGACTCGGCATCGACCTGCAGTGCACTGGCCCCTGATGGCAGC
                                                                                                                                                                GACATGGAGGTGCCAGACTCGGGCATCGACCTGCAGTGCACACTGGCCCCCTGATGGAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTCAACAGCCTGTCCCAGCCATTTTCTCTGGAGGAGCAGGAGCAAATTCTCTCGTGCC
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22.4%; Score 588.2; DB 8; Length 722;
Best Local Similarity 92.4%; Pred. No. 6e-131;
Matches 668; Conservative 2; Mismatches 43; Indels 10
                                                                                                                                                                                                                                                                                                                                                                            A PEDELICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                ; Sequence 15296, Application US/10450763; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: SIMILAR
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US-10-450-763-15296
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  APPLICANT: Kinch, Deborah
APPLICANT: Rosenberg, Michael
APPLICANT: Subramaniam, S. Sai
APPLICANT: Subramaniam, S. Sai
APPLICANT: Subramaniam, S. Sai
APPLICANT: Li, Huo
APPLICANT: Li, Huo
APPLICANT: Li, Huo
APPLICANT: Derbel, Maher
TITLE OF INVENTION: Pragments of, Cynomolgus Monkey Genes and the Use Thereof
TITLE OF INVENTION: Pragments of, Cynomolgus Monkey Genes and the Use Thereof
TITLE OF INVENTION: NUMBER: US/60/680,473
CURRENT APPLICATION NUMBER: US/60/680,473
KUMBER OF SEQ ID NOS: 48714
SOFTWARE: Patent Sequence Analysis Tool Version 1.0
SEQ ID NO 32424
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Pred. No. 1.4e-60;
1; Mismatches 1491; Indels 107;
                                                                                                                                                                                                                                                                                 LOCATION: (1)...(3658)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 28.7%;
Matches 645; Conservative
                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Macaca Mulatta
                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
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APPLICANT: Kinch, Deborah
APPLICANT: Rosenberg, Michael
APPLICANT: Rosenberg, Michael
APPLICANT: Sazk, Suzanne
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APPLICANT: Li, Huo
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APPLICANTON: Nucleotide Array Containing Polynucleotide Prob
TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Prob
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TITLE OF INVENTION: Number: 2052-05-13
NUMBER OF SEQ ID NOS: 487114
SOFTWARE: Patent Sequence Analysis Tool Version 1.0
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APPLICANT: Li, Huo
APPLICANT: Li, Huo
APPLICANT: Bandaru, Raj
APPLICANT: Bendaru, Raj
APPLICANT: Derbel, Maher
TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide
TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide
TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide
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GENERAL INFORMATION:
APPLICANT: Cooper, Matthew
APPLICANT: Kinch, Deborah
APPLICANT: Rosenberg, Michael
APPLICANT: Subramaniam, S. Sai
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OTHER INFORMATION: n = A,T,C
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Pred. No. 1.4e-51;
1; Mismatches 269; Indels
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; OTHER INFORMATION: n = A,T,C or
US-60-680-544-11056
                           TYPE: DNA ORGANISM: Macaca Fascicularis
                                                                                                                                        Query Match 9.8%;
Best Local Similarity 59.8%;
Matches 490; Conservative
                                                                   NAME/KEY: misc_feature
SEQ ID NO 11056
LENGTH: 761
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RESULT 15 US-60-680-473-10785/c

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APPLICANT: Kinch, Deborah
APPLICANT: Kinch, Deborah
APPLICANT: Rosenberg, Michael
APPLICANT: Scak, Suzanne
APPLICANT: Subramaniam, S. Sai
APPLICANT: Stak, Suzanne
APPLICANT: Li, Huo
APPLICANT: Li, Huo
APPLICANT: Derbel, Maher
TITLE OF INVENTION: Raj
APPLICANT: S15902000
CURRENT APPLICATION NUMBER: US/60/680,473
CURRENT FILING DATE: 2005-05-13
NUMBER OF SEQ ID NOS: 48714
SOFTWARE: Patent Sequence Analysis Tool Version 1.0
SEQ ID NO 10785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2319 CAGCTGTGNAATCGTCAGGGGGTGTCTGCTAGCCTCAACCTCCTGGGGCAGGGGACGCCG 2378
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Sequence 10785, Application US/60680473 GENERAL INFORMATION:
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                                                                     APPLICANT: Cooper, Matthew . . APPLICANT: Kinch, Deborah APPLICANT: Rosenberg, Michael APPLICANT: Subramaniam, S. Sai
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ORGANISM: Macaca Fascicularis
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, OTHER INFORMATION: n = A,T,C
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1 (bases 1 to 1253)
Wallach, D. Mallini,N., Boldin,M., Kovalenko,A. and Mett,I. MoDULATORS OF TNF RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR PREPARATION AND USE
PATENTY MO 9737016.A 4 09-OCT-1997;
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1253; Conservative 0; Mismatches
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LOCUS
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TITLE
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CQ700802 Sequence
BV17772 sqmm6310
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Copyright (c) 1993 - 2005
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/trānslation="MAPAQRCPLCRQTFFCGRGHVYSRKHQRQLKEALERLLPQVEAA RKAIRAAQVERYVPEHERCCWCLCGGCEVREHLSHONLTVLYGGLLEHLASPEHKKAT WKFWRENKEAYQMKEKFLYPPQDYARFKKSMYKGLDSYERKENKVIKEMAAQIREVEQ SRQEYVESVLEPQAVPDPEGGSAPRRKGMYSKGLDSYEREKBYLVIKEMAAQIREVEQ GREYTYRSVLEPQAVPDPEGSSAPRKGMYSKGLSSZLQQPSNLDLPPAFELDWMET GPSLTFIGHQDIPQVGNIHSCATPPPMYIQDERYIAGNGSIGPSYEFLKEKEKGKCKLKK LPPDRYGANFDHSSRTSAGWLDSFGRVWNNGRRWQSRHQFKTEAAAMKKQSHTEKS"
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                               Arai Y. Kubo, T., Ohira, M., Gamou, T., Maeno, G., Sakiyama, T., Toyoda, A., Hattori, M., Nakagawara, A. and Ohki, M.
Direct Submission
Submission
Submitted (17-007-2002) Yasuhito Arai, National Cancer Center Research Institute, Molecular Oncology Division; 5-1-1 Tsukiji, Chuou-ku, Tokyo 104-0045, Japan (B-mail:yarai@ganz.ncc.go.jp, Tel:81-3-3542-2511(ex.4752), Fax:813-3542-0688)
This gene was identified within a LOH region at 11q23.3 of neuroblastoma. Reference sequence was predicted from genomic sequences of a BAC contig mapped at 11q23.3 using several gene prediction programs. Expression was analyzed by RT-PCR and Northern blot.. Then, a part of this CDNA was obtained by CDNA
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cds.
                 DLNB14 mRNA, complete
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mol_type="mRNR"
db_xref="taxon:9606"
/chromosome="11"
/map="11q23.3"
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scherfin, M.J., Usdin, T.B., Toshiyuti, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Morkernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
WWb Site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQVEAARRAVRAAQVERYVPEHDRČCWCPCCGCEVRKHLSHGNLTVLHGGLLEHLASP
EHKKATNKFWWENKANAQMKEKFLISPQDYARFKKSMVKGLDSYEEKEDEVIKEMAAQ
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/translation="PPGPGSMAPPQRCPLCRQTPFCGRGHVYSHKHQRQLKGALERLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (01-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 120 Row: j Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction.
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/clone_lib="NCICGAP_Co24"
/lab_host="PH10B"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
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/protein id="AAH5529.1"
/db_xref="G1:33416550"
/db_xref="LocusID:382073"
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/db_xref="LocusID:382073"
/db_xref="MGI:2685960"
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/clone="IMAGE:4205568"
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/strain="FVB/N"
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AUTHORS
TITLE
JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1175)
                                                                                                                                                                  813 GCTGGGAACCAAGAAATAGGACCATCCTATGAAGAATTTCTTAAAGAAAAGGAAAAAAGG
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                                                            GTCCAGATGAAAGAAGTTTCTGGTCACTCCCCAGGATTATGCGCGATTCAAGAAATCC
                                                                                           GTCCAGATGAAAGAGAAGTTTCTGGTCACTCCCCAGGATTATGCGCGATTCAAGAAATCC
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CAGACATCAACTCCAAAACTGAAGCTGCAGCAATGAAGAAGCAGTCACATACAGAAAAA 1039
IREVEGSRQEVVRSVLEPQAESDPEEGSSAPESWKATNGHVASSSQOVSHLALQPVAE
KLOWETGQQLIFIGHQDTPGIGNIHSCATPPWNIQEERHSSGSLPIGPSYEEFLKEKE
KQKLKKLPPDRVGANFDHSSNTSAGWLPSFGRVWNNGRRWQSRHQFKTEAATRSKQPR
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                                                                                                                 Gaps
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6
                                                                                    Length 1175;
                                                                                                                Indels
                                                                                     DB 10;
                                                                                     Score 723.8; DB 10;
Pred. No. 7.9e-181;
0; Mismatches 197;
                                                                                       57.8%;
81.4%;
                                                                                                      Similarity 81.4
01, Conservative
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Direct Submission

Direct Submission

Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jul 22, 2000 this sequence version replaced gi:5777578.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em; EmBL; Sw., SWISSPROT; Tr., TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence that of constructed by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence is the entire information can be found at http://www.sanger.ac.uk/HGP/Chr20 of Clone RPF-107712 is at 71329 in this sequence. This sequence is the entire insert of clone RPF-107712 is at 71329 in this sequence. This sequence was finished as follows unless otherwise noted; all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality = compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mis subclone; and the assembly was confirmed by restriction digest. RP4-718P11 is from the library RPCI-4 constructed by the group of Pieter de Jong. For http://www.databac./home.htm
                                                                                                                          1159
                                                         1014 echgaagerneccaggegearnecanementeargeccaacaarrecagia 1073
                                                                                                                                                                                    TTATTCCTAAGACCAAA----TCCTCCCGGCTGCCTTAGGAAACAGATGCACCCATTC 1128
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 104913)
GCTAATCATGCTCTCTACCAACTACCATGAGGCTAAAAGCCAAAGTCAACCCCTA
                                                                                                                             TTATACCTTCCACCCAAATTCTTTATCATTGTCTTTAGGAAACAGACATACTCATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSJ718P11

Human DNA sequence from clone RP4-718P11 on chromosome

20p12.1-12.3. Contains part of the gene for a novel class II
aminotransferase similar to serine palmotyltransferase, ESTS, and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL109983.2 GI:9368492
HTG; aminotransferase; serine palmotyltransferase.
Homo sapiens (human)
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VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
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/map="p12.1-12.3"
/clone="RP4-718P11"
/clone_lib="RPCI-4"
                                                                                                                                                                                                                                                       1160 ATTIGATITAATAAAGTITTATITIC
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gene

TITLE Homo sapiens chromosome 20, clone RP11-303K20 JOURNAL Unpublished Cloases 1 to 192748 MUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Bardwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewert, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Leho, C., Locke, K., Macdonald, P., Marquis, N., McLaughlin, J., Meldrim, J., McDawan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,	Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subreamanian, A., Talamas, J., Tasfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wymn, D., Ye, W.J., Zimmer, A. and Zody, M. TITLE Direct Submission JOURNAL Submission JOURNAL Submission JOURNAL Street, Cambridge, MA 02141, USA RESEARCH, 32 Charles Street, Cambridge, MA 02141, USA JATHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brom, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Donino, M., Doyle, M., Rerreira, P., FitzHugh, W., Gage, D., Gaaldgan, J., Grand, P., Horton, L., Grand, C., Hagos, B., Heaford, A., Horton, L.,	<pre>Howland,JC., Illev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRocque,K., Lamazares,R., Janders,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrin,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Schlauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., LE Direct Submission</pre>	∢
TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS	TITLE	TITLE JOURNAL COMMENT
Matches 672; Conservative 0; Mismatches 105; Indels 40; Gaps 8; QY 406 CACTCCCCAGGATTATGCACGATTCAAGAAATCCCTGGTGGAAGATTCCTATGA 465 Db 15503 CCCTCCCCAGGATTATGCACGATTCAAAAATCCCTGGTGGAAGCTTCCTATGA 15444 QY 466 AGAAAAAGAGGATAAAGTGATCAAGAGAAGAGAGATGGCAGCTCAGATCTGTGAGCTGAACAAGAGGAGTGCAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	15323 15323 630 15263 690 15204 750		990 CICARANGICIGAGGAATGAAGGAGGATGACATAGAAAAAG 14905 CT-CAGAACTGAAGCTGCAGCAATGAACGAGTCACATAGAAAAAAG 14905 CT-CAGAACTGAAGCTGCAGCAACTACAGATAAAAAAATG 1041 CTAATCATGCTCTCTACCAACTACCATGAGGCTAAAAGCCAAGTCAACTCACTACTACTACTACTCACTACTACTCACTACTA

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144360 GGCTGCCCTC-TTTGGACCGTGTCTGGAATAATGGATACTGTTGGCAGTTCAGGCGGTCAA 144418
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                               143941 CTGGCAGGAGGAGGTTCAGTCTTGTCTAGAGGTTGGTTTCCCTCGGAGGATCCAGACCCC
                                                                                                                                                                                                                                                                                                       AAGAAATAGGACCATCCTATGAAGAATTTCTTAAAGAAAAGGAAAAACAGAAGTTGAAAA
                                                                                                                                                                                                        TCCACTCAGGTGCCACACCTCCCTGGATGATCCAAGATGAAGAATACATTGCTGGGAACC
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                                                                         AGAAAAGGAGGATAAAGTGATCAAGGAGATGGCAGCTCAGATCCGTGAGGTGGAGCAGAG
                                                                                                                                CCGACAGGAGGTGGTTCGGTCTTTAGAGCCT--------CAGGCAGTGC
                                                                                                                                                                                         CAGACCCAGAAGAGGCCTCTTCAGCACCTAGAAGCTGGAAAGGGATGAACAGCCAAGTAG
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 45728 12-SEP-2002;
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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39.0%; Score 489; DB 2; Length 192748;
Best Local Similarity 82.3%; Pred. No. 4e-118;
Matches 672; Conservative 0; Mismatches 105; Indels 40;
                                                                                                                                                                                                                                                                                                                    48774: Contig of 8458 bp in length
48874: gap of 100 bp
79145: contig of 30271 bp in length
79245: gap of 100 bp
132530: contig of 53285 bp in length
132630: gap of 100 bp
192748: contig of 60118 bp in length.
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of 7078 bp in length
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of 5690 bp in length
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of 3957 bp in length
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of 6125 bp in length
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of 8458 bp in length
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/note="assembly_fragment"
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'note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/mol_type="genomic DNA"
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/chromosome="20"
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1 (bases 1 to 1191)
1 (bases 1 to 1191)
2 (Asson, Marrellos, Kammerer, S., Hoyal, C.R., Shi, M.M., Cantor, C.R. and Braun, A. Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
                                                                                                                                                                                                                                                                                                                                     CAGGATATACCAGGAGTTGGTAACATCCACTCAGGTGCCACACCTCCCTGGATGATGCAA
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Best Local Similarity 97.0%; Pred. No. 7.3e-95;
Matches 448; Conservative 1; Mismatches 8; Indels
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/db_xref="taxon:9606"
/clone lib="Human DNA (Sequenom)"
<1. .>601
                     Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 601.
                                                                                          Location/Qualifiers
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Pharmaceuticals division
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       Fax: 18582029020
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Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M., Cantor,C.R. and Braun,A.
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene Regions
                                                                                                                                                                                                                       GGTAACATCCACTCAGGTGCCACACCTCCCTGGATGATCCAAGATGAAGAATACATTGCT
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                                                                                                                                    Score 444.4; DB 6;
Pred. No. 1.1e-106;
0; Mismatches 6;
          Location/Qualifiers
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3595 John Hopkins Court, San Diego,
Tel: 18582029018
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Pharmaceuticals division
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Matches 493; Conservative
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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llarity 83.0%; Pred. No. 1.3e-75;
Conservative 0; Mismatches 66;
                                                                                                                        Score 392; DB 6;
Pred. No. 9.1e-93;
0; Mismatches 5;
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PE Corporation (NY) (US)
Location/Qualifiers
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CQ752826

    .401
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98.8%;
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Matches 395; Conserv
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0102568-A 2032 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 GATGAAGAATACATGCTGGGAACCAAGAAATAGGACCATCCTATGAAGAATTCTTAAA
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/mol type="genomic DNA"
/mol type="genomic DNA"
/b xref="taxon:9606"
/clone lib="Human DNA (Sequenom)"
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Pred. No. 8.1e-95;
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1595 John Hopkins Court, San Diego, CA
Tel: 188282029018
Fax: 18582029020
Email: abraun@sequenom.com
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 1191.
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SM Gallus gallus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

1 (bases it or 130)

S Boardman, P. E., Bonfield, J. K., Brown, W. R. A., Carder, C., Chalk, S. E., Croning, M. D. R., Davies, R. M., Francis, M. D., Grafham, D. V., Humbray, S. J., Humbray, S. J., Munt, P. J., Maddison, M., McLaren, S. R., Niblett, D., Overton, I. M., Rogers, J., Scott, C. E., Taylor, R. G., Tickle, C. and Wilson, S. A.

Direct Submission

Submitted (04-MAY-2004) Sanger Institute, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: chickest@bms.umist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequencing project.
This sequencing project.
This sequence is from the
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
from a library constructed by Elizabeth Bosch. CDNA was prepared
from a Na extracted from heads, normalised, and poly A-trimmed.
ECORI-NotI cut CDNA was then ligated into the vector. Vector:
pBluescript II KS(+); Site_1: ECORI; Site_2: NotI Host: Escherichia
coli DH10B.
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/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
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/db_xref="taxon:9031" /clone="ChEST321117" /clone_lib="CSEQCHN24" /dev_stage="stage 22"

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                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGAGGTCCAGATGAAAGAGATTTCTGGTCACTCCCCAGGATTATGCGCGATTCAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   615 TGAACAGCCAAGTAGCTTCCAGCTTACAGCAGCCCTCAAATTTGGACCTGCCACCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAPATITIAAGCIGGAIGGAAICAGGCCAGGCIIIGACCIICAIIGGCCACCAGGAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGAGTTGGTAACATCCACTCAGGTGCCACACCTCCCTGGATGATCCAAGATGAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        751 AGGATGGAAGCAACAACAAATTGGTCCTTCATATGAGGAATTTCTCAAGCAAAAGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     871 AGACAGGAGACAGCTGCCTTCCTTT-GGCCGGGTTTGGAATCACGGCAGGAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACATTGCTGGGAACCAAGAAATAGGACCATCCTATGAAGAATTTCTTAAAGAAAAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              855 AACAGAAGTIGAAAAACTCCCCCCAGACCGAGITGGGGCCAACTITGAICACAGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             930 cagriccaggcaric-agrirragagccgaarcaggaggaaagaagaaggrgarcaga
                                         Gaps
                                        5;
   Length 1390;
                                                                                                                                                                                                                   198 AGGIGGAGCGCTAIGIGCCC---GAACACGAGCGAIGCIGCIGGIGCCIGI
                                      Indels
 Score 309; DB 5; L
Pred. No. 1.2e-70;
O; Mismatches 390;
Query Match
Best Local Similarity 59.4%;
Matches 578; Conservative
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966 CGCCGCTGGCAGTCCAGACATCAACTCCAAAACTGAAGCTGCAGTGAAGAAGCAGTC 1025
                                                                   Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 ATGAAGAATACATTGCTGGGAACCAAGAAATAGGACCATCCTATGAAGAATTTCTTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        846 AAAAGGAAAAACAGAAGTTGAAAAACTCCCCCAGACCGAGTTGGGGCCAACTTTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.7 ADAAGGAAAACAGAAGTTGAAAAAACTCCCCCCAGACCGAGTTGGGGCCAACTTTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 ACAGCTCCAGGACCAGTGCAGGCTGGCTGCCCTCTTTT-GGCCGCGTCTGGAATAATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 CGCCGCTGGCAGTCCAGACATCAAA-TTCAAAACTGAAGCTGCAGCAAGGAAGAAGCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                         117 GGATATACCAGGAGTIGGTAACATCCACTICAGGIGCCACACCTCCTGGATGATCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                786 ATGAAGAATACATTGCTGGGAACCAAGAAATAGGACCATCCTATGAAGAATTTCTTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               906 ACAGCTCCAGGACCAGTGCAGGCTGGCTGCCTCTTTTGGGCCGCGTCTGGAATAATGGA
                                                                                                                                                                                                                                                                                                                                                                                         GGATATACCAGGAGTTGGTAACATCCAC-TCAGGTGCCACACCTCCCTGGATGATCCAAG
                                                                                                                                           Patent: WO 02068579-A 13377 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                                                                                                   1. .433
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                            Query Match 22.5%;
Best Local Similarity 98.7%;
Matches 315; Conservative
 Homo sapiens
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Best Local Similarity
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CQ728296
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F 10-APR-1999 UP 1998543068
F 10-APR-1997 US 08/835913
I KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI DAVID MERBERG,
                                    PAT 27-AUG-2002
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                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    (bases 1 to 421)

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C12N15/12, C12NS/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:
Double;
CC Tpology: Linear;
FH Key Location/Qualifiers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGATGAAGAATACATTGCTGGGAACCAAGAAATAGGACCATCCTATGAAGAATTTCTTAA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAAAAGGAAAAACAGAAGTTGAAAAACTCCCCCCAGACCGAGTTGGGGCCAACTTTGA 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 AGAAAAGGAAAAACAGAAGTTGAAAAACTCCCCCCAGACCGAGTTGGGGCCCAACTTTGA 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 CTGGCTCATGTTTTCAGCCAAGTAGCTTCCAGCTTACAGCAGCCCTCAAATTTGGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAGGATATACCAGGAGTTGGTAACATCCACTCAGGTGCCACACCTCCCTGGATGATCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                   Jacobs, K., Mccoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D. Treacy, M., Spaulding, V. and Agostino, M.J. Secreted expressed sequence tags (BESTs)
Patent: JP 2001519666-A 410 23-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 421;
                                    linear
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                                  421 bp DNA expressed sequence tags (sESTs).
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tt WO02068579.

    .421
    /organism="Zea mays"
    /mol_type="genomic DNA"
    /db_xref="taxon:4577"

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                                                                    BD058555 BD058555.1 GI:22604161
JP 2001519666-A/410.
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CQ727443.1 GI:42293443
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Matches 303; Conserv
                                                                                                                            Zea mays
                                                                                                                                           Zea mays
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LOCUS
DEFINITION
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RESULT 12
               BD058555
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176 845 236 905 296

785

Gaps

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Indels

Score 281.4; DB 6; Pred. No. 2.2e-63; 0; Mismatches 1;

Length 433;

414

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PAT 03-FEB-2004
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent: WO 02068579-A 14230 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                                                                                                CQ728296 263 bp DNA Sequence 14230 from Patent WO02068579. CQ728296

    .263
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

1026 ACATACAGAAAAAGCTAA 1044
                                                     ACATACAGAAAAAAGCTAA 433
                                                                                                                                                                                                                                                                                      CQ728296.1 GI:42296746
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Homo sapiens
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us-09-155-676b-4.rge

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139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 GTGCGGGAACACCTGAGCCATGGAACCTGACGGTGCTGTACGGGGGGCTGCTGTAGGGT 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 CCTTCTTCTGTGGTCGCGGGCACGTTTACAGCCGCAAGCA-CCAGCGGCAGCTGAAGGAG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 grititgagaggcrccrccccccaggrggaggcgccccccaaggccarccgcgcccrcag 199
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                                                                                    344 GCAACCAACAAATTCTGGTGGGAGAACAAAGCTGAGGTCCAGATGAAAAAAAGAGTTTCTG 403
                                                                                                                                                                                                                             284 AACCTGACGGTGCTGTACGGGGGGGTGCTGGAGCATCTGGCCAGCCCAGAGAAA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 CCTTCTTCTGTGGTCGC-GGCACGTTTACAGCCGCAAGCACCCCAGCGGCAGCTGAAGGAG
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                                                      1 GIGGAGGCGGCCGCAAGGCCATCCGCGCTCAGGTGGAGCGCTATGTGCCCGAACAC
                                                                                                                                                                   164 GTGGAGGCGGCCCGCAAGGCCATCCGCGCCGCTCAGGTGGAGCGCTATGTGCCCCGAACAC
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Gaps
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19.5%; Score 244.8; DB 6; Length 374;
Best Local Similarity 98.5%; Pred. No. 1.1e-53;
Matches 268; Conservative 0; Mismatches 2; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 22599 06-SEP-2000; Genset (FR)
                                                                                                                                                                                                                                                                                                                                                                                   linear
0; Indels
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                                                                                                                                                                                                                                                                                                                                                                           374 bp DN Sequence 22599 from Patent EP1033401.

    .374
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

 Mismatches
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44 43.2 3.4 468 5 ABV40808 Abv40808 Human pro ALIGNMENTS RESULT 1 AAV03325 XX AAV03325 XX AAV03325 XX AAV03325 XX AAV03325 XX AAV03325 XX AAV03325 XX AAV03325 XX AAV03325 XX AAV03325 XX AUDIAMENT COLOR 15, Which encodes a TRAF2 binding protein. XX Human tumour necrosis factor receptor-associated factor 2; TRAF2; XX Human tumour necrosis factor receptor-associated factor 2; TRAF2; XX Human tumour necrosis factor receptor-associated factor 2; TRAF2; XX Human tumour necrosis factor receptor-associated factor 2; TRAF2; XX Human tumour necrosis factor receptor-associated factor 2; TRAF2; XX Homo sapiens. XX Homo sapiens. XX HOS 09-OCT-1997; XX 09-OCT-1997; XX 01-APR-1997; 97WO-IL000117. XX 02-APR-1996; 96IL-00119133. XX YEDA NEDA RES & DEV CO LTD. XX YEDA PEDA RES & DEV CO LTD. XX WALL 1997-503101/46. DR P-PSDB; AAM42401. XX NA HAM42401. XX NA HAM42401. XX NA HAM42401. XX NA HAM42401. XX NA HAM42401. XX NA HAM42401. XX NA HAM42401. XX NA HAM42401. XX NA HAM42401. XX NA HAM42401. XX NA HAM42401. XX NA HAM42401. XX XX NA HAM42401. XX XX XX XX XX XX XX XX XX X
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The present sequence is that of clone 15, which encodes a TRAP2 binding protein. Clone 15 is a partial clone, which lacks most of its 5' end of the coding DNA sequence. A cDNA library prepared from B-cells was corrended for proteins that associate with TRAP2, and the present sequence isolated. The clone 15 protein is capable of binding to at least amino cids 222-501 of TRAP2. The TRAP-2 binding proteins can be used for mediation or mediation in cells of the activity of NF-kappaB or any other intracellular signalling activity modulated or mediated by TRAP2. TRAP-binding proteins are especially used for prevention or treatment of pathological conditions associated with NF-kB induction, e.g. acute comparable of conditions associated with NF-kB induction, e.g. acute comparable of the pancreas that results in diabetes, the death of cells in graft rejection, the death of cligodendrocytes in the brain in multiple sclerosis, and AlDS-inhibited T cell suicide which causes conflict in for modulating of ligands capable of binding to a protein, which are useful for modulating cellular activity modulated by TRAP2.
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                                  The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating of polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The colypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                     and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
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0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.1%; Score 514.6;
SEQ ID NO 19571; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 97.4%;
Matches 568; Conservative
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                                                                                                                                                                                                                                                           Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                              DNA encoding novel human diagnostic protein #23046.
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84.9%; Pred. No. 1.1e-129;
tive 0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 23046; 103pp; English
AAS87242 standard; cDNA; 2557 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259
                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (1gs) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have growth of many human tamoers are used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence encodes the human legless (1gs) protein homologue higs-1 described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                    Novel polypeptide useful in therapeutic method for treating disorders of cell fate such as cell differentiation or cell proliferation.
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                                                                                                                                   28-JUL-2000; 2000US-0221502P
AAB71230"
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BRUNNER E.
FROESCH B.
KRAMPS T.
PETER O.
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                                   US2002086986-A1
                                                                  04-JUL-2002
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(FROE/)
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(PETE/)
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1. :3948
//t-tag= a /product= "hlsg-1"
601. :3948
//t-tag= "region encoding protein represented in protein
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                               156 CIGICITAGAGGIIGGIIIICCIICGGAGGAICCAGACCACCICAGGCAGIGCCAGACCCA
                                                                      GAAGAGGCCTCTTCAGCACCTA-GAAGCTGGAAAGGGATGAACAGCCAAGTAGCTT-CCA
                                                                                       GAAGAGGCTCTTCAGCACCTAGGAAGCTGGAAAGGGATGAACAGCCAAGTAGCTTCCCA
                                                                                                                                     CAGGACCATCTCTGACATTCATTGGCCATCAGGATATA-CCAGGAGTTGGTAACATCCAC
                                                                                                                                                                                                                                                                          TCAGGTGCCACACCCCCCTGGATGATCCAAGATGAAGAATACAT----TGCTGGGAACCA
                                                                                                                                                                                                                                                                                            516 AGAGGAAAAACAGAAGTTGAAAAACTCCCCCCCCAGACCCGAGTTGGGGGCCAACTTT
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                                                 GTGGAGCGCTATGTGCCCCGAACACGAGCGATGCTGCTGCTGCTGCTGCTGCGGCTGTGAG
                                                                                                                                                 260 GIGCGGGAACACCTGAGCCAIGGAAACCIGACGGGGTGCTGTACGGGGGGCTGCTGGAGCAI
                                                                                                                                                                                                  3259 GTGCGGGAACACTGAGCCATGGAAACCTGACGGTGCTGTACGGGGGGGCTGCTGCAGCAT
                                                                                                                                                                                                                                                      320 CTGGCCAGCCCAGAGCACAAGAAAGCAACCAACAAATTCTGGTGGGAGAAACAAAGCTGAG
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                    Legless protein; 1gs; cell fate disorder; blood disease; gene therapy; cancer; tissue regeneration; tissue repair; cytostatic; gene; ss.
Novel Lgs polypeptide useful for isolation of Lgs-binding proteins, diagnosing disorders of cell fate, treating diseases such as cancer
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                                                                                                                                                                        AAD62643 standard; cDNA; 3948
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27-JUL-2001; 2001US-00915543.
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Matches 475; Conserv
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3439 ATGGTGAAAGGTTTGGATTCCTATGAAGAAAAGGAGGATAAAGTGATCAAGGAGATGGCA 3498
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                                                                                                                                                                              Human; legless; lgs; gene; ss; cell differentiation disorder; cell prollferation disorder; cancer; Wnt pathway; medulloblastoma; colon; breast; head; neck; brain; thyroid; skin; blood disease; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissue regeneration; tissu
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500 GCTCAGATCCGTGAGGTGGAGCAGACAGGAGGTGGTTCGGTCTTTAGAGCC
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/product= "Human Lgs/Bc19"
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27-JUL-2001; 2001US-00915543.
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P-PSDB; ADJ71905.
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140 GCTTTTGAGAGGCTCCTGCCCCAGGTGGAGGCGGCCCGCAAGGCCATCCGCGCCCGCTCAG 199

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3198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3199 GTGGAGCGCTATGTGCCCGAACACGAGCGATGCTGCTGGTGCCTGTGCTGCGGCTGTGAG 3258
                                                                                                               organisms, the nuclectide sequence encoding a protein comprising a positive function in a regulatory pathway and the use of the polypeptide for the isolation of Igs-binding proteins by carrying out an assay chosen from an in vitro binding assay with such a peptide or a co-immunoprecipitation from vertebrate or invertebrate cell lysates or a mammalian or yeast two hybrid assay. The polypeptide and polymolectide are useful for treating disorders of cell fate, which involves administering therapeutic compounds chosen from invertebrate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCGGGAACACCTGAGCCATGGAAACCTGACGGGGTGCTGTACGGGGGGGCTGCTGGAGCAT 3318
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                                                                                                                                                                                                                                                                                                                 vertebrate Lgs protein homologues or fragments, antibodies, antibody fragments, lgs antisense DNA, lgs antisense RNA, lgs double-stranded RNA, fragments, lgs antisense DNA, lgs antisense RNA, lgs double-stranded RNA, and lpsptides or chemical and natural compounds being capable of interfering with Lgs function, synthesis and degradation. The compound is administered to cell differentiation or cell proliferation. The compound from a pre-neoplastic or non-malignant condition by preventing progression from a pre-neoplastic or non-malignant condition to a neoplastic or malignant state. The cancerous condition is characterised by overstimulation of the Wnt pathway and is medulloblastoma or cancer of the colon, breast, head and neck, brain, thyroid or skin. The therapeutic compound may also be administered to a blood disease to promote tissue regeneration and repair. This sequence represents cDNA encoding a human Lgs/Bc19 partial polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 GCTTTTGAGAGGCTCCTGCCCCAGGTGGAGGCGCCCGCAAGGCCCATCCGCGCCGCTCAG 199
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                                           amino acid domains with a Legless (Lgs) protein and is therefore a functional homologue of Lgs. The invention also relates to a nucleotide sequence encoding a protein present in invertebrate and/or vertebrate
                               or more homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3139 GCTTTGGAGAGGCTCCTGCCCCAGGTGGAGGCGGCCCGCAAGGCCATCCGCGCGCCTCAG
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                         invention relates to a polypeptide sharing one
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36.1%; Score 451.8; DB 12
Best Local Similarity 99.2%; Pred. No. 2.1e-121;
Matches 475; Conservative 0; Mismatches 2;
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objunctions are deposited under the accession intumers ALC 90000. Into sequences are used as tissue markers, chromosomal tags, for altibodies, also as nutritional sources and supplements and in gene therapy. The secreted proteins are useful therapeutically, in human or veterinary medicine, e.g. for modulating cell proliferation or infections, autoimmune disease, organ rejection, or to induce tumour immunity), as regulators of haematopoiesis (e.g. for treating anemia or inconjunction with tumour therapy), to stimulate growth of tissue for wound healing, as fertility control agents, for regulating demonstais or chemokines (e.g. for direction), as necessatic and thrombolytic agents (e.g. in treatment of haemophilia or infarctions), as antimicrobial agents, for modifying biorhythms, as pepetite, or metabolism, as analgesics and many other uses. The proteins are also used to raise antibidies, used as diagnostic immunoassay care also used to raise antibizing) for treating e.g. cancer 2089 2149 2209 844 964 veterinary medicine; cell proliferation; immunostimulant; infection; immunosuppressant; autofimmune disease; organ rejection; tumour; anemia; haematopoiesis; wound healing; fertility control; chemotaxis; analgesic; thrombolytic; haemophilia; infarction; antimicrobial agent; cancer; se Secreted protein; human; tissue marker; genetic disease; gene therapy; 2210 CACAGCTCCAGGACCAGTGCAGGCTGCCTTTT-GGCGTGTCTGGAATAATGG 2090 GATGAAGAATACATTGCTGGGAACCAAGAAATAGGACCATCCTATGAAGAATTTCTTAAA 2150 GAAAAGGAAAAACAGAAGTTGAAAAACTCCCCCCAGACCGAGTTGGGGCCAACTTTGAT CAGGATATACCAGGAGTTGGTAACATCCACTCCAGGTGCCACACCTCCCTGGATGATCCAA 785 GATGAAGAATACATTGCTGGGAACCAAGAAATAGGACCATCCTATGAAGAATTTCTTAAA 905 CACAGCTCCAGGACCAGTGCAGGCTGGCTGCCCTCTTTTGGGGCCGCGTCTGGAATAATGG Gaps ä The invention provides polynucleotides (AAX60579-X60687) encoding specific secreted human proteins (AAY16779-Y16787). The nucleic aci sequences are deposited under the accession number ATCC 98580. The Merberg 2, Length 2556; Sequence 2556 BP; 722 A; 569 C; 520 G; 740 T; 0 U; 5 Other; Indels Evans C, Human secreted protein encoding DNA (clone as20_2). Score 400.8; DB 2; Pred. No. 1.6e-106; 0; Mismatches 7; Racie LA, Nucleic acid encoding secreted human proteins ER, Claim 1; Page 91-92; 107pp; English. Mccoy JM, Lavallie Agostino MJ; 98WO-US023829, 97US-00965789. 98US-00185936, 32.0%; Best Local Similarity 97.4%; Matches 450; Conservative (GEMY) GENETICS INST INC. WPI; 1999-327362/27. P-PSDB; AAY16779 Homo sapiens, WO9924469-A1 06-NOV-1998; 07-NOV-1997; 04-NOV-1998; 20-MAY-1999. χΣ 725 Query Match Jacobs Treacy NAME OF THE PROPERTY OF THE PR ð 셤 g g ò ઠે 엄 ò

2268

AAX60579 standard; DNA; 2556

(first entry)

27-JUL-1999

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Length 401; Indels

76 T; 0 U; 0 Other;

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GGATAAAGTGATCAAGGAGATGGCAGCTCAGATCCGTGAGGTGGAGCAGAGCCGACAGGA
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Pred. No. 2.2e-104;
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23-AUG-2000; 2000US-00649167
                                               98.86;
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                                                                         2328 CACATACAGAAAAAAGCTAATCATGCTCTCTACCAACTACCATGAGGCTAAAAAGC--AAA 2385
                                                                                                           2386 GTCAACACCCCTATTATATACCTTCCA-CCAAATTCTTTATCATTGTCTTTCTTAGGAAA 2444
                                  ACCCCCCTGCCAGTCCAGACTCAA-TTCAAAACTGAAGCTGCAGCAATGAAGAAGCAGT
                                                          CACATACAGAAAAAGCTAATCATGCTCTCTACCAACTACCATGAGGCTAAAAGCCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                          Human; cytostatic; gene therapy; colon cancer; prostate cancer;
                                                                                                                                                              CAGACATACTCATTTGATTTAATAAAGTTTTATTTTC 1186
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                                                                                                                                                                                                                                                                                                                                                                       breast cancer; lung cancer; cancer detection; ss
                                                                                                                                                                                                                                                                                                                                  human polynucleotide, SEQ ID NO: 2032
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                                                                                                                                                                                                                                                      AAF66276 standard; cDNA; 401 BP
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99US-0142311P.
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GCACGAGGTGATCAAGGAGATGGCAGCTCATATCCGTGAGGTGGAGCAGAGGCCGACAGGA
                                                                 GGTGGTTCGGTCTGTCTTAGAGCCTCAGGCAGTGCCAGACCCCAGAAGAGGGCTCTTCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             874
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cerivity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics forensics, gene mapping, identification of mutations and the contained of the processing contained that it is an expression or contained the assess biodiversity and the contained of the contained that it is an expression or contained the assess biodiversity and the contained that it is an expression or contained the contained that it is an expression and contained the contained that it is an expression or contained the contained that it is an expression or contained the contained that it is an expression and contained that it is an expression and contained the contained that it is an expression and contained the contained that it is an expression and contained the contained that it is an expression and contained the contained that it is an expression and contained the contained that it is an expression and contained the contained that it is an expression and contained the contained that it is an expression and contained the contained that it is an expression and contained the contained that it is an expression and contained the contained that it is a contained to the contained that it is an expression and contai
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                                                                                                                                                                                                                                                                                                                                                                                                                                               and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    757 AGGTGCCACACCTCCCTGGATGATCCAAGAAGAATACATTGCTGGGAACCAAGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCTTTTGGGCCGCGTCTGGAATAATGGACGCCGCTGGCAGTCCAGACATCAACTCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1057 CCAACTACCATGAGGCTAAAAGCCAAAGTCAACCAAACCCCTATTATACCTTCCACCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            604 CCAACTACCATGAGGCTAAAAGC--AAAGTCAACAAACCCCTATTATACCTTCCA-CCAA
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Matches 419; Conserv
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corde. The polymucleotides can be used to express recombinant proteins for analysis, characterisation or therapeutic use, as markers for tissues in which the corresponding protein is expressed, as molecular weight markers on Southern gels, as chromosome markers or tags to identify chromosomes or to map related gene positions, to compare with endogenous Chromosomes or to map related gene positions, to compare with endogenous DNA sequences in patients to identify potential genetic disorders, as a source probes to hybridise and discover novel related DNA sequences, as a source of information to derive PCR primers for genetic fingerprinting, to raise anti-protein antibodies and in gene therapy. The proteins can be used to raise antibodies or to elicit another immune response, as reagents in biological fluids, as markers for tissues in which the corresponding protein is preferentially expressed and to treat autoimmune disorders (e.g. multiple sclerosis, systemic lupus erythematosus, insulin dependent diseases, bone fractures, cartilage damage, central nervous system clasorders (e.g. Alzheimer's disease or Parkinson's disease) and cancers. The proteins and polymucleotides are also useful as nutritional sources or sequence represents a human polymucleotide of the invention.
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Human; gene; ss; genetic disorder; genetic fingerprinting;

ADA45162 standard; cDNA; 2489 BP.

ADA45162

(first entry)

20-NOV-2003

EXEXEXEXEX

ADA45162;

Human polynucleotide #72.

autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; insulin dependent diabetes mellitus; graft.versus-host disease; anaemia; periodontal disease; bone fracture; cartilage damage; central nervous system disorder; Alzheimer's disease; Parkinson's disease; cancer; nutrition; carbon source; nitrogen source; New polypeptides and polynucleotides having biological activities, useful as nutritional sources or supplements, or for treating e.g. autoimmune diseases, cancers, bone fractures or damages, or central nervous system The invention relates to human polynucleotides and the polypeptides they ΰ Evans Collins-Racie LA, Disclosure; Page 237-238; 288pp; English La Vallie ER, Spaulding V; 9705-0093045P. 9705-0090100P. 9705-00958304. 9705-0090111P. 9805-00095272. 9805-00096287. 97US-0086234P. 2000US-00746783 98US-00149633 98US-00165960 98US-00130189 98US-00185936 MCCOY J M.
LA VALLIE E R.
COLLINS-RACIE L A. Mccoy JM, I WPI; 2003-521754/49. P-PSDB; ADA45163. TREACY M. SPAULDING V. carbohydrate source EVANS C. MERBERG D. US2003044935-A1. JACOBS 21-DEC-2000; 06-MAR-2003 , K, 11-JUN-1997 08-JUL-1997 02-OCT-1997 27-OCT-1997 08-SEP-1998 01-OCT-1998 08-SEP-1997 07-NOV-1997 05-JUN-1998 11-JUN-1998 17-JUN-1998 04-AUG-1998 04-NOV-1998 disorders. Merberg (JACO/) (TREA/) (SPAU/) Jacobs LVAL, COLL EVAN/ Ношо

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This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include mutritional activity, tissue growth activity, activity, activity, tissue growth activity, activity, activity, receptor/ligand activity, and activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 AGAAAAGGAAAAAACAGAAGTTGAAAAAAACTCCCCCCAGACCGAGGTTGGGGCCAACTTTGA 399
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human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA.libraries.
                                                                                                                                                                                                                                                                                                                                                     23.7%; Score 297; DB 2; Length 421;
llarity 96.8%; Pred. No. 2e-76;
Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                      Sequence 421 BP; 128 A; 110 C; 88 G; 95 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #13671.
                                                    Claim 1; Page 232; 633pp; English
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23-AUG-2000; 2000US-00649167.
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es 303; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                      GGAATAATGGACGCCGCTGGCAGTCCAGACATCAACTCCAAAACTGAAGCTGCAGCAATG 1014
                                                                                                                                                                                                                                                                                                                                                                                                         GGAATAATGGACGCCGCTGG--GTCCAGACATCAA-TTCAAAACTGAAGCTGCAGCAATG 2258
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGAAGCAGTCACATACAGAAAAAAGCTAATCATGCTCTCTACCAACTACCATGAGGCTA 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGCCAAAGTCAACCAAACCCCTATTATACCTTCCACCCCAAATTCTTTATCATTGTCTT 1134
                                                                                                                                                   1969 CATTTCCAACTACAGGATATAAGGAGTTGGTAACATCCACTCAGGTGCCACACCTCCCTG
                                                                                                                                                                                                                   2029 GATGATCCAAGATGAAGA--ACATTGCTGGGAACCAAGAAATAGGACCATCCTATGAAGA 2086
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                                                                                                                  CATTGGCCATCAGGATATACCAGGAGTTGGTAACATCCACTCAGGTGCCACACCTCCCTG
                                                                                                                                                                                  GATGATCCAAGATGAAGAATACATTGCTGGGAACCAAGAAATAGGACCATCCTATGAAGA
                                                                                                                                                                                                                                                    ATTTCTTAAAGAAAAGGAAAAACAGAAGTTGAAAAAACTCCCCCCAGACCGAGTTGGGGC
                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTTAGGAAACAGACATACTCATTTGATTTAATAAAGTTTTATTTTC 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTTAGGAAACAGACATACTCATT--TTTGATTTAATAAAGTTTTTATTTTTC 2421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treacy
                                                                                   19;
                                                  DB 9; Length 2489;
                 699 A; 556 C; 506 G; 723 T; 0 U; 5 Other;
                                                Score 300.4; DB 9; Length
Pred. No. 5.4e-77;
0; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccoy JM, Lavallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV86432 standard; cDNA; 421 BP.
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                                                Query Match
Best Local Similarity 91.5%;
Matches 432; Conservative
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                 Sequence 2489 BP;
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                                                                                                                                                                                                                                    The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbrrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cappendiable for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in the winted specification, but was obtained in the winted specification, but was obtained in the winted specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 GAAACCTGACGGTGCTGTACGGGGGCTGCTGGAGCATCTGGCCAGCCCAGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342 AAGCAACCAACAAATTCTGGTGGGAGAACAAAGCTGAGGTCCAGATGAAAGAAGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    569 AAGCAACCAACAAATTCTGGTGGTAGAACAAAGCTGAGGTCCAGATGAAAGAGAAGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 AGGTGGAGGCGCCCCCCAAGGCCATCCGCGCCCTCAGGTGGAGCGCTATGTGCCCGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGAGCGATGCTGCTGTGCTGCTGCGGCTGTGAGGTGCGGGAACACCTGAGCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 ACGAGCGATGCTGCTGCTGTGCTGCGGCTGTGAGGTGCGGGAACACCTGAGCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 509 GAAACCTGACGGGCTGTACGGGGGGCTGCTGGAGCATCTGGCCAGCCCAGAGAACAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.0%; Score 263.4; DB 5; Length 3100; 99.6%; Pred. No. 4.7e-66; 1.ve 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3100 BP; 759 A; 849 C; 927 G; 564 T; 0 U; 1 Other;
                                                                                                                                                                                                            Claim 1; SEQ ID NO 13671; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                629 TGGTCACTCCCCAGGATTATGCGCG 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402 TGGTCACTCCCCAGGATTATGCGCG 426
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                                                 Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.6
Matches 264; Conservative
                                               Liu C,
                                                                               2001-639362/73
                (HYSE-) HYSEQ INC.
                                                                             WPI; 2001-639362/
P-PSDB; ABG13680
                                           Drmanac RT,
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à 셤 ò g à Human secreted protein 5' EST, SEQ ID NO: 22599.

(first entry)

06-OCT-2000 AAC18524;

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNAs sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199
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Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 CCTTCTTCTGTGGTCGCGGGCACGTTTACAGCCGCAAGCA-CCAGCGGCAGCTGAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 GCTTTGGAGAGGCTCCTGCCCCAGGTGGAGGCGGCCGCAGGCCATCCGCGCCGCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGAGCGCTATGTGCCCCGAACACGAGCGATGCTGCTGGTGCCTGTGCTGCGGCTGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGCGGGAACACCTGAGCCATGGAAACCTGACGGTGCTGTACGGGGGGGCTGCTGGAGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 CCTTCTTCTGTGGTCGC-GGCACGTTTACAGCCGCAAGCACCCAGCGGCAGCAGCTGAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 22599; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 374 BP; 66 A; 109 C; 139 G; 59 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 244.8; DB 3
Pred. No. 4.1e-61;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.5%;
98.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 268; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-500381/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                     (GEST ) GENSET
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AAT24301
ID AAT24
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AC AAT24
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ВP.

603/c ADB49603 standard; DNA; 584

ADB49603;

us-09-155-676b-4.rng

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RESULT 15
ADB49603/c
                                      A single-stranded DNA (or its complementary strand or the corresp. double stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented CDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell cuction or for recognising different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGTCAACCAAACCCCTATTATACCTTCCACCCAAATTCTTTATCATTGTCTTTAGG 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTCACATACAGAAAAAAGCTAATCATGCTCTCTACCAACTACCATGAGGCTAAAAGCCA 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGACGCCGCTGGCAGTCCAGACATCAACTCCAAAACTGAAGCTGCAGCAATGAAGAAGC 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 AGTCACATACAGAAAAAGCTAATCATGCTCTTACCAACTACCATGAGGCTAGNAAGCA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGTCAA-CAAACCCCTATTATACCTTCCA-CCAAATTCTTTATCATTGTCTTTCTTAGG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                                                                                                                    Single-stranded DNA for identifying gene signatures - isolated from 3'-directed human cDNA library that reflects relative abundance of corresp. mRNA in specific human tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        902 GATCACAGCTCCAGGACCAGTGCAGGCTGGCTGCCCTCTTTTGGGCCGCGTCTGGAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATCACAGCTCCAGGACCAGTGCAGGCTGCCCCTCTTTT-GGCCGCGCTCTGGAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 TGGACGCCGCTGGCAGTCCAGACATCAA-TTCAAAACTGAAGCTGCAGCAATGAAGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                 Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.0%; Score 226; DB 2; Length 326; 95.8%; Pred. No. 1.3e-55; ive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAACAGACATACTCATTTGATTTAATAAAGTTTTATTTTTC 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 AAACAGNCATACTCATTCATTTGATTTANTAAGGTTTTATTTTC 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 326 BP; 87 A; 71 C; 64 G; 87 T; 0 U; 17 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1578; 2245pp; Japanese.
                                Human gene signature HUMGS06324.
                                                                                                                                                                                                                                                94WO-JP001916.
                                                                                                                                                                                                                                                                                 93JP-00355504.
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                        Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                 (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                        Matsubara K,
                                                                                                                                          Homo sapiens.
                                                                                                                                                                         WO9514772-A1
                                                                                                                                                                                                                                            11-NOV-1994;
                                                                                                                                                                                                                                                                                 12-NOV-1993;
22-SEP-1996
                                                                                                                                                                                                             01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Simi
Matches 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              962
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The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                diagnostic marker;
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                                                     Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:145
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                                                                                                          toxic effect, gene expression profile, hepatotoxicity, toxicity marker, toxicity progression, drug screening, primary rat hepatocyte toxicity modelling, gene; ds.
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GenCore v Copyright (c) 1993	Ow nucleic - nucleic search, using sw model Run on: June 8, 2005, 23:20:34 ; Search time 2640.16 Seconds (without alignments) 18065.048 Million cell updates/sec	Title: Perfect score: 1253 Sequence: 1 catiggagtacgcggtggcggggggccgtacccacttt 1253	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	ned: 34239544 seqs, 19032134700 residues	Total number of hits satisfying chosen parameters: 68479088 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	EST:* : gb_est1:* : gb_est2:* : gb_htc:* : gb_est3:*		verg .		Result Query No. Score Match Length DB ID	755.6 60.3 926 2 BE796421 713.2 56.9 884 4 BI859740 694 55.4 1066 4 BG403663	4 616.8 49.2 714 5 BQ006160 BQ006160 5 587 46.8 816 4 B1769735 B1769735 6 578.4 46.2 652 5 BM972124 BM972124	576.4 46.0 758 5 BQ007036 BQ007036 U 572 45.7 760 4 BM682005 BM682005 U 565 45.1 878 4 B1414452 B1414452 6	553.8 45.0 652 7 CNZ91332 CNZ91332 CNZ91332 3258.4 44.6 743 5 BUG08980 BUG08980 BUG08980 BUG08980 BUG08980 BUG08980 BUG08985 BUG0	14 541.4 43.2 596 5 BM929870 BM929870 UI-E-EJI- C 15 531.8 42.4 668 4 BIO46666 BIO46566 MR3-FN020 16 530.8 42.4 870 3 AKO52757 AKO52757 MR3 muscu C 17 519.4 41.5 599 6 CB321979 CB321979 UI-CF-FN0	509 40.6 629 6 CA438500 CA438500 U 507.4 40.5 706 5 BQ006283 BQ006283 U 495.4 39.5 634 6 CA748930 CA748930 U 486.4 38.8 680 5 BU733365 BU733355 U	22 486.4 38.8 759 5 BU733404 UI-E-COI	484.4 38.7 635 6 CA424880 CA424880 U

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BI859740 884 bp mRNA linear EST 10-OCT-2001 603387142F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5395906 5',

GI:16000487

mRNA sequence. BI859740 BI859740.1

DEFINITION RESULT 2 BI859740 LOCUS

ACCESSION

Homo sapiens (human) Homo sapiens

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

Homo sapiens Vakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 884)

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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.c.column: 11
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llarity 93.0%; Pred. No. 4.4e-184;
Conservative 0; Mismatches 28;
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Location/Qualifiers
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UI-H-EII-ayy-j-22-0-UI.81 NCI_CGAP_EII Homo sapiens CDNA clone
IMAGE:5845365 3', mRNA sequence.
BQ006160
BQ006160.1 GI:19731060
EST.
                                                                                                                120 AACACGAGCGAIGCTGCTGCTGCTGTGCGGCTGTGAGGTGCGGGAACACCCTGAGCC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Close Distribution: Clone distribution information can be found
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 714)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Caner Institute, Cancer Genome Anatomy Project (CGAP),

        59
        CCCAGGTGGAGGCGCCCCCATCCGCGCCCCTCAGGTGGACGCTTTGTGCCCG

        60
        CCCAGGTGGAGGCGCCCGCATCCGCGCCCCCTCAGGTGGAGCGCTTATGTGCCC

                                                                                                                                                                           180 ATGGAAACCTGACGGTGCTGTACGGGGGCTGCTGGAGCATCTGGCCAGCCCAGAGCACA
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                                                                                                                                                                                                                                                     300 TICTGGTCACTCCCCAGGATTATGCGCGATTCAAGAAATCCATGGTGAAAGGTTTGGATT
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Unpublished (1997)
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B. (Dasses 1 to 1066)

S. NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Onpublished (1999)

L. Ontact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Tissue Procurement: ATCC

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.llnl.gov

Plate: LLAM10433 row: j column: 21

High quality sequence stop: 735.

Location/Qualifiers

T. 1066

//organism=-Homo sapiens"
                                                                                                                                                                       1037
                                                                                                                                                                                                                                                 AAGCTAATCATGCTCTCTACCAACTACCATGAGGCTAAAAGCCAAAGTCAACCAAACCCC 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG403663 1066 bp mRNA linear EST 12-MAR-2001 602419385F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4526324 5', mRNA sequence.
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/lab host="DHIOB (phage-resistant)"
/clone_lib="NIH MGC_93"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                             TCCAGACATCAA-TTCAAAACTGAAGCTGCAGCAATGAAGAAGCAGTCACATACAGAAAA
                                                                                                                                                                                                                                                                   GAAGTTGAAAAACTCCCCCCAGACCGAGTTGGGGCCCAACTTTGATCACAGCTCCAGGAC
                                  GAAGTTGAAAAACTCCCCCCGGAGACCGAGTTGGGGCCAACTTTGATCACAGCTCCAGGAC
                                                                                                                CAGTGCAGGCTGCCCTCTTTT-GGCCGCGTCTGGAATAATGGACGCCCGTTGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4526324"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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Best Local S:
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BG403663
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658

817

698 598 757

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/ r. 510.
/ Organism="Homo sapiens"
/ wol_type="mRNA"
/ wol_type="mRNA"
/ db_tref="taxon:9606"
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/ clone lib="NIH MGC 122"
/ lab_host="DH10B"
/ clone lib="NIH MGC 122"
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/ note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: Not!; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                    BI769735
603055036F1 NIH_MGC_122 Homo sapiens CDNA clone IMAGE:5204408 5',
mRNA sequence.
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                                                                                                                       CTATTATACCTTCCACCCAAATTCTTTATCATTGTCTTTAGGAAACAGACATACTCA 1156
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1512 row: h column: 09
High quality sequence stop: 790.
Location/Qualifiers
                                                           166 AAAGCTAATCATGCTCTACCAACTACCATGAGGCTAAAAGC--AAAGTCAACAAACC 109
                                                                                                                                                                     CTATTATACCTTCCA-CCAAATTCTTTATCATTGTCTTTCTTAGGAAACAGACATACTCA 50
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                   1037 AAAGCTAATCATGCTCTCTACCAACTACCATGAGGCTAAAAAGCCAAAGTCAAACCC
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NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 1.8e-149;
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Best Local Similarity 91.6%;
Matches 721; Conservative (
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/clone="Intage: 845365"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH108 (Life Technologies)"
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov The following repetitive elements were found in this cDNA sequence: 1-41, >AT_rich#Low_complexity Seq primer: MI3 FORWARD POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGCTCAGATCCGTGAGTTGGAGCAGAGCCGACAGGAGGAGGAGGTGGTTTGGTCTTAGAG
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0; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.2%; Score 616.8; 98.1%; Pred. No. 1.20
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TAG_LIB=UI-H-EI1
                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                       Location/Qualifiers
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77, Conservative
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Best Local Simi
Matches 677;
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Email: paul-mccray@uiowa.edu
Tissue Procuray@uiowa.edu
Tissue Procurament: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this CDNA
sequence: 1-41, AT rich#Low_complexity
Seg primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGTGCTTAC.
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
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                                                                                                                                                                                                                                         1. .652
/organism="Homo sapiens"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Normalization and subtraction: two approaches to facilitate gene
                                                                                    CTGGCCAGCCCAGAGCACAAGAAAGCAACCAACAAATTCTGGTGGGGAGAACAAAGCTGAG
                                                                                                                                                                                                                       GTCCAGATGAAAGAGAAGTTTCTGGTCACTCCCCAGGATTATGCGCGATTCAAGAAATCC
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 GTGGAGCGCTATGTGCCCCGAACACGAGCGATGCTGCTGGTGCCTGTGCGGCTGTGAG
                     GTGCGGGAACACCTGAGCCATGGAAACCTGACGGTGCTGTACGGGGGGCTGCTGGAGCAT
                                                                                                                                                                      CTGGCCAGCCCAGAGCACAAGAAGCAACCAACAAATTCTGGTGGGAGAACAAAGCTGAG
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UI-CF-ECI-abp-m-17-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
UI-CF-EC1-abp-m-17-0-UI 3', mRNA sequence.
BM972124
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2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
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UI-E-EO1-aiw-c-24-0-UI.sl UI-E-EO1 Homo sapiens cDNA clone
UI-E-EO1-aiw-c-24-0-UI 3', mRNA sequence.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                              466 AGAAAAGGAGGATAAAGTGATCAAGGAGATGGCAGCTCAGATCCGTGAGGTGGAGCAGAG
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                                                                                                               Indels
                                                                                  Length
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                                                                                 Score 576.4; DB 5;
Pred. No. 1.5e-146;
0; Mismatches 6;
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      TAG_TISSUE=chondrosarcoma
TAG_LIB=UI-H-EI1
TAG_SEQ=ACACTTGCAC"
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                                                                              tch 46.0%;
al Similarity 94.4%;
706; Conservative
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                                                                                  Query Match
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                                                                                                          TACAGAAAAAAGCTAATCATGCTCTCTACCAACTACCATGAGGCTAAAAGCCAAAGTCAA 1088
                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Issue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov

The following repetitive elements were found in this cDNA

Seq primer: M13 FORWARD

POLYA-Yes.
                     234
                                                                                                                                                                                  116 ACAAACCCCTATTATACCTTCCA-CCAAATTCTTTATCATTGTCTTTCTTAGGAAACGA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 758)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
cecrescastroa-troadacteadecresadroadradadecastroadadecastroada
                                                CGCTGGCAGTCCAGACATCAACTCCAAAACTGAAGCTGCAGCAATGAAGAAGCAGTCACA
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/mol_type="mRNA"
/db_xref="taxon:9606"
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BQ007036.1 GI:19731936
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Unpublished (1997)
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/mol_type="mRNA"
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/dev_stage="fetal"
/dev_stage="fetal"
/dev_stage="fetal"
/dev_stage="fetal"
/dev_stage="fetal"
/dob host="blub" (Life Technologies) (Tl phage resistant)"
/clone lib="UI-E-EOI"
/note="Organ: eys, Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EOI is a normalized CDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996, First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The olignoucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye magning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                    University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA 1911 319 318 8265
Fax: 319 315 9265
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 GAAGAAAAGGAGATAAAGTGATCAAGGAGATGGCAGCTCAGATCCGTGAGGTGGAGCAG 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 617 AACAGCCAAGTAGCTTCCAGCTTACAGCAGCCCTCAAATTTGGACCTGCCACCAGCTCCA 676
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 760)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The following repetitive elements were found in this cDNA sequence: 1-41, >AT rich#Low_complexity
Seq primer: M13 Forward
POLYA-Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.7%; Score 572; DB 4; Length 760; 93.9%; Pred. No. 2.4e-145; live 0; Mismatches 10; Indels
                                                                                                                                                                Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. 760
/organism="Homo sapiens"
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/db xref="texon:9606"
/clone="UI-E-E01-aiw-c-24-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCCGACAGGAGGTGGTTCGGTCTGTCTTAGAG-
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TISSUE=human fetal eye
                                                                                                 Genome Res. 6 (9), 791-806 (1996)
97044477
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TAG_LIB=UI-E-E01
TAG_SEQ=CGCGTATACC"
                                                                                                                                                                                                                                                                                                                                                                                                                         (www.resgen.com).
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In (Dates 1 to 8 18)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Nobert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Inoryte Genomics, Ino.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMI1350 row: e column: 18

High quality sequence start: 4

High quality sequence start: 4

High quality sequence start: 4

High quality sequence start: 4
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602986667F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5142137 5',
BI414452
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 878)
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                                                                                                              GAGCTTGACTGGGATGGAGACCAGGACCATCTCTGACATTGGCCATCAGGATATACCA
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AACAGCCAAGTAGCTTCCAGCTTACAGCAGCCTCAAATTTGGACCTGCCACCAGCTCCA
                                                                       464 GGAGTTGGTAACATCCACTCCAGGTGCCACACCTCCCTGGATGATCCAAGATGAAGATAC
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99.0%; Pred. No. 4-
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                                                                                                                     CN291332.1 GI:47307746
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                                                                                                                                                        Homo sapiens
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Best Local Similarity
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Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 652)
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17000600024907 GRN_PREHEP Homo sapiens CDNA 5', mRNA sequence.
CN291332
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230 Constitution Drive, Menlo Park, CA 940
210 Constitution Drive, Menlo Park, CA 940
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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2024 University of Iowa
2024 University of Iowa
2024 University of Secure
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLONA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLONA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
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CLONA Library Arrayed by: Dr. M. Bento Soares
CLONA Library Arrayed
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                                                                      455
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Bonaldo, M. F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                          AGCCAAGTAGCTTCCAGCTTACAGCAGCCCTCAAAATTTGGGACCTGCCACCAGGCTCCAG
                             CAGGCAGTGCCAGAAGAGGGCTCTTCAGCACCTAGAAGCTGGAAAGGGATGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                          AGCCAAGTAGCTTCCAGCTTACAGCAGCCCTCAAA - - TTTGGACCTGCCACCAGCTCCAG

    .743
    /organism="Homo sapiens"

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Homo sapiens
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TITLE
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UI-CF-FNO-aeq-1-18-0-UI.S1 UI-CF-FNO Homo sapiens CDNA clone
UI-CF-FNO-aeq-1-18-0-UI 3', mRNA sequence.
                   bento-soares@uiowa.edu
TAG_TISSUD=Human Lung Epithelial Cell Lines untreated LPS
Abr to LPS 24h
TAG_LIB-UT-CF-FNO
TAG_SEQ=CTGCTCAGGT"
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1 (Dases 1 to 747)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene discovery
                                                                                                                                                                                                                                                                                                        GGAGTTGGTAACATCCACTCAGTGCCACACCTCCCTGGATGATCCAAGATGAAGAATAC
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                                                                                                                                                                                                                                                                                557 CCTCAGGCAGTGCCAGACCCAGAAGAGGGCTCTTCAGCACCTAGAAGCTGGAAAGGGATG
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                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                      Length 743;
1996. For additional information, contact:
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                                                                                                                                                                                   Score 558.4; DB 5;
Pred. No. 1.3e-141;
0; Mismatches 6;
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ilarity 98.1%;
Conservative
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BM684305 656 bp mRNA linear EST 27-FEB-2002
UI-E-EJI-aji-1-23-0-UI.sl UI-E-EJI Homo sapiens cDNA clone
UI-E-EJI-aji-1-23-0-UI 3', mRNA sequence.
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/lab host="DH10B (Life Technologies) (T1 phage resistant)"
/lab host="DH10B (Life Technologies) (T1 phage resistant)"
/lone=lib="U1-E-E1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
U1-E-E2I is a subtracted ODNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
                                                                                                                                                                                                                 AAAGCTAATCATGCTCTCTACCAACTACCATGAGGCTAAAAGCCAAAGTCAACCAAACCC 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA 1911: 319 315 8250
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arraged by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 65), Bonaldo, M.F., Lennon, G. and Soares, M.B.
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/tissue type="fetal eyes, lens, eye anterior segment,
optio nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
                                                                                                                                                                                                                                     GTCCAGACATCAACTCCAAAACTGAAGCTGCAGCAATGAAGAAGCAGTCACATACAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics (www.resgen.com).
The following repetitive elements were found in this CDNA gequence: 1-47, AT_rich#Low_complexity
Seq primer: M13 Forward
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                         TTCATTTGATTTAATAAGTTTTTATTTTC 1186
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97044477
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/db_xref="taxon:9606"
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Homo sapiens
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AUTHORS
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                                                                                                                                                                  Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CONE Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com)
The following repetitive elements were found in this cDNA
sequence: 147, AT rich#Low_complexity
Seq primer: M13 FORWARD
POLYA=Yes.
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                                                                        McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
  Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
                                                          Contact: McCray, PB
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first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence between the Not I site and the (dT)18 tail. The sequence between the Not I site and the (dT)18 tail. The sequence between the Not I site and the (dT)18 tail. The AGANTCAAGA; lens. CGATTAAGCA; eve anterior segment, AATACCGCAT; optic nerve, CCATTAAGTG; retina, CGCGG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG_INB-UI-E-EVI TAG_LES-Foveal and Macular Retina TAG_LES-GTCC"
with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT/T3-Pac vector. The oligonucleotide used to prime the synthesis of
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                                                                                                                                                                                                                                                                                                                                                                                    Score 548.6; DB 4; Length 656;
Pred. No. 6e-139;
0; Mismatches 14; Indels 6;
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96.8%;
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BM929870 596 bp mRNA linear EST 13-MAR-2002 UI-E-EJ1-aji-1-23-0-UI.rl UI-E-EJ1 Homo sapiens cDNA clone UI-E-EJ1-aji-1-23-0-UI 5', mRNA sequence.

BM929870.1 GI:19389043

DEFINITION RESULT 14 BM929870

LOCUS

ACCESSION VERSION

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/dev stage="fetal and adult"
//dev stage="fetal and adult"
//lab_host="DH10B (Life Technologies) (TI phage resistant)"
//clone llb="UIT-S-L31"
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
// UI-E-EJI is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
strande cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector: The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)1B tail. The
sequence tags for this library are: fetal eyes,
AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,
AAGACCCAT; optic nerve, CCATTAAGTG; retina, CCGGG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                             University of Iona (1156 MEBRF, Iowa City, IA 52242, USA 1913 1335 8250
Fax: 319 315 8250
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
DNA sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
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                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/do xref="taxon:9606"
/db xref="taxon:9606"
/clone="VI-E-Ed1-aji-1-23-0-UI"
/tiseut type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                            1 (bases 1 to 596)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                             Genome Res. 6 (9), 791-806 (1996) 97044477
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                               Homo sapiens (human)
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                                                           Homo sapiens
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TITLE
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KEYWORDS
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

(bases 1 to 668)
Dias Neto.B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Silva,W., Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                                                                                                      GGCAGTCCAGACATCAACTCCAAAACTGAAGCTGCAGCAATGAAGAAGAAGCAGTCACATACA 1032
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mRNA sequence.
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Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was prived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-FN0209-060201-016-f06&t3=2001-02-06&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 668.
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ACCAGGAGTTGGTAACATCCACTCAGGTGCCACACCTCCCTGGATGATCCAAGATGAAGA
                ACCAGGAGTTGGTAACATCCACTCAGGTGCCACACCTCCCTGGATGATCATCCAAGATGAAGA
                                                          ATACATTGCTGGGAACCAAGAAATAGGACCATCCTATGAAGAATTTCTTAAAGAAAAGGA
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020263
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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MR3-FN0209-060201-016-f06 FN0209 Homo sapiens CDNA,
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BI046266.1 GI:14452888
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Smal; Site 2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
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                                                                                                                                                                                                                            42.4%; Score 531.8; DB 4; 91.6%; Pred. No. 2.4e-134; ive 0; Mismatches 28;
/mol type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FN0209"
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Best Local Similarity 91.6
Matches 613; Conservative
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-232-463-14

US-08-232-463-14

US-09-232-857-1

US-09-232-857-1

US-09-206-115-1

US-09-206-115-1

US-09-206-115-1

US-09-206-115-1

US-08-981-322-26

US-09-981-322-26

US-08-981-322-26

US-08-948-176-21

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US-09-636-4422

US-09-636-492-20

US-09-636-492-20
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Listing first 45 summaries
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Maximum DB R
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41 3.3 51259 4 US-09-618-166-209 Sequence 209, App 40.8 3.3 71278 4 US-09-949-016-11851 Sequence 17563, A 40.8 3.3 16873 4 US-09-949-016-11851 Sequence 17563, A 40.8 3.3 16873 4 US-09-016-11853 Sequence 17563, A 40.6 3.2 148 4 US-10-071-411A-63 Sequence 6, Appli 40.6 3.2 148 4 US-10-071-411A-63 Sequence 6, Appli 6 40.6 3.2 148 4 US-10-034-350A-6 Sequence 7, Appli 6 40.6 3.2 148 4 US-10-034-350A-7 Sequence 7, Appli 6 40.6 3.2 149 4 US-10-034-350A-7 Sequence 7, Appli 6 40.6 3.2 149 4 US-10-034-350A-9 Sequence 8, Appli 6 40.6 3.2 149 4 US-10-034-350A-9 Sequence 9, Appli 6 40.6 3.2 150 4 US-0-822-250A-9 Sequence 9, Appli 7 40.6 3.2 150 4 US-0-822-250A-9 Sequence 9, Appli 7 40.4 3.2 3751 4 US-09-140-378A-1 Sequence 1, Appli 7 40.4 3.2 3363 4 US-09-949-016-2495 Sequence 2495, Appli 7 40.4 3.2 3343 4 US-09-949-016-2495 Sequence 2495, Appli 7 40.4 3.2 3343 4 US-09-949-016-2495 Sequence 2497, Appli 7 40.4 3.2 3343 4 US-09-949-016-2495 Sequence 2497, Appli 7 40.4 3.2 3343 4 US-09-949-016-2495 Sequence 2497, Appli 7 40.4 3.2 3343 4 US-09-949-016-2495 Sequence 2497, Appli 7 40.4 3.2 3343 4 US-09-949-016-2495 Sequence 2497, Appli 7 40.4 3.2 3343 4 US-09-949-016-2495 Sequence 2497, Appli 7 40.4 3.2 3943 4 US-09-949-016-2495	ALIGNMENTS	ISSULT 1 Sequence 3437, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION: APPLICANT: VENATION: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307 CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT PILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR APPLICATION NUMBER: 60/241,768 PRIOR PILING DATE: 2000-10-03 PRIOR APPLICATION NUMBER: 60/231,498 PRIOR PILING DATE: 2000-09-08 PRIOR PILING DATE: 2000-10-03 PRIOR PILING DATE: 2000-10-03 PRIOR PILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 SOFTWARE: PASISEQ for Windows Version 4.0 SEQ ID NO 3437 LENGTH: 816 TYPE: DNA ORGANISM: Human (S-09-949-016-3437	Query Match 22.2%; Score 278.4; DB 4; Length 816; Best Local Similarity 96.7%; Pred. No. 1.1e-71; Matches 327; Conservative 0; Mismatches 6; Indels 5; Gaps 4;	849 AGGAAAAACAGAAGTIGAAAAAACTCCCCCCAGACCGAGTITGGGGCCAACTITGATCACA 908 	909 GCTCCAGGACCAGTGCAGGCTGCCCTCTTTTGGCCGCGTCTGGAATAATGGACGC 968	969 CGCTGGCAGTCCAGACATCAACTGAAGCTGCAGCAATGAAGAAGCAGTCACA 1028 	1029 TACAGAAAAAGCTAATCATGCTCTACCAACTACCATGAGGCTAAAAGCCAAAGTCAA 1088 	0 0	
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| Sequence 1621, Application US/09949016
| Patent No. 641239
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| CURRENT APPLICATION NUMBER: US/09/949,016
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR FILING DATE: 2000-10-20
| PRIOR APPLICATION NUMBER: 60/237,768
| PRIOR PRILNG DATE: 2000-10-03
| PRIOR PILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                              Sequence 22599, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT APPLICATION NUMBER: US 60/122,487

PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 22599
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296 CATACTCATTCATTTGATTTAATAAAGTTTTATTTTT 333
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Best Local Similarity 98.5%; Pred. No. 5.7e-62;
Matches 268; Conservative 0; Mismatches 2
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ORGANISM: Homo sapiens
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US-09-949-016-16221/c
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Sequence 15179, Application US/09949016

j Batent No. 6812339

j GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: US/09/949,016
    CURRENT APPLICATION NUMBER: US/09/949,016
    CURRENT FILING DATE: 2000-04-14
    PRIOR APPLICATION NUMBER: 60/231,758
    PRIOR PILING DATE: 2000-10-03
    PRIOR PILING DATE: 2000-10-03
    NUMBER OF SEQ ID NOS: 207012
    SOFTWARE: FastSEQ for Windows Version 4.0
    SOFTWARE: ASSOCIATION NOS: 207012
    SOFTWARE: ASSOCIATION NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                             4972 CAGCTCCAGGACCAGTGCAGGCTGCCTGTTTT-GGCCGCGTCTGGATAATGGAC 4914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCTCTACCAACTACCATGAGGCTAAAAGCCAAAGTCAACCAAACCCCTATTATACCTTC 1109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1913 GCCGCTGGCAGTCCAGGTATGTGTTCAGTGCCGGGTCTCCAACCTACCCATCCAACCT 4854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4853 CCTTTTTGGAGATGTCACCCTTCATCATGGTTAACCCTTTATTTCCTTTCAGACATCA 4794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4793 ATTCAAAACTGAAGCTGCAGCAATGAAGAAGCAGTCACATACAGAAAAAAGCTAATCATG 4734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4733 CTCTCTACCAACTACCATGAGGCTAAAAGC--AAAGTCAACAAACCCCTATTATACCTTC 4676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             907 CAGCTCCAGGACCAGTGCAGGCTGGCTGCCTCTTTTGGGCCGCGCTCTGGAATAATGGAC 966
                                                                                                                                                                                                                                                                                                                                                            847 AAAGGAAAAACAGAAGTTGAAAAACTCCCCCCAGACCGAGTTGGGGCCAACTTTGATCA
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                                                                                                                                                                                                                                                                                                     12; Indels 101;
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                                                                                                                                                                                                                                              Length 6623;
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                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                           Score 175.8; DB 4
Pred. No. 7.7e-41;
                                                                                                                                                                                                                                                                                                  0; Mismatches
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRSESEQ for Windows Version
SEQ ID NO 16221
LENGTH: 6623
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                                                                                                                                                                                                                                        14.0%;
74.1%;
                                                                                                                                                                                                                                                                                                     Matches 324; Conservative
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Best Local Similarity 74.1
Matches 324; Conservative
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                          TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-949-016-15179
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US-09-949-016-15179
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US-09-949-016-16221
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Sequence 15628, Application US/09513999C

| Sequence 15628, Application US/09513999C
| Patent No. 6783961
| GENERAL INFORMATION:
| APPLICANT: Dunas Milne Edwards, J.B.
| APPLICANT: Dunas Milne Edwards, J.B.
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| Patent No. 678399L
| FILE REFERENCE: 59.US2.REG
| CURRENT FILING DATE: 2000-02-24
| PRIOR PPLICATION NUMBER: US 60/122,487
| PRIOR FILING DATE: 1999-02-26
| NUMBER OF SEQ ID NOS: 36681
| SEQ ID NO 15628
| LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    976 AGTCCAGACATCAACTCCAAAACTGAAGCTGCAGCAATGAAGAAGCAGTCACATACAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.7%; Score 83.4; DB 4; Length 97; 97.9%; Pred. No. 1.2e-14; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1036 AAAAGCTAATCATGCTCTCTACCAACTACCATGAGGC 1072
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
PAPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PILING DATE:
APPLICATION WUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
967 GCCGCTGGCAGTCCAGACAT 986
                                               300 GCCGCTGGCAGTCCAGGTAW 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 97.9
Matches 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-513-999C-15628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-232-463-14/c
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                    CTCTCTACCAACTACCATGAGGCTAAAAGCCAAAGTCAACCAAACCCCTATTATACCTTC 1109
                                                                                                                                                                 2059 CAGCICCAGGACCAGTGCAGGCTGGCTGCTTTT-GGCGGCGTCTGGAATAATGGAC 2117
                                                                                                                                                                                                                                                                                                                                                                                                                                            2238 ATTCAAAACTGAAGCTGCAGCAATGAAGAAGCAGTCACATACAGAAAAAGCTAATCATG 2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCTCTACCAACTACCATGAGGCTAAAAGC--AAAGTCAACAAACCCCTATTATACCTTC 2355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2118 GCCGCTGGCAGTCCAGGTATGTGTTCAGTGCCGGGTCTCCAACCTACCCATCCAACCT 2177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                847 AAAGGAAAAACAGAAGTTGAAAAAACTCCCCCCAGACCTGGGGCCCAACTTTGATCA 906
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PALEAR NO. 6783961

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT PELING DATE: 1000-02-24

FRIOR PLING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: PALEATION

SEQ ID NO 34197

LENGTH: 328
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                                                                                                                                                                                                                                                                                                                                                                                                                 990 CTCCAAAACTGAAGCTGCAGCAATGAAGAAGCAGTCACATACAGAAAAAAGCTAATCATG
                                                                                                                    CAGCTCCAGGACCAGTGCAGGCTGCCTCTTTTTGGGCCGCGTCTGGAATAATGGAC
                                                                                                                                                                                                                                                                                                                                                                 2178 CCTTTTTGGAGATGTCACCCTTCATCGTGTTAACCCCTTTATTTCGTTTCAGACATCA
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Pred. No. 5.7e-26;
1; Mismatches 3; Indels 1:
                                                                                                                                                                                                                   GCCGCTGGCAGTCCAGACATCA-----
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; Patent No. 6783961
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Best Local Similarity 96.4%;
Matches 135; Conservative
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US-09-513-999C-34197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: 319
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48; Conservative
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US-09-110-937-1
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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Matches 48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                      363 GGGAGAACAAAGCTGAGGTCCAGATGAAAGAGATTTCTGGTCACTCCCCAGGATTATG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 CGCGATTCAAGAAATCCATGGTGAAAGGTTTGGATTCCTATGAAGAAAAGGAGGATAAAG 482
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                                                                                                                                                                                                                                                                                      DB 1; Length 7218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Shabon, Usman
APPLICANT: Bergsma, Derk
TITLE OF INVENTION: Cloning of Human GPR14 Re
TITLE OF INVENTION: ceptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSED: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
          REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)833-4109
TELEFAX: (703)833-4109
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08789354
Patent No. 5851798
                                                                                                                                        LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
BENT, Stephen A.
                                                                                                                                                                                                                          US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.7%; Score 46.8; DB 3; Length 2126; 96.0%; Pred. No. 0.0049; 1.ve 0; Mismatches 2; Indels 0
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APPLICANT: Sarau, Henry
APPLICANT: Sarau, Henry
APPLICANT: Chales
APPLICANT: Chales
APPLICANT: Chales
TITLE OF INVENTION: A Method of Finding Angonist
TITLE OF INVENTION: and Antagonist To Human and Rat GPR 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 Arcadectrarcearacerceaecreeaeeeecceraeccaerrr
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; Sequence 1, Application US/09110937A
; Patent No. 6005074
; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; APPLICANT: SHABON, USMAN
; TITLE OF INVENTION: CLONING OF HUMAN GPR14 RECEPTOR
; FILE REFERENCE: P50610-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/110,937A CURRENT FILING DATE: 1998-07-06 NUMBER OF SEQ ID NOS: 2 SEQ ID NO 1 SEQ ID NO 1 LENGTH: 2126
FILING DATE: 27-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONEY/AGENT INFORMATION:
NAME: HAN, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: P50610
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-058-725B-1/c
; Sequence 1, Application US/09058725B
; Patent No. 6133420
                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2126 base pairs
TYPE: nucleic acid
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1204 ATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCGTACCCACTTTT 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46.8; DB 3; Length 2126;
Pred. No. 0.0049;
0; Mismatches 2; Indels 0
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APPLICANT: Zalacain, Magdalena
APPLICANT: Zalacain, Magdalena
APPLICANT: Brown, James R.
ITILE OF INVENTION:
CORRESPONDENCES: 5
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Dechart Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                              OPERATING STEM: COMPACTED OF SOFTWARE: FASE SEG for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/232,857
FILING DATE: 15-JAN-1998
CLASSIFICATION: DATA:
APPLICATION NUMBER: 08/789,354
FILING DATE: 27-JAN-1997
APPLICATION NUMBER: 60/074,075
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 09/058,725
FILING DATE: 10-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: PEFSET AND NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 23,031
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
COFTWARE: FastSED for Windows Version 2.0
SUSTEMT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,115
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.7%;
96.0%;
              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2126 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.7%
Dest Local Similarity 96.0%
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 846169
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2126 base pai
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear HOLECULE TYPE: CDNA US-09-232-857-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
MEDIUM TYPE:
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TELEX: 8'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.7%; Score 46.8; DB 3; Length 2126; 96.0%; Pred. No. 0.0049; tive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BERGSMA, DERK
TITLE OF INVENTION: A METHOD OF FINDING AGONIST
TITLE OF INVENTION: AND ANTAGONIST TO HUMAN AND RAT GPR14
                                                                                      COUNTY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASELSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,725B
FILING DATE: April 10, 1998
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/789,354
FILING DATE: APPLICATION NUMBER: 08/789,354
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKTR NUMBER: 34,344
REFERENCE/DOCKTR NUMBER: GP50005-1
TELEDRIVOR: 610-270-5219
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WILLETTE, ROBERT
AIYAR, NAMBI
ROMANIC, ANNE
KHANDOUDI, NASSIRAH
GOUT, BERNARD
AL-BRAZANJI, KAMAL
AMES, ROBERT S.
FOLEY, JAMES J.
SARAU, HENRY
CHAMBERS, JON K.
SHABON, USMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09232857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOUGLAS, STEPHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 48; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: DOUGLAS
APPLICANT: WILLETS
                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6159700
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US-09-232-857-1/c
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                                                                                COUNTRY:
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STATE:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                         STATE:
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RESULT 14
US-09-206-115-1/c
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                                                                                                                                                                                                                                                                                                                              1203 AATCAAGCTIATCGAIACCGICGACCTCGAGGGGGGGGGCCGIACCCACT 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1203 AATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCGTACCCACT 1250
                                                                                                                                                                                                                                                 Length 1236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.6%; Score 44.8; DB 3; Length 1236; 95.8%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                       48 AATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCCCGTACCAAT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 AATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCCCGTACCCAAT 1
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Brown, James R.
TITLE OF INVENTION: NOVEL AmpS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                             Query Match
3.6%; Score 44.8; DB 2; 1
Best Local Similarity 95.8%; Pred. No. 0.014;
Matches 46; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FestesC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,115
FLING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GM10099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09205008
Patent No. 6297039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: GN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                         TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1236 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1236 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.8
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 215-994-22:
TELEFAX: 215-994-2222
                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-933-115-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOPOLOGY: linear
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APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LiP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                             GENERAL INFORMATION:
APPLICANT: Zalacain, Magdalena
APPLICANT: Zalacain, Magdalena
APPLICANT: Brown, James R.
APPLICANT: Brown, James R.
APPLICANT: Brown, James R.
APPLICANT: Brown, JAMES S.
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%; Score 44.8; DB 4;
95.8%; Pred. No. 0.014;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                  ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GM10099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APFLLCATE
FILING DATE:
ATTORNEY, TOGG O
NAME: DICKINSON, TOGG O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/08981392
Patent No. 6262025
GENERAL INFORMATION:
; Sequence 1, Application US/09206115; Patent No. 6558919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1236 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : TOPOLOGY: linear
US-09-206-115-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 46; Conserv
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                                                                                                                                                                                                                                               CITY: Ph:
STATE: Pi
COUNTRY:
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Search completed: June 10, 2005, 20:46:47 Job time: 140.386 secs

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June 10, 2005, 14:23:14; Search time 476.179 Seconds (without alignments) 16311.995 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpna/US07_BUBCOMB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US08_BUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_BUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_BUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_BUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US08_BUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US08_BUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US08_BUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US08_BUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	!		Sequence 16, Appl		Sequence		Sequence 3344, Ap
ΙD	8 9 US-09-915-543-16	US-10-322-579-16	US-10-664-859-16	US-10-242-535A-45728	US-10-085-783A-45728	US-09-746-783-205	US-09-796-692-3344
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Query Match 36.1%; Score 451.8; DB 9; Length 3948; Best Local Similarity 99.2%; Pred. No. 6.8e-126; Matches 475; Conservative 0; Mismatches 2; Indels 2;

SOFTWARE: PatentIn version 3.1; SEQ ID NO 16; LENGTH: 3948

; TYPE: DNA ; ORGANISM: Human lgs-1 US-09-915-543-16

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	: GENE	RAL INFC	DRMATION:					
	; APP	LICANT:	APPLICANT: BASLER, Konrad	Konrad				
	; APP	LICANT:	BRUNNER, Erich	, Erich				
	APP:	LICANT:		, Barbara	ra			
	; APP	APPLICANT:	KRAMPS, T	Thomas				
	: APP	LICANT:	PETER, (Dliver				
	TIL	LE OF IN	VENTION:	ESSENT	IAL	DOWNSTREAM COMPONENT OF TH	HE WINGLESS SIGNALIN	NG PATHWAY
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APPLICANT: BASLER, Brich
APPLICANT: FROBCH, Barbara
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APPLICANT: FROBCH, Barbara
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TILE REFERENCE: 060361
CURRENT RAPLICATION NUMBER: US/09/915,543
PRIOR APPLICATION NUMBER: US/09/915,543
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
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99.2%; Pred. No. 6.8e-126;
tive 0; Mismatches 2;
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; Sequence 16, Application US/1032579
; Publication No. US2003011441341
; Publication No. US2003011441341
; GENERAL INFORMATION:
; APPLICANT: BASIER, Konrad
; APPLICANT: RRAWES, Thomas
APPLICANT: RRAWES, Thomas
; APPLICANT: RRAWES, Thomas
; APPLICANT: RRAWES, Thomas
; APPLICANT: PETER, Oliver:
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATION NUMBER: US/10/322,579
; CURRENT FILING DATE: 2002-12-19
; CURRENT FILING DATE: 2001-07-27
; PRIOR FILING DATE: 2001-07-27
; PRIOR PAPLICATION NUMBER: 60/221,502
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Pred. No. 6.8e-126;
0; Mismatches 2;
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SEQ ID NO 16
LENGTH: 3948
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Best Local Similarity 99.2
Matches 475; Conservative
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US-10-322-579-16
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RESULT 5
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1 Sequence 45728, Application US/10085783A

1 Sequence 45728, Application No. US20040037841A1

2 Sequence 45728, TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN TO COMPAN T
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Pred. No. 3.7e-124;
0; Mismatches 6;
                                                                                                  TGATTTAATAAAGTTTTATTTTC 1186
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Matches 493; Conservative
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APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR PILING DATE: 2002-02-28
PRIOR FILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR APPLICATION NUMBER: US 60/271,955
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin version 3.2
LENGREN PATENTING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
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                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 45728, Application US/10242535A; Publication No. US20040013663A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                US-10-242-535A-45728
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US-10-242-535A-45728
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ORGANISM: Human
                                                                                                                                                                         3439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 785 GATGAAGAATACATTGCTGGGAACCAAGAAATAGGACCATCCTATGAAGAATTTCTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2030 CAGGATATACCAGGAGTTGGTAACATCCACTCAGGTGCCACACCTCCCTGGATGATCCAA
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                                                                                                                                                                                                                                                                   PROTEINS AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: ...

ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RE-Base #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: AUTHORNATION:
NAME: Milasincic, Debra J.
REGISTRATION NUMBER: 46,931
TELEPHONE: (617) 242-7400
TELEPHONE: (617) 242-414

INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LENGTH: 2556 basis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 205:
US-09-746-783-205
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
                                                                                                             McCoy, John M.
LaVallie, Edward R.
Racie, Lisa A.
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael J.
Howes, Steven H.
Fechtel, Kim
                                   Sequence 205, Application US/09746783 Publication No. USZ0030044935A1 GENERAL INFORMATION: GENERAL TAGODS, Kenneth
                                                                                                                                                                                                                                                                 INVENTION: SECRETED ENCODING
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
             US-09-746-783-205
                                                                                                                                                                                                                                                                   TITLE OF
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Sequence 3344, Application US/09796692
| Publication No. US20020198362A1
| GENERAL INPORMATION: Alexander Application No. US20020198362A1
| APPLICANT: Adjace, Paul A. APPLICANT: Adjace, Paul A. APPLICANT: Adjace, Paul A. APPLICANT: Adjace, Paul A. APPLICANT: Mannion, Jame COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY ITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
| TILE REFERENCE: 2077, 00120
| CURRENT APPLICATION NUMBER: US/09/796,692
| CURRENT FILING DATE: 2000-03-01
| PRIOR FILING DATE: 2000-03-01
| PRIOR FILING DATE: 2000-04-28
| PRIOR FILING DATE: 2000-04-28
| PRIOR FILING DATE: 2000-04-28
| PRIOR PAPLICATION NUMBER: 60/200,999
| PRIOR PILING DATE: 2000-05-22
| PRIOR PILING DATE: 2000-05-22
| PRIOR PILING DATE: 2000-05-22
| PRIOR PILING DATE: 2000-05-24
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| PRIOR PILING DATE: 2000-06-32
| PRIOR PI
2269 ACGCCGCTGGCAGTCCAGACATCAA-TTCAAAACTGAAGCTGCAGCAATGAAGAAGCAGT 2327
                                                                       1025 CACATACAGAAAAAGCTAATCATGCTCTTCTACCAACTACCATGAGGCTAAAAGCCAAAG 1084
                                                                                                                                                                                                                          2386 GTCAACAAACCCCTATTATATACCTTCCA-CCAAATTCTTTATCATTGTCTTTCTTAGGAAA 2444
                                                                                                                       2328 CACATACAGAAAAAAGCTAATCATGCTCTCCTACCAACTACCATGAGGCTAAAAGC--AAA
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: (92)
OTHER INFORMATION: IN
NAME/KEY: unsure
LOCATION: (187)
OTHER INFORMATION: IN
NAME/KEY: unsure
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LOCATION: (242)
OTHER INFORMATION: n
NAME/KEY: unsure
LOCATION: (318)
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-796-692-3344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 AGATGAAAGAAGTTTCTGGTCACTCCCCAGGATTATGCGCGATTCAAGAAATCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TGAAAGGTTTGGATTCCTATGAAGAAAAGGAGGATAAAGTGATCAAGGAGATGGCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCAGTGCCAGACCCAGAAGAGGGCTCTTCAGCACCTAGAAGC-TGGAAAGGGATGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 CCAGCCCAGAGCACAAGAAAGCAACCAACAAATTCTGGGGGGGAAACAAAGCTGAGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 TGAAAGGTTTGGATTCCTATGAAGAAAGGAGGATAAAGTGATCAAGGAGATGGCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 AGATCC-GTGAGGTGGAGCAGAG-CCGACAGGAGGTGGTTCGGTCTGTCTTAGA-GCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.5%; Score 256.4; DB 14; Length 352; 97.2%; Pred. No. 5.1e-67; Live 0; Mismatches 4; Indels 5;
     PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3344
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3344, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            620 AG-CCAAGTAGCTTCCAGCTT 639
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
                                                                                                                                                                                                                                                                                                                                                                                                                            Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (329)
; OTHER INFORMATION: n=A,T,C or
US-10-040-862-3344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n=A, T, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: n=A, T, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: unsure
LOCATION: (235)
OTHER INFORMATION: n=A,T,C
                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: n=A, T, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 97.2
Matches 312; Conservative
                                                                                                                                                                                                               ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: unsure
LOCATION: (242)
OTHER INFORMATION: n
                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (187)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                        NAME/KEY: unsure
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                                                                                                                                                                                            TYPE: DNA
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APPLICANT: Algales, Paul A.
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APPLICANT: Algales, Paul A.
APPLICANT: Marmion, Jane
APPLICANT: Cortse, Mac
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APPLICANT: Cortse, Mac
APPLICANTON: Compositions and Methods for the Detection, Disgnosis and Therapy
ITILE OF INVENTION: Head and Methods for the Detection, Disgnosis and Therapy
ITILE OF INVENTION: Algorithm Analysis us 60/100,479
FRIOR APPLICATION NUMBER: US 60/100,479
FRIOR APPLICATION NUMBER: US 60/200,303
FRIOR APPLICATION NUMBER: US 60/200,303
FRIOR PILING DATE: 2000-04-27
FRIOR PELING DATE: 2000-04-28
FRIOR PELING DATE: 2000-06-04
FRIOR FILING DATE: 2000-06-04
FRIOR FILING DATE: 2000-05-04
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FRIOR PELING DATE: 2000-05-04
FRIOR PELING DATE: 2000-06-04
FRIOR APPLICATION NUMBER: US 60/202,903
FRIOR PELING DATE: 2000-09-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                503
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                                                                                                                                                                                                                                                                                                      1 CCAGCCCAGAGCACAAGAAAGCAACCAACAAATTCTGGTGGGAGAACAAAAAGCTGAGGTCC
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                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                 Length 352;
                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                 Score 256.4; DB 9;
Pred. No. 5.1e-67;
                                                                                                                                               20.5%; Scc. No. 5...
97.2%; Pred. No. 5...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3344, Application US/10040862; Publication No. US20030078396A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              620 AG-CCAAGTAGCTTCCAGCTT 639
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; OTHER INFORMATION: n=A,T,C or G; NAME/KEY: unsure; LOCATION: (329); OTHER INFORMATION: n=A,T,C or GUS-09-796-692-3344
                                                                                                                                                                                       Best Local Similarity 97.2
Matches 312; Conservative
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DUBLICATE SHAPE STATE AND CONTROL OF SEQUENCE 3144, Application US/10154084B

| PUblication No. US20040005561A1
| GENERAL INFORMATION: Algace Paul A. |
| APPLICANT: Gaiger, Alexander |
| APPLICANT: Algace Paul A. |
| APPLICANT: Marc W. |
| APPLICANT: Marc W. |
| APPLICANT: Marc W. |
| APPLICANT: Retere, Marc W. |
| APPLICANT: Corisa Corporation |
| TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy |
| TITLE OF INVENTION: Hematological Malignancies |
| TITLE OF INVENTION: Hematological Malignancies |
| TITLE OF INVENTION: Hematological Malignancies |
| TITLE OF INVENTION: WIMMER: US/01/0154,884B |
| CURRENT FILING DATE: 2000-05-23 |
| PRIOR APPLICATION NUMBER: US 60/186,126 |
| PRIOR APPLICATION NUMBER: US 60/186,126 |
| PRIOR APPLICATION NUMBER: US 60/200,303 |
| PRIOR FILING DATE: 2000-04-28 |
| PRIOR FILING DATE: 2000-04-28 |
| PRIOR FILING DATE: 2000-04-28 |
| PRIOR FILING DATE: 2000-04-28 |
| PRIOR FILING DATE: 2000-05-01 |
| PRIOR APPLICATION NUMBER: US 60/200,709 |
| PRIOR APPLICATION NUMBER: US 60/200,209 |
| PRIOR APPLICATION NUMBER: US 60/200,209 |
| PRIOR PILING DATE: 2000-05-01 |
| PRIOR APPLICATION NUMBER: US 60/200,209 |
| PRIOR PILING DATE: 2000-06-01 |
| PRIOR PILING DATE: 2000-06-01 |
| PRIOR PILING DATE: 2000-06-01 |
| PRIOR PILING DATE: 2000-09-03 |
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Pred. No. 5.1e-67;
0; Mismatches 4; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AG-CCAAGTAGCTTCCAGCTT 639
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; OTHER INFORMATION: n = g, a, c or
US-10-154-884B-3344
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Best Local Similarity 97.2%;
Matches 312; Conservative (
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LENGTH: 352
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                                                    ## APPLICANT: Carter, iauren
### APPLICANT: Correr, iauren
### APPLICANT: Corriva Corporation
#### Corriva Corporation
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Pred. No. 5.1e-67;
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               Ordonez, Nadia
Carter, Lauren
McNeill, Patricia Dianne
Corixa Corporation
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OTHER INFORMATION: n = g, a, c or
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97.2%;
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Best Local Similarity 97.2
Matches 312; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-057-475B-3344
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Delymorphisms in the Human Genome
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR PLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-00-22
PRIOR PRIOR DATE: 2000-00-22
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR PLICATION NUMBER: US 60/195,218
PRIOR PLICATION NUMBER: US 60/195,218
PRIOR PLICATION NUMBER: US 60/165,363
PRIOR PLICATION NUMBER: US 60/166,363
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-24
PRIOR FILING DATE: 1999-10-24
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 1999-09-80
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       Gaps
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81.8%; Pred. No. 1.5e-55;
tive 1; Mismatches 50; Indels 23;
       4; Indels
       0; Mismatches
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Publication No. US20020198371A1
GENERAL INFORMATION:
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Best Local Similarity 81.8<sup>†</sup>
Matches 332; Conservative
       Matches 312; Conservative
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APPLICANT: Adagte, Paul A.
APPLICANT: Adagte, Paul A.
APPLICANT: Manion, Jane
APPLICANT: Manion, Jane
APPLICANT: Manion, Jane
APPLICANT: Reteer, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Composition Malignancies
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION NUMBER: US/10/040,862
PRIOR PPLICATION NUMBER: US/10/040,862
PRIOR PILING DATE: 2000-01-11-06
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,99
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,099
PRIOR APPLICATION NUMBER: US 60/200,094
PRIOR APPLICATION NUMBER: US 60/200,004
PRIOR APPLICATION NUMBER: US 60/200,004
PRIOR APPLICATION NUMBER: US 60/200,004
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,004
PRIOR APPLICATION NUMBER: US 60/200,004
PRIOR PILING DATE: 2000-05-01
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                                                                                                                                                                     Sequence 3344, Application US/10764324 Publication No. US20040175739A1 GENERAL INFORMATION: APPLICANT: Gaiger, Alexander
301 AGCCCAAGTAGCTTCCANCTT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (329)
; OTHER INFORMATION: n=A,T,C or G
US-10-764-324-3344
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OTHER INFORMATION: n=A,T,C or
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OTHER INFORMATION: n=A, T, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n=A, T, C or
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: unsure
LOCATION: (318)
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NAME/KEY: unsure
LOCATION: (329)
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LOCATION: (187)
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NAME/KEY: unsure
LOCATION: (242)
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RESULT 14

US-10-956-157-3788/C

US-10-956-157-3788/C

Sequence 3788, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Weeth

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WIT:

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: UNDER: US/10/956,157

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 GCAGGAGGTGGTTCAGTCTGTCCTAGAGGTTTCCCTCGGAGGATCCAGACCCCTC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 AGCCAGTGTCCGGGCACTTTAGTCCTGGAAGCTGGAAAGGATGAACAGCCAGGTAGCT 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 GAGACAGGACTATCTCCCGATATTCATTGGTTATCAGGATATACCAGGAGTTGGTAACATC 14
                                                                                                             241 AAAAAATGTTAATCATTCCCTGATGCTCTACCAACTACCGTGAGGCTAAAAGCAAAGTC
                                                                                        AAAGTCAACCAAACCCCTATTATACCTTCCACCCAAATTCTTTATCATTGTCTTTAG
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                                                                                                                                                                  GAAACAGACATACTCCATTTGATTTAATAAAGTTTTTATTTTC
            1032 AGAAAAAGCTAATCATGC-----TCTCTACCAAC
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US-10-956-157-9023
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                                                                                                                                          1032 AGAAAAAAGCTAATCATGC----TCTCTACCAACTACCATGAGGCTAAAAGC----C 1080
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GTGCAGGCTGGCTGCCTCTTTTGGGCCGCGTCTGGAATAATGGACGCCGCTGGCAGTCC 980
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                                                                                  APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE NUMBERION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
FRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FEBELSEQ for Windows Version 4.0
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1; Mismatches 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 120356, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
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Best Local Similarity 81.8
Matches 332; Conservative
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US-10-027-632-120356
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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 0319895-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 567
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                                                                                                                                                                                                                                                                                                                                                                            471 AGGAGGATAAAG--TGATCAAGGAGATGGCAGCTCAGATCCGTGAGGTGGAGCAGAGCCG 528
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                                                                                                                                                                                                                                                                   Query Match
16.4%; Score 205; DB 21; Length 567;
Best Local Similarity 79.9%; Pred. No. 3e-51;
Matches 298; Conservative 0; Mismatches 55; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9023
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Search completed: June 11, 2005, 06:13:08 Job time : 478.179 secs

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Sequence 13672, A Sequence 8756, Ap Sequence 8756, Ap Sequence 8756, Ap Sequence 30183, A Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 1735, Appl Sequence 1753, Appl Sequence 1851, A Sequence 59, Appl Sequence 59, Appl Sequence 59, Appl Sequence 59, Appl Sequence 5496, Appl Sequence 5496, Appl Sequence 5

Sequence Sequence Sequence

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Minimum | Maximum |

Database

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Sequence:

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Sequence 4, Application US/09155676B

Sequence 4, Application US/09155676B

GENERAL INFORMATION:
APPLICANT: WALLACH, Bavid
APPLICANT: WALLACH, Mark
APPLICANT: WALLACH, Mark
APPLICANT: METI, Iggor
TITLE OF INVENTION: MODULATORS OF TWF RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR
TITLE OF INVENTION: PREPARATION AND USE
FILE REFERENCE: WALLACH=21
CURRENT FALLICATION NUMBER: US/09/155,676B
CURRENT FILING DATE: 1999-01-04
PRIOR FILING DATE: 1999-01-04
PRIOR FILING DATE: 1996-04-02
PRIOR FILING DATE: 1996-04-02
PRIOR FILING DATE: 1996-04-02
PRIOR FILING DATE: 1996-08-26
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VERSION 3.3
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US-10-990-228-8756
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US-00-880-544-30183
US-09-155-6768-1
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US-10-703-032-17036
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US-10-990-774A-11851
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Matches 1253; Conservative
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ORGANISM: Homo sapiens
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1: /cgn2_6/ptodata/2/pna/PCT NEW COMB.seq:*
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15: /cgn2_6/ptodata/2/pna/USO8_NEW COMB.seq:*
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GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles
TITLE OF INVENTION: Target Genes
FILE REPRENEUR: AMAIO1033 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PRECENTIN version 3.2
SEQ ID NO 1553
LENGTH: 1253
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ORGANISM: Homo sapiens
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APPLICANT: Wyeth APPLICANT: Wheth APPLICANT: Wheth APPLICANT: Wheth APPLICANT: Wounts, William Martin APPLICANT: Wounts, Milliam Martin TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug TITLE OF INVENTION: Target Genes (PRESERVE: AM101083 (031896-042000) CURRENT APPLICATION NUMBER: US/11/060,756 CURRENT FILING DATE: 2005-02-18 NUMBER OF SEQ ID NOS: 303284 SOFTWARE: Patentin version 3.2 SEQ ID NO 5826 LENGTH: 1253
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APPLICANT: Wyerh
APPLICANT: Wounts, William Martin
APPLICANT: Wounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles
TITLE OF INVENTION: Target Genes
FILE REPERENCE: AMIO1083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PATENTIN version 3.2
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                                                                                                                                                                                        RESULT 4
US-11-060-756-5825
; Sequence 5825, Application US/11060756
; GENERAL INFORMATION:
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OTHER INFORMATION: n is a,
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LENGTH: 1253
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LOCATION: (187)...(675)
COTHER INFORMATION: 78% homologous to Homo sapiens TRAF2 binding protein encoded
COTHER INFORMATION: by clone 15, accession number W42401, Smith-Waterman Score=665.
US-10-450-763-19571
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               CAGTCACATACAGAAAAAAGCTAATCATGCTCTCTACCAACTACCATGAGGCTAAAAAGCC
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                                                                                                                                                                                                                                                                           APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POL.
FILE REPERENCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
FRIOR PELLOR ION NUMBER: PCT/US01/08631
FRIOR FILING DATE: 2001-03-30
FRIOR FILING DATE: 2000-03-31
FRIOR FILING DATE: 2000-03-31
FRIOR APPLICATION NUMBER: 09/649,167
FRIOR APPLICATION NUMBER: 09/649,167
FRIOR APPLICATION NUMBER: 09/649,167
FRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSCOM
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US-10-450-763-19571
; Sequence 19571, Application US/10450763
; GENERAL INFORMATION:
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FEATURE:
NAME/KEY: SIMILAR
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. LOCATION: (307)..(642)
; CTHER INFORMATION: 67% homologous to Homo sapiens TRAF2 binding protein encoded
; OTHER INFORMATION: by clone 15, accession number W42401, Smith-Waterman Score=349.
US-10-450-763-19570
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        CAGGACCATCTCTGACATTCATTGGCCATCAGGATATA-CCAGGAGTTGGTAACATCCAC
                                                                                                                                                                                                           TCAGGIGCCACACCTCCCTGGATGATCAAGAAGAATACATTGGCTGGGGGACCCCA
                                                                                                                                                                                                                                                                                                                                                                              456 AGAAATHCCCCATCCCTATGAAGAATTTCCTTAAAGAAATTTCCCCTATGTAC
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                                                                                                                                                              TCAGGTGCCACACCTCCCTGGATGATCCAAGATGAAGAATACAT----TGCTGGGAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -CCAACTT
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TILLE REFERENCE: 790CTP3/US
FILLE REFERENCE: 790CTP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR PILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-31
PRIOR PLILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NOS: 60736
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LENGTH: 742
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NAME/KEY: SIMILAR
LOCATION: (307)..
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US-10-450-763-19570
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Matches 419
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NAME/KEY: SIMILAR
LOCATION: (1885)...(2196)
OTHER INFORMATION: 40% homologous to Mus musculus synbindin, accession number OTHER INFORMATION: A7233340, Smith-Waterman Score=116.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2557)
OTHER INFORMATION: n = a,t,c or g
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AGAAATCCATGGTGAAAGGTTTGGATTCCTATGAAGAAAAGGAGGATAAAGTGATCAAGG
                                                                                                                                                                                                                                                                                                                                                                                               Tragageerecageerecagaceeagagegeerecteerecageerecagaaa
                                                                                                                                                      AGATGGCAGCTCAGATCCGTGAGGTGGAGCAGAGCCGACA-GGAGGTGGTTCGGTCTGTC
                                                                                                                                                                                                           518 AGATGGCAGCTCAGATCCGTGAGGTGGAGCAGCAGAGCGAAGGTGGTTCGGTCTGTC
                                                36 GATTCAAGAAATCCATGGTGAAAGGTTTGGATTCCTATGAAGAAAGGAGGATAAAAGGA
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38.3%; Score 479.6; DB 8; Length 2557;
Best Local Similarity 84.9%; Pred. No. 1.8e-114;
Matches 702; Conservative 0; Mismatches 55; Indels 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23046, Application US/10450763
GENERAL INFORMATION:
APPLICANT: Hyseq.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES:
FILE REFERRINCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR PLING DATE: 2000-03-31
PRIOR PLING DATE: 2000-03-31
PRIOR PLING DATE: 2000-03-31
PRIOR PLING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 23046
LENGTH: 2557
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ORGANISM: Homo sapiens
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US-10-450-763-23046
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JOHNSTON COOPER, Matthew

JAPPLICANT: Kinch, Deborah

JAPPLICANT: Kinch, Deborah

JAPPLICANT: Subramaniam, S. Sai

APPLICANT: Subramaniam, S. Sai

APPLICANT: Sak, Suzanne

JAPPLICANT: Sak, Suzanne

APPLICANT: Bandaru, Raj

APPLICANT: Bandaru, Raj

JAPPLICANT: Bandaru, Raj

APPLICANT: Bandaru, Raj

APPLICANT: Derbel, Maher

TITLE OF INVENTION: Nucleotide Array Containing Polymucleotide Probes Complementary t

TITLE OF INVENTION: Nucleotide Array Containing Polymucleotide Probes Complementary t

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TITLE OF INVENTION: Nucleotide Array Containing Polymucleotide Array Containing Polymucleotide Array Containing Polymucleotide Array Containing Polymucleotide Array Containing Polymucleotide Array Containing Polymucleotide Array Containing Polymucleotide Array Containing Polymucleotide Array Containing Polymucleotide Array Containing Polymucleotide Array Containing Polymucleotide Array Containing Polymucleotide Polymucleotide Polymucleotide Polymucleotide Polymucleotide Polymucleotide Polymucleotid
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                                                                                                                                                                       559 ACGACGCTGGCAGTCCAGACATCAA - TTCAAAACTGAAGCTGCAGCAATGAAGAAGAAGT
                                                                                                                                                                                                                                                                              618 CACATACAGAAAAAAGCTAATCATG--CTTTACCAACTACCATGAGGCTAAAAG-CAAAG
                                                                                                                                                                                                                                                                                                                                                                                        675 TCAACAAACCCC-----TACTTTCCACCGAATTCTTTATCATTGTCTTTCTTTAGGAAA
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                                                                                   500 CACAGCTCCAGGACCAGTGCAGGCTGGCTGCCCTCTTTT-GGCCGAGTCTGGAATAATGG
                                                                                                                                        965 ACGCCGCTGGCAGTCCAGACATCAACTCCAAAACTGAAGCTGCAGCAATGAAGAAGCAGT
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Best Local Similarity 93.3%; Pred. No. 5.5e-74;
Matches 407; Conservative 0; Mismatches 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 7415, Application US/60680544; GENERAL INFORMATION:
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LOCATION: (1)...(743)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1145 CAGACATACTCATTCA 1160
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ORGANISM: Macaca Fascicularis
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US-60-680-544-7415/c
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General INFORMATION:
APPLICANT: Cooper, Matthew
APPLICANT: Cooper, Matthew
APPLICANT: Cooper, Matchew
APPLICANT: Subramaniam, S. Sai
APPLICANT: Subramaniam, S. Sai
APPLICANT: Sak, Susanne
APPLICANT: Bandaru, Raj
APPLICANT: Lorder, Matcher
TITLE OF INVENTION: Pragments of, Cynomolgus Monkey Genes and the Use Thereof
TITLE OF INVENTION: Pragments of, Cynomolgus Monkey Genes and the Use Thereof
TITLE OF INVENTION: US/60/680,544
CURRENT FILING DATE: 2005-05-13
NUMBER OF SEQ ID NOS: 48714
SOFTWARE: Patent Sequence Analysis Tool Version 1.0
SEQ ID NO 781
LENTH: 743
LENTH: 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTGAAGCTGCAGCAATGAAGAAGCAGTCACATACAGAAAAAAGCTAATCATGCTCTTA 1056
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CTCTTTTGGGCCGCGTCTGGAATAATGGACGCCGCTGGCAGTCCAGACATCAACTCCAAA
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25.8%; Score 323.6; DB 15; Length
al Similarity 93.3%; Pred. No. 5.5e-74;
407; Conservative 0; Mismatches 14; Indels
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LOCATION: (1)...(743)
CTHER INFORMATION: n = A,T,C or G
US-60-680-544-781
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US-60-680-544-781
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Best Local S
Matches 407
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APPLICANT: Subramaniam, S. Sai
APPLICANT: Szak, Suzanne
APPLICANT: Szak, Suzanne
APPLICANT: Li, Huo
APPLICANT: Bandaru, Raj
APPLICANT: Derbel, Maher
TITLE OF INVENTION: Nucleotide Array Containing Polymucleotide Probes Complementary t
TITLE OF INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       965 ACGCCGCTGGCAGTCCAGACATCAACTCCAAAACTGAAGCTGCAGCAATGAAGAAGCAGT 1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 CACATACAGAAAAAAGCTAATCATG--CTTTACCAACTACCATGAGGCTAAAAG-CAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 25.8%; Score 323.6; DB 15; Length 743; al Similarity 93.3%; Pred. No. 5.5e-74; 407; Conservative 0; Mismatches 14; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 21590290000
CURRENT APPLICATION NUMBER: US/60/680,473
CURRENT FILING DATE: 2005-05-13
NUMBER OF SEQ ID NOS: 48714
SOFTWARE: Patent Sequence Analysis Tool Version 1.0
                                                                                                                                                                                                             ; Sequence 7415, Application US/60680473; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature;
COCATION: (1)...(743)
COTHER INFORMATION: n = A,T,C or G
US-60-680-473-7415
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                                                                                          728 CAGACATACTCATTCA 743
                                                                                                                                                                                                                                                    APPLICANT: Cooper, Matthew
APPLICANT: Kinch, Deborah
APPLICANT: Rosenberg, Michael
APPLICANT: Subramaniam, S. Sai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Macaca Fascicularis
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                                                                1145 CAGACATACTCATTCA
  675 TCAACAAACCCC
                                                                                                                                                                     RESULT 12
US-60-680-473-7415/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 7415
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Best Local Si
Matches 407;
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APPLICANT: Cooper, Matthew
APPLICANT: Rosemberg, Michael
APPLICANT: Subramaniam, S. Sai
APPLICANT: Subramaniam, S. Sai
APPLICANT: Subramaniam, S. Sai
APPLICANT: Bandaru, Raj
APPLICANT: Bandaru, Raj
APPLICANT: Darbel, Maher
ITILE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary t
ITILE OF INVENTION: Pragments of, Cynomolgus Monkey Genes and the Use Thereof
ITILE OF INVENTION: VIDEOCOME
CURRENT APPLICATION NUMBER: US/60/680,473
CURRENT FILING DATE: 2005-05-13
NUMBER OF SEQ ID NOS: 48714
SOFTWARE: Patent Sequence Analysis Tool Version 1.0
SEQ ID NO 781
LENGTH: 743
                                                                                                                     9
                                          CACATACAGAAAAAAGCTAATCATGCTCTCTACCAACTACCATGAGGCTAAAAGCCAAAG 1084
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185 ACGACGCTGGCAGTCCAGACATCAA-TTCAAAACTGAAGCTGCAGCAATGAAGAAGCAGT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  905 CACAGCTCCAGGACCAGTGCAGGCTGGCTGCCCTCTTTTGGGCCGCGCTCTGGAATAATGG 964
                                                                                                                                                   69 TCAACAAACCCC-----TACTTTCCACCGAATTCTTTATCATTGTCTTTCTTAGGAAA 17
                                                                126 CACATACAGAAAAAAGCTAATCATG--CTTTACCAACTACCATGAGGCTAAAAG-CAAAG
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Best Local Similarity 93.3%; Pred. No. 5.5e-74;
Matches 407; Conservative 0; Mismatches 14,
                                                                                                                                                                                                                                                                                                                                                    Application US/60680473
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OTHER INFORMATION: n = A,T,C
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LOCATION: (1)...(743)
                                                                                                                                                                                                                                                                                                                                                       Sequence 781, Applica
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            RESULT 11
US-60-680-473-781
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                                          1025
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LOCATION: (1342)...(2190)

CTHER INFORMATION: 99% homologous to Homo sapiens 29-MAR-1991 New platelet
OTHER INFORMATION: factor 4 receptor superfamily member PF4ARii, accession number
CTHER INFORMATION: Q37107_cdl,Smith-Waterman Score=1468.
US-10-450-763-19572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569 AAGCAACCAACAAATTCTGGTGGGAGAACAAAGCTGAGGTCCAGATGAAAGAGAAAGTTTC 628
                                                 FEATURE:
NAME/KEY: SIMILAR
LOCATION: (277).. (525)
OTHER INFORMATION: 40% homologous to Mus musculus punc,accession number OTHER INFORMATION: AF026465,Smith-Waterman Score=175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 ACGAGCGATGCTGCTGCTGTGCCTGTGCGGCTGTGAGGTGCGGGAACACCTGAGCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 ACGAGCGATGCTGCTGGTGCCTGTGCTGCGGCTGTGAGGTGCGGGAACACACCTGAGCCATG
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                                                                                                                                                                                                                                                                                                                                                                     Length 3100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILLE REFERENCE: 790C193/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSCOR
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                                                                                                                                                                                                                                                                                                                                                                Query Match 21.0%; Score 263.4; DB 8; Best Local Similarity 99.6%; Pred. No. 4.5e-58; Matches 264; Conservative 0; Mismatches 1;
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; Sequence 19572, Application US/10450763
; GENERAL INFORMATION:
                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(3100)
CTHER INFORMATION: n = a,t,c or g
TYPE: DNA
ORGANISM: Homo sapiens
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SEQ ID NO 19572
LENGTH: 4017
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                                                                                                                           APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/10/940,774A
CURRENT FILING DATE: 2004-09-15
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: US/TUSO1/08631
PRIOR PILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
LENGTH: 3100
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                                                                               ; Sequence 3437, Application US/10940774A; GENERAL INFORMATION:
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Best Local Similarity 96.7
Matches 327, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Human
US-10-940-774A-3437
                                                 US-10-940-774A-3437
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US-10-450-763-13671
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Search completed: June 11, 2005, 05:07:14 Job time : 482.315 secs

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June 10, 2005, 06:13:19; Search time 3133.95 Seconds (without alignments) 16321.674 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Sequence 45728, A
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124 US-60-545-213-5826

125 US-09-471-275-1856

126 US-09-471-275-1856

127 US-09-552-317-6921

128 US-09-552-317-6921

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100 US-60-213-362-7089

101 US-60-213-362-1179

102 US-60-213-362-1179

103 US-60-213-362-1179

104 US-60-213-362-1179

105 US-60-213-362-1179

107 US-60-213-362-1179

108-09-340-623-11304

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GATICGAGCCCACGAAGGCCCCTICITCTGTGGTCGCGGCACGTTTACAGCCGCAAGCAC 120 180 61 GATTCGAGCCCACGAAGGCCCCTTCTTCTGTGGTCGCGGCACGTTTACAGCCGCAAGCAC 181 GGCCATCCGCGCCCGCTCAGGTGGAGCGCTATGTGCCCCGAACACGAGCGATGCTGCTGGTG 1 carridgagricacecegregedececreradaaracregarececegecrecangeaarre 121 CCAGCGGCAGCTGAAGGAGGCTTTTGAGAGGCTCCTGCCCCAGGTGGAGGCGGCCCCCAA 1 CATTGGAGTCACGCGCGCGCGCTCTAGAATAGTGGATCCCCGGGCTGCANGGAATTC Gaps ; 0 DB 17; Length 1253; Sequence 4, Application US/09155676

Sequence 4, Application US/09155676

GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: WALLACH, Nikolai
APPLICANT: WALLNIN, Mark
TAPLICANT: MCVALENKO, Andrei
APPLICANT: MCVALENKO, Andrei
TITLE OF INVENTION: FACTOR (TRAF), THEIR PREPARATION AND USE
TITLE OF INVENTION: FACTOR (TRAF), THEIR PREPARATION AND USE
CORRESPONDENCE ADDRESS:
ADDRESSER: BROWDY AND NEIMAR, P.L.L.C. Indels STREET: 624 NINTHA STREET, N.W., Suite 300
CITY: Washington
STATE: 0.C.
COUNTRY. USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/09/155,676
FILING DATE: 04-JAN-1999
CLASSIFTCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IL97/00117
FILING DATE: 101-APR-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: IL 117800
FILING DATE: 02-APR-1996
ATTORNEY/AGENT INFORMATION:
NUMBER: BROWNY, ROGER L. . 0 E: BROWDY AND NEIMAR, P.L.L.C. 624 Ninth Street, N.W., Suite 300 Query Match
99.9%; Score 1252; D.
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1253; Conservative 0; Mismatches WALLACH=21 REFERENCE/DOCKET NUMBER: WALL TELECOMMUNICATION INFORMATION: TELEFAK: 202-628-5197 TELEFAK: 202-737-35-38 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: 25,618 1253 base pairs NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 2 TYPE: nucleic acid STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: CDNA US-09-155-676-4 61 셤 q ò 엄 셤 ò ઠે Š

	COUNTRY: Mashington STATE: D.C. COUNTRY: USA ZIP: 20001 COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/09/155,676A	X 5 5 5 5 H	NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25,618 REFERENCE/DOCKET NUMBER: WALLACH=21 TELEPHONE: 202-737-3528 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 1253 base pairs TYPE: nucleic acid STRANDEDNESS: single TYPE: MOLECULE TYPE: CDNA	Ouery Match Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1253; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1253; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY CATTGGAGTCAGGGGGGGCTCTAGAATAGTGGATCCCGGGGTGCANGGAATTC 60 DD CATTGGAGTCAGGGGGGGCTTTTTTGGAGTAGGGTGCCGGGGTGCANGGAATTC 60 QY 61 GATTGGAGCCCACGAAGGCCCTTTTTTTTGGAGTGGGCGCGCAGGTGCAAGCAC 120 QY 61 GATTGGAGCCCACGAAGGCCCTTTTTTTTTTTTTTTTTT
Qy 241 CCTGTGCTGCGGCTGTGGGAACACCTGAGCCATGGAAACCTGACGTGCTGTA 300 Db 241 CCTGTGCTGCGGCTGTGAGTGCGGGAACCCTGAGCCATGGAAACCTGACGTGCTGTA 300 Cy 301 CGGGGGCTGCTGGAGCATCTGGCCAGCCCAGAGCAACAACAACAAATTCTG 360 Db 301 CGGGGGCTGCTGGAGCATCTGGCCAGCCCAGAGCACAACAACAACAAAATTCTG 360 CGGGGGGCTGCTGGAGCATCTGGCCAGCCCAGAGCACAACAACAACAACAACAACAACAAC	421 TGCGCGATTCAAGAAATCCATGGTGAAAGGTTTGGATTCCTATGAAGAAAAGGAGATAA 480	AGCTGGAAAGGGATGAACAGCCAAGTAGCTTCCAGCTTACAGAGCCCTCAAATTTGGA	721 CCATCAGGATATACCAGGAGTTGGTAACATCCACTCAGGTGCCACCTCCCTGGATGAT 780 781 CCAAGATGAAGAATACATTGCTGGGAACCAAGAATACGACCATCCTATGAAGAATTTCT 840 781 CCAAGATGAAGAATACATTGCTGGGAACCAAGAAATAGGACCATCCTATGAAGAATTTCT 840 781 TAAAGAAAAGAAAAACAGAAATTGAAAAAATCCCCCCAACTT 900 841 TAAAGAAAAGGAAAAATGAAAAAAACTCCCCCCAACTT 900 841 TAAAGAAAAAGAAAAAATTGAAAAAAATCCCCCCCAAGATTGGGGCCCAACTT 900 901 TGATCACAGGCCCAGGACGATGCAGGCTGGCTGCCTCTTTTTGGGCCGCCTCTGGAATA 960 901 TGATCACAGCTCCAGGACCAGTGCAGGCTGGCTGCCTCTTTTTGGGCCGCGTCTGGAATA 960 901 TGATCACAGCTCCAGGACCAGTGCAGGCTGGCTGCCTCTTTTGGGCCGCGTCTGGAATA 960	961 ATGGACGCGCTGGCAGTCCAGACTCCAAACTGAAGCTGCAGCAATGAAGAAG 1020

RESULT 2 US-09-155-676A-4 ; Sequence 4, Application US/09155676A ; GENERAL INFORMATION:

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Gaps

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120 180 180 240 240 300

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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SEQ ID NO 1553
LENGTH: 1253
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NAME/KEY: misc_feature
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US-60-545-213-1553
US-60-545-213-1553
Sequence 1553, Application US/60545213
SEQUENCE 1 INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wouth
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
APPLICANT: Mounter Sequence Acid Arrays for Monitoring Expression
TITLE OF INVENTION: Target Genes
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APPLICANT: Wyeth
APPLICANT: Wouth
APPLICANT: Would and Martin
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
APPLICANT: Mounts
TITLE OF INVENTION: Target Genes
FILE REFRENCE: AMIJIO83 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT APPLICATION NUMBER: US/60/545,213
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1253; Conservative 0; Mismatches
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8-60-545-213-5826
9-60-545-213-5826
Sequence 5826, Application US/60545213
GENERAL INFORMATION:
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; OTHER INFORMATION: n is a, c,
US-60-545-213-5826
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ORGANISM: Homo sapiens
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99.9%; Score 1252; DB 124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1253; Conservative 0; Mismatches 0;
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FBATURE:
NAME/KEY: misc feature
LOCATION: (1135)...(127)
OTHER INFORMATION: similar to gi4455233 in the genepept database release 114,
OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
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98.7%; Pred. No. 4.5e-262;
ive 0; Mismatches 7; Indels
                                                                                                                    APPLICANT: Hyeeq, inc.
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FIER REFERENCE: 782
CURRENT PELLING NOWBER: US/09/471,275
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/234,611
EARLIER FILING DATE: 1999-01-20
EARLIER FILING DATE: 1999-01-22
EARLIER FILING DATE: 1999-01-22
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                                                    Sequence 1856, Application US/09471275 GENERAL INFORMATION:
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OTHER INFORMATION: n = a,t,c or
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Matches 1093; Conservative
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
                                                                                                                 APPLICANT: Hyseg,
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                          GGCCATCCGCGCCGCTCAGGTGGAGCGCTATGTGCCCGAACACGAGCGATGCTGCTGGTG 240
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LOCATION: (1135)...(127)
OTHER INFORMATION: similar to gi4455233 in the genepept database release 114,
OTHER INFORMATION: Run with FASTXY 3.3100, default parameters
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98.7%; Pred. No. 4.5e-262;
ive 0; Mismatches 7; Indels
TITLE OF INVENTION: From Various Libraries FILE REFERENCE: 784
CURRENT APPLICATION NUMBER: US/09/488,725B
CURRENT FILING DATE: 2000-01-21
PRIOR PILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-02-13
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; Sequence 6991, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Sinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
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NAME/KEY: misc_feature

LOCATION: (1)...(1201)

OTHER INFORMATION: n = a,t,c or g

FRATURE:

NAME/KEY: misc_feature

LOCATION: (1135)...(127)

OTHER INFORMATION: similar to gi4455233 in the genepept database release 114,

OTHER INFORMATION: Run with FASTXY 3.3100, default parameters

US-09-552-317-6991
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                                                                                                                                                                                                       Query Match 81.5%; Score 1021.8; DB 26; Lengt Best Local Similarity 98.7%; Pred. No. 4.5e-262; Matches 1093; Conservative 0; Mismatches 7; Indels
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                         RESULT 9
US-09-552-317-6991/C
Sequence 6991, Application US/09552317
GENERAL INFORMATION:
APPLICANT: Tailinghast, John
APPLICANT: Tilinghast, John
APPLICANT: Liu, Chenghus
TITLE OF INVENTION: Novel Nucleic Acids
TITLE OF INVENTION: Novel Nucleic Acids
TITLE OF INVENTION: and Polypeptides
FILE REFERENCE: 784CIP
CURRENT APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 10289
SOUTHWARE: PL CT_genes Version 1.01
LENGTH: 1200
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ORGANISM: Homo sapiens
FEATURE:
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SGUENCE 382, Application US/10217607

SGUENCE 382, Application US/10217607

STILL NFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PMOLICIN

CURRENT APPLICATION NUMBER: US/10/217,607

CURRENT APPLICATION NUMBER: 09/758,463

PRIOR PILING DATE: 2001-01-11

PRIOR PILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

SRIOR PLING DATE: 2000-01-31

SRIOR APPLICATION NUMBER: 60/180,628

NUMBER OF SEQ ID NOS: 1304

SSCPUMARE: PATENTIN VET: 2.0

SEQ ID NOS: 1304
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Pred. No. 1.6e-255;
1; Mismatches 7;
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Best Local Similarity 98.5
Matches 1090; Conservative
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; ORGANISM: Homo sapiens
US-10-217-607-382
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US-10-217-607-382
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                                   81 CCTTCTTCTGTGGTCGC-GGCACGTTTACAGCCGCAAGCACCCAGCGGCAGCTGAAGGAG
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                                                                                                                                                                                                                                                                                                                                                                Sequence 382, Application US/09758463
GENERAL INFORMATION:
FEDERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM011
CURRENT APPLICATION NUMBER: US/09/758,463
CURRENT FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 382
LENGTH: 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 1.6e-255;
1; Mismatches 7;
                                                                                                                                                                                                                                      ATTIGATITAATAAAGTITTATTITC 1186
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Best Local Similarity 98.5%;
Matches 1090; Conservative
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ORGANISM: Homo sapiens
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US-09-758-463-382
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Sequence 7088 Application US/60213362
| Sequence 7088 Application US/60213362
| GENERAL INFORMATION:
| APPLICANT: Morris, MacDonald
| APPLICANT: Morris, MacDonald
| APPLICANT: Lal, Preet;
| APPLICANT: Lal, Preet;
| APPLICANT: Lal, Preet;
| APPLICANT: Lal, Preet;
| TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using TITLE OF INVENTION: Delynucleotide Sequence Databases, and Single Nucleotide Polymor TITLE OF INVENTION: Identified Thereby
| TITLE OF INVENTION: APPLICATION NUMBER: US/60/213,362
| CURRENT APPLICATION NUMBER: US/60/213,362
| CURRENT PILING DATE: 2000-06-21
| NUMBER OF SEQ ID NOS: 8429
| SEQ ID NO 7088
| LENGTH: 1415
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                                                                                                                                                                                                                                                                                                                                                       Query Match 52.9%; Score 663.4; DB 90
Best Local Similarity 95.1%; Pred. No. 4.8e-166;
Matches 750; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                        ) NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 468318.12
US-60-213-362-7088
 1160 ATTTGATTTAATAAAGTTTTATTTTC
            ATTTGATTTAATAAGTTTTATTTTC
                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                       GCTTTGGAGAGGCTCCTGCCCCAGGTGGAGGGGCCCCGCAAGGCCATCCGCGCCCCTCAG 299
                                                                                                                       GTGGAGCGCTATGTGCCCGAACACGAGCGATGCTGCTGGTGCTGTGCTGCGGCTGTGAG 359
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Sequence 2059, Application US/60278561

GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Disp, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polymorphisms Identified Thereby
TITLE OF INVENTION: Polymorphisms Identified Thereby
TITLE OF INVENTION: Polymorphisms Identified Thereby
TITLE OF INVENTION: Polymorphisms Identified Thereby
TITLE OF INVENTION: Polymorphisms Identified Thereby
TITLE OF INVENTION: Polymorphisms Identified Thereby
TITLE OF INVENTION: Polymorphisms Identified Thereby
TITLE OF INVENTION UNDER: US/60/278,561
CUBRENT FILING DATE: 2001-03-23
SOFURARE: PERL PROGRAM
SEQ ID NOS: 15598
SEQ ID NO 2059
IENGTH: 3216
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938 TCTTTTGGGCCGCGTCTGGAATAATGGACGCCGCTGGCAGTCCAGACATCAACTCCAAAA
                                                                                                 2167 GGACCATCCTATGAAGAATTTCTTAAAGAAAAGGAAAAAACAGAAGTTGAAAAAACTCCCC
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Pred. No. 7.2e-166;
0; Mismatches 6;
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OTHER INFORMATION: Incyte ID No: 1000026.9
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US-60-278-561-2059
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95.1%;
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Best Local Similarity 95.1
Matches 750; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTATTTTC 1186
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ORGANISM: Homo sapiens
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US-60-278-561-2059/c
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US-60-213-362-1179/C
US-60-213-362-1179/C
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
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TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
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                        CTGAAGCTGCAGCAATGAAGAAGCAGTCACATACAGAAAAAAGCTAATCATGCTCTCTAC
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OTHER INFORMATION: Incyte ID No: 1000026
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APPLICANT: Lal, Preeti
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APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYNORPHISMS IDENTIFIED THEREBY
TITLE OF INVENTION: POLYNORPHISMS IDENTIFIED THEREBY
TITLE OF INVENTION: POLYNORPHISMS IDENTIFIED THEREBY
TITLE OF INVENTION: POLYNORPHISMS IDENTIFIED THEREBY
TITLE OF INVENTION NUMBER: US/60/324,185
CURRENT FILING DATE: 2001-09-21
SOFTWARE: PEEL PROGram
SEQ ID NOS: 35862
SOFTWARE: PEEL PROGram
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, OTHER INFORMATION: Incyte ID No: 1301765.9
US-60-324-185-7629
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ORGANISM: Homo sapiens
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	Description	Aaw42401 TRAF2 bin	Aab71230 Human leg	Abw01535 Human 1gs	Adj71905 Human Lgs	Novel l	Abg19581 Novel hum	Abg13680 Novel hum	Aam89643 Human imm	Aay16779 Human sec		Abb68702 Drosophil	Abb64668 Drosophil	Adi28627 Mycoplasm		Adp68294 Human NOV	Adl25642 Human dia		Novel	Aab07973 A human n		Abg04996 Novel hum	Human	Human	5 Mycopl	Aab68357 Amino aci
SUMMARIES	ID	AAW42401	AAB71230	ABW01535	ADJ71905	ABG19580	ABG19581	ABG13680	AAM89643	AAY16779	ADA45163	ABB68702	ABB64668	AD128627	ADH47759	ADP68294	ADL25642	ADH48828	ABG08145	AAB07973	ADF09504	ABG04996	ABP69840	ABP69842	ADI28615	AAB68357
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ALIGNMENTS

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Human tumour necrosis factor receptor-associated factor 2; TRAF2; TRAF-2 binding protein; NF-kappaB activity; NF-kappaB induction; intracellular signalling activity; acute hepatitis; autoimmune-induced cell death.
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                                                               TRAF2 binding protein encoded by clone 15.
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                                                                                                                                                                                                                                                                                                                                                                                              Boldin M,
                                                                                                                                                                                                                                                                                                                                                                           (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                              96IL-00117800.
96IL-00119133.
                                                                                                                                                                                                                                                                                                                             97WO-IL000117.
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              Malinin N,
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-503101/46.
N-PSDB; AAV03325.
                                                                                                                                                                                                                      Misc-difference 356
                                                                                                                                                                                Misc-difference 320
                                                                                                                                                                                                   Misc-difference 338
                                                                                                                                                                                                                                         Misc-difference 358
                                                                                                                                                                                                                                                            Misc-difference 388
                                                                                                                                                             Misc-difference 18
                                              15-APR-1998
                                                                                                                                                                                                                                                                                                                                              02-APR-1996;
26-AUG-1996;
                                                                                                                                                                                                                                                                                                                           01-APR-1997;
                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                       WO9737016-A1
                                                                                                                                                                                                                                                                                                         09-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                              Wallach D,
                          AAW42401;
AAW42401
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DNA encoding tumour necrosis factor receptor-associated factor binding

Homo sapiens.

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The present sequence represents a TRAF2 binding protein, which is encoded by clone 15. Clone 15 is a partial clone, which lacks most of its 5' end of the coding DNA sequence. A cDNA library prepared from B-cells was cornened for proteins that associate with TRAF2, and clone 15 was carded as associate with TRAF2, and clone 15 was caids 222-501 of TRAF2. The TRAF-2 binding proteins can be used for modulation or mediation in cells of the activity of NF-kappas or any content intracellular signalling activity modulated or mediated by TRAF2. TARF-binding proteins are especially used for prevention or treatment of pathological conditions associated with NF-KB induction, e.g. acute pathological conditions associated with NF-KB induction, e.g. acute comparities, autoimmune-induced cell death, e.g. death of the beta langerhans cells or the panceas that results in diabetes, the death of langerhans cells or the death of oligodendrocytes in the brain in cells in graft rejection, the death of oligodendrocytes in the brain in proliferation of the AIDS virus and hence the AIDS disease. The proteins are also useful for screening of ligands capable of binding to a protein, which are useful for modulating cellular activity modulated/mediated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HODIPGVGNIHSGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEKQKLKKLPPDRVGANF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSHIQKKANHALYQLPXGXKP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WENKAEVOMKEKFLVTPQDYARFKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AIRAAQVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLYGGLLEHLASPEHKKATNKFW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSTKPLLYLPPKFFIIVFLRKQTYSFIXFNKVLFFGLRGLESSLSIPSTSRGGRTHF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Legless; human; 1gs; Wnt/Wingless signaling pathway; Wnt; Wg; tissue proliferation; tumour; cytostatic; cellular disorder; colon; blood disorder; cancer; breast; head and neck cancer; brain; thyroid; medulloblastoma; skin cancer; tissue regeneration; tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSVLEPQAVPDPEEGSSAPRSWKGMNSQVASSLQQPSNLDLPPAPELDWMETGPSLTFIG
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- used for modulation or mediation in cells of the activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.5%; Score 2178; DB 2; L
100.0%; Pred. No. 6.2e-190;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human legless homologue hlgs-1 partial protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB71230 standard; protein; 1115 AA
                                                          Disclosure, Fig 5, 127pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 417; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 417 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB71230;
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-----RTLKSGAFPQ--TPEAHPQ 1021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 QVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPPWMIQDEEYIA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 GNQEIGPSYEEFLKEKEKQKLK-KLPPDRVGANFDHSSRTSAGWLPSFGPRLEXWTPLAV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 VKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNS 207
                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (1gs) protein, a downstream component of the Wnt/Wingless (Mnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention has eyestatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the human legless (1gs) protein homologue higs-1 described in the disclosure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 REHLSHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 FFCGRGTFTAASTQRQLKEAFERLLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.3%; Score 795; DB 5; Length 1115; illarity 55.6%; Pred. No. 7e-63; Conservative 17; Mismatches 67; Indels 60
                                                                                                                                                                                                                                                                                                                                    Novel polypeptide useful in therapeutic method for treating ocil fate such as cell differentiation or cell proliferation.
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                                                                                                                                                                                                                                                            Peter
                                                                                                                                                                                                                                                          Kramps T,
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991 -YALTVRSPAVLSR------
                                                                                                                                                                                                                                                                                                                                                                                       Example II; Fig 10B; 41pp; English.
                                                                                                                                                                                                                                                             В,
                                                                                                                                                                                                                                                             Froesch
                                                                                                                                     28-JUL-2000; 2000US-0221502P
                                                                                                       27-JUL-2001; 2001US-00915543
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                                                                                                                                                                                                                                                               Basler K, Brunner
                                                                                                                                                                   BASLER K.
BRUNNER E.
FROESCH B.
KRAMPS T.
PETER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1115 AA;
                                                                                                                                                                                                                                                                                                             N-PSDB; AAF88468
                                            US2002086986-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 180;
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                                                                                                                                                                                                  (FROE/)
(KRAM/)
(PETE/)
                                                                                                                                                                    (BASL/)
(BRUN/)
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The invention relates to a polypeptide sharing one or more homologous amino acid domains with a Legless (Lgs) protein and is therefore a functional homologue of Lgs. The invention also relates to a nucleotide eccentrate corganisms, the nucleotide sequence encoding a protein present in invertebrate and/or vertebrate corganisms, the nucleotide sequence encoding a protein comprising a constitute function in a regulatory pathway and the use of the polypeptide from the isolation of Lgs-binding proteins by carrying out an assay chosen from an in vitro binding assay with such a peptide or a coformannest two hybrid assay. The polypeptide and polymucleotide are useful for treating disorders of cell fate, which involves are useful for treating disorders of cell fate, which involves are useful for treating disorders of resquents, antibodies, antibody fragments, 1gs antisense DNA, 1gs antisense RNA, 1gs double-stranded RNA, correlated to cell differentiation or cell proliferation. The compound are related to cell differentiation or cell proliferation. The compound are related to cell differentiation or cell proliferation. The compound for malignant state. The cancerous condition to a neoplastic or malignant state. The cancerous condition is characterised by overmalignant state. The cancerous condition is characterised by overmalignant replace to present a maniation of the Wnt pathway and is medulloblastoms or cancer of the colon, breast, head and neck, brain, thyroid or skin. The therspeutic compound may also be administered to a blood disease to promote tissue compound and repair. This sequence represents a human Lgs/Bc19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; SEQ ID NO 17; 62pp; English.
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                                                                                                                                                                                                          RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 QVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPPWMIQDEEYIA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 FFCGRGTFTAASTQRQLKEAFERLLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEV 87
                                                                                                                                                                                                                             Legless protein; 1gs; cell fate disorder; blood disease; gene therapy; cancer; tissue regeneration; tissue repair; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      828 FFCGRGHVYSRKHQRQLKEALERLLPQVEAARKAJRAAQVERYVPEHERCCWCLCCGCEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Lgs polypeptide useful for isolation of Lgs-binding proteins, diagnosing disorders of cell fate, treating diseases such as cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.3%; Score 795; DB 7; Length 1115; 55.6%; Pred. No. 7e-63; ive 17; Mismatches 67; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peter 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kramps T,
                       ABW01535 standard; protein; 1115 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Froesch B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Fig 10B; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000; 2000US-0221502P.
27-JUL-2001; 2001US-00915543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          .9-DEC-2002; 2002US-00322579.
                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brunner E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-829432/77.
                                                                                                                                                                                Human lgs-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYZU-) UNIV ZURICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD62643
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                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                            ABW01535;
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ABW01535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; legless; lgs; cell differentiation disorder;
cell proliferation disorder; cancer; Wht pathway, medulloblastoma;
breast; head; neck; brain; thyroid; skin; blood disease;
tissue regeneration; tissue repair; cytostatic; Lgs/Bc19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peter
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                                                                                                                           1073 -NKTOSLOLAGKARKTALHLÓTKA 1095
                                                                         327 QTSTPKLKL---QQXRSSHIQKKA 347
                                                                                                                                                                                                                                                      ADJ71905 standard; protein; 1115 AA
                                                                                                                                                                                                                                                                                                                                                                                                         Human Lgs/Bc19 partial polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-2000; 2000US-0221502P.
27-JUL-2001; 2001US-00915543.
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                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brunner E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-203288/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                        ADJ71905;
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                         ABG19581;
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                                                                                                                                                                                                                                     1022 ARCLCAFRRGALKPEPPGRTLKLGVPPHTTRKARPHAAKTSP-----RPRCTRQAP--- 1072
                                                                                                                                                                                                -----RTLKSGAFPPQ--TPEAHPQ 1021
                                       8
                                                                                                                                                                            208 QVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPPWMIQDEEYIA 267
                                                                                                                                                                                                                    268 GNQEIGPSYEEFLKEKEKQKLK-KLPPDRVGANFDHSSRTSAGWLPSFGPRLEXWTPLAV 326
                                                                                                           88 REHLSHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSM 147
                                                                                                                                      148 VKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNS 207
                                                                                                                                                 28 FFCGRGTFTAASTOROLKEAFERLLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEV
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                           n; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
                                       90;
                    Length 1115;
                   36.3%; Score 795; DB 8; Length 111
55.6%; Pred. No. 7e-63;
ive 17; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 49939; 103pp; English.
                                                                                                                                                                                                                                                                              1073 -NKTOSLOLAGKARKTALHLÖTKA 1095
                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #19571.
                                                                                                                                                                                                                                                            327 OTSTPKLKL---QOXRSSHIOKKA 347
                                                                                                                                                                                             | ::: |: |
991 -YALTVRSPAVLSR-------
                                                                                                                                                                                                                                                                                                                                  A.
                                                                                                                                                                                                                                                                                                                                  ABG19580 standard; protein; 156
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                                          Matches 180; Conservative
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                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS83767.
     Sequence 1115 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
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in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal continuity of (II) or to treat disease states involving (II). (II) is secrivity of (II) or to treat disease states involving (II). (II) is considered in the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 QVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLYGGLLEHLASPEHKKATNKFWWENKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 WRRSRIVDPRAAXNSIRAHEGPFFCGRGTFTAASTORQLKEAFERLLPQVEAARKAIRAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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23-AUG-2000; 2000US-00649167.
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Best Local Similarity 77.93
Matches 134; Conservative
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N-PSDB; AAS83768.
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Tang YT;

Liu C,

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 44039; 103pp; English.
                   30-MAR-2001; 2001WO-US008631.
                                                  31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                   WPI; 2001-639362/73.
                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                   N-PSDB; AAS77867.
                                                                                                                                                                                                                                                                          biodiversity.
                                                                                                                                     Drmanac RT,
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 ATNKFWWENKAEVQMKEKFLVTPQDYARFKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 STGK--WINNG-----IVFQDEDRI-----IDTYDTDES------QK 263
                                         sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNSQVASSLQQPSNLDLPPAPELDWMETGP 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVGANFDHSSRTSAGWLPSFG---RVWN-----NGRRWQSRAPEGEREVPWSEEQT 359
                                                                                                                                                                                                                                                                                  and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                 The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                  polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                      25.3%; Score 554.5; DB 4; Length 741;
40.7%; Pred. No. 3.7e-41;
ive 18; Mismatches 52; Indels 127; Gaps
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food supplement; medical imaging; diagnostic; genetic disorder.
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Claim 20; SEQ ID NO 49940; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 40.7'
Matches 135; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 741 AA;
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reaction (PCR) primers, oligomers, and for chromosome and gene mapping, reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II) The polymotectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal critisty of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful in medical imaging polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Abgrollo-Abg30377 represent movel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 SHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARSHLYGTPMG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 SAVPSQACLEALLLIVPWGACGVSQEEEES------PAEGSKDEPGEQVELKEEA 276
polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KKSMVKGL-----DSYEEKEDKVIKEMAAQIREVEQSRQEVVRSV-LEPQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 TOROLKEAFERL-----LPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEVREHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -------PPEPKGDATPEGEKAT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.0%; Score 503; DB 4; Length 312; 49.3%; Pred. No. 5.2e-37; ative 14; Mismatches 38; Indels
The invention relates to isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM89643 standard; protein; 65 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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2000US-023484P

2000US-0235834P

2000US-0235834P

2000US-0236347P

2000US-0236367P

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2000US-0236369P

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2000US-0236369P

2000US-023703P

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2000US-023703P

2000US-023703P

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2000US-0251869P.
2000US-0251989P.
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08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
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 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
Human immune/haematopoietic antigen SEQ ID NO:17236
                                                                                                                                                                      2000US-0179065P.
2000US-0186658P.
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2000US-0198123P.
2000US-0198123P.
2000US-0198123P.
2000US-0205515P.
2000US-021513F.
2000US-021513F.
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2000US-0233063P.
2000US-0233064P.
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                                                                                          WO200157182-A2
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23-AUG-2000;
23-AUG-2000;
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14-SEP-2000;
14-SEP-2000;
                                                                 sapiens
                                                                                                                   09-AUG-2001
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Evans C,

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The invention provides polynucleotides (AAX60579-X60687) encoding specific secreted human proteins (AAY16779-Y16787). The nucleic acid specific secreted human proteins (AAY16779-Y16787). The nucleic acid sequences are deposited under the accession number AFTC 98880. The polynucleotides are used as tissue markers, chromosomal tags, for diagnosis of genetic diseases, to generate anti-protein or anti-DNA antibiodies, also as nutritional sources and supplements and in gene therapy. The secreted proteins are useful therapeutically, in human or vectrinary medicine, e.g. for modulating cell proliferation or therapy. The secreted proteins are useful therapeutically, in human or vectrinary medicine, e.g. for modulating cell proliferation or infections, autoimmune disease, organ rejection, or to induce tumour immunity), as regulators of heemicopolesis (e.g. for treating anemia or inconjunction with tumour therapy), to stimulate growth of tissue for owund healing, as fertility control agents, for regulating encounted the memobalitic and thrombolytic agents (e.g. in treatment of heemophilia or infarctions), as antimicrobial agents, for modifying biorhythms, are appetite, or metabolism, as analgesics and many other uses. The proteins are also used to raise antibodies, used as diagnostic immunoassay reagents also (when neutralizing) for treating e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 SWKGMNSQVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPPWMI 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; genetic disorder; genetic fingerprinting; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; insulin dependent diabetes mellitus; graft-versus-host disease; anaemia periodontal disease; bone fracture; cartilage damage; central nervous system disorder; Alzheimer's disease; Parkinson's disease; cancer; nutrition; carbon source; nitrogen source;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.0%; Score 198; DB 2; Length 104;
llarity 62.5%; Pred. No. 7.9e-10;
Conservative 5; Mismatches 15; Indels
                                                                                                                                          Lavallie ER, Racie LA,
                                                                                                                                                                                                                                                                                                       Nucleic acid encoding secreted human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA45163 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 92; 107pp; English
        97US-00965789.
98US-00185936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-2003 (first entry)
                                                                                    (GEMY ) GENETICS INST INC
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                                                                                                                                          Mccoy JM,
Agostino N
                                                                                                                                                                                                                         WPI; 1999-327362/27.
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nes 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 QDEE 264
                                                                                                                                                                                                                                                     N-PSDB; AAX60579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSQD 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003044935-A1
        07-NOV-1997;
                                 04-NOV-1998;
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                                                                                                                                          Jacobs K,
Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA45163;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                              AAX54951 to AAX64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
c polynucleotides may be used to produce the secreted (I), by inserting the
nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
c ancers and cancer metastases of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK849492 to AAK84950 and AAM82169
represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 FIGH---QDIPGVGNIHSGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEKQKLKKLPPD 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FFSHFQLQDIPGVGNIHSGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEKGKLKKLPPD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secreted protein, human, tissue marker, genetic disease, gene therapy, veterinary medicine, cell proliferation, immunostimulant, infection; immunosuppressant, autoimmune disease, organ rejection; tumour, anemia, haemalopoiesis, wound healing, fertility control; chemotaxis, analgesic; thrombolytic; haemophilis; infarction; antimicrobial agent, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 17236; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.1%; Score 309.5; DB 4; Length 65; 92.2%; Pred. No. 2.5e-20; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein (clone as20_2)
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                                                                                                                                                                   Ruben SM
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08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                   Barash SC,
                                                                                                                                                                                                                      2001-483426/52
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Matches

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RESULT 9
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ID AAX1
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AC AAX1.
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DT 27-J
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DD Huma
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Drosophila; developmental biology; cell signalling; insecticide;

Drosophila melanogaster

pharmaceutical

WO200171042-A2

27-SEP-2001

Drosophila melanogaster polypeptide SEQ ID NO 32898

(first entry)

26-MAR-2002

ABB68702;

ABB68702 standard; protein; 850 AA

: :: RSQD 78

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RESULT 11

ABB68702

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The invention relates to human polymuclectides and the polypeptides they encode. The polymuclectides can be used to express recombinant proteins for analysis. Characterisation or therapeutic use, as markers for tissues in which the corresponding protein is expressed, as markers for tissues in which the corresponding protein is expressed as molecular weight markers on Southern gels, as chromosome markers or tags to identify chromosomes or to map related gene positions, to compare with endogenous DNA sequences in patients to identify potential genetic disorders, as probes to hybridise and discover novel related DNA sequences, as a source of information to derive PCR primers for genetic fingerprinting, to raise anti-protein antibodies and in gene therapy. The proteins can be used to raise antibodies or to elicit another immune response, as reagents in assays designed to quantitatively determine levels of the protein in perferentially expressed and to treat autoimmune disorders (e.g. multiple sclerosis, systemic lupus erythematosus, insulin dependent disorders mellitus or graft-versus-host disease), anaemias, periodontal diseases, bone fractures, cartilage damage, central nervous system classes or parkinson's disease) and cancers. The proteins and polymucleotides are also useful as nutritions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptides and polynucleotides having biological activities, useful as nutritional sources or supplements, or for treating e.g. autoimmune diseases, cancers, bone fractures or damages, or central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or supplements, e.g. as carbon, nitrogen or carbohydrate sources. This sequence represents a human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Evans C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Collins-Racie LA,
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Spaulding V;
                                                             97US-0086234P.
97US-0092115P.
97US-0093045P.
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97US-00958304.
97US-0090111P.
98US-00092722.
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98US-00130189.
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98US-00165960
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COLLINS-RACIE L A.
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Treacy M,
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TREACY M.
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               21-DEC-2000;
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                                                               12-JUN-1997
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(MERB/) I
(TREA/)
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(COLL/)
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Myers EW;

PWD,

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Adams M,

Venter JC,

(PEKE) PE CORP NY

WPI; 2001-656860/75.

N-PSDB; ABL12805

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150. 23-MAR-2001; 2001WO-US009231

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequence (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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23.2%; Pred. No. 1.4;
+ive. 52; Mismatches 151;
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nes 89; Conservative
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Indels

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Conservative

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Local Similarity

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SYEEFLKEKEKQKLKKLPPDRVGANPDHSSRTSAGWLPSF-GPRLEXWTPLAVQTS----
                                       ---TPKLKLQQXRSSH--IQKKANHALYQLPXGXKPKSTKPLLYLPPKFFIIVFLRKQTY
                                                                                                                                                                                                                                developmental biology; cell signalling; insecticide;
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                                                    519 APLAPTLSVDQEAEDFDPFDTSAVSALVQ-----PKSTE---
                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 20796
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29.7%; Pred. No. 1.5;
iive 21; Mismatches 39;
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                                                                                          ABB64668 standard; protein; 838
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                                                                                                                                                                                                                                                              Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 SFGPRLEXWTPLA----VQTSTPKLKLQQXRSS----HIQKKANHALYQLPXGXKPKST 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pneumonia, vaccine, diagnosis, C28-MHP545; immunogen; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 RFKKSMVKGLDSYEEKE-DKVIKEMAAQI-REVEQSRQEVVRSVLEPQAVPDPEEGS-SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             474 LFEKEVTFKLDNFRDVEIEKAFGLLYPGVNEELEQARREQRASLEKEKAKKGLKEFSQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534 DENLKAINNÓ--DGLEEDDNITERLPENSPIQY-------OGEKAGLG---SSPDK
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                                                     336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1878;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma hyopneumoniae immunogen protein C28-MHP545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 110.5; DB 8;
Pred. No. 5.6;
5; Mismatches 132;
299 LPSDIPPPSQLPSDIPPPSQL----PS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 20; 81pp; English.
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(NSWA-) NSW AGRIC.
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                                                                                                                                                                                                                                                                                                                ADI28627 standard; protein; 1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasma hyopneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mahairas GG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2004-083044/08.
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nes 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiinflammatory.
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N-PSDB; ADI28626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004003161-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                     ADI28627;
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152 DSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLE---PQAVPDPEEGSSAPRSWKGMNSQ 208

Indels

39;

Conservative

Matches

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209 VASSLQQPSNL--DLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPP 257

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The present invention relates to novel proteins (I) referred to as NOVX, where X is any number from 1 to 18, and their coding sequences (III). The proteins and their coding sequences are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder such as metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Padigaru M, Alsobrook JP, Colman SD, Spytek KA, Boldog F; Vernet CAM, Li L, Shenoy S, Casman S, Guo X, Edinger S; Macdougall J, Malyankar U, Parturajan M, Shinkets RA, Pena C; Tchernev V, Zerhusen BD, Millett I, Miller C, Lepley DM, Smithson G; Baumgartner J, Herrman J, Peyman JA, Gorman L, Mezes P, Kekuda R; Taupier RJ, Gerlach V, Grosse WM, Liu X, Ellerman K, Rothenberg M;
                                                                                                                                                                                                                               Antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthic; antiinflammatory; dermatological; antiasthmatic; antiinflammatory; dermatological; antiasthmatic; antiinflammatory; metabolic disorder; diabetes; obesity; viral infection; bacterial infection; fungal infection; norection; protozoal infection; anorexia; cancer; cardiovascular disease; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; epilepsy; immune disorder; haematopoietic disorder; inflammatory skin disorder; asthma; dyslipidaemia; NOV18;
EVNPRIPSSRDIENAKFVLDKTEKNKYWQIYSSASPAFQNKWSLFGYYRYLLGLDPKQT 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 159-160; 380pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              ARL-like protein; chromosome 12q12-q14
                                                                                            ADH47759 standard; protein; 4952 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-0262454P.
2001US-0262597P.
2001US-0265530P.
2001US-0265530P.
2001US-0276777P.
2001US-0276777P.
2001US-02303030336P.
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                                                                                                                                                                     (first entry)
                                                                                                                                                                                                        NOV18 protein, SEQ ID 56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baumyu--
Taupier RJ, Gerruc.
-- hJ, Burgess CE;
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28-FEB-2001;
16-MAR-2001;
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18-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens,
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31-JAN-2001;
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                                                                                                                                                                     25-MAR-2004
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2841 IGPIAKAKMVALKGIKKV------MAQGSIGVAPGMNRQ------QVSLLAQ 2880
                                                                                                                                                                                                                                                                                                                                                                                                                          2781 HGGQAGLVPQQSSQPVLSQKPMGTMPPSMCMKPQQLAMQQQLANSFFPDTDLDKFAAEDI 2840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGPPAHLLTPSPLSGPGGSSLLEKFELESGALTLPGGPAASGDELDKMESSLVASE---- 2664
                                                                                                                                                                                                                                                                                                                         242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 KLQQXRSSHIQKKANHALYQLPXGXKPKSTKPLLYLPPKFF--IIVFLRKQTYSFIXFN- 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 LKEKEKOK-----LKKLPPDRVGANFDHSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKL 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           crohn's disease; rheumatoid arthritis; immunological; endocrine; pigmentation; haematopoietic; psychotic; autoimmune; muscular; posteoporosis; angina pectoris; hypotension; anxiety; allopecia; bulimia; cancer; manic depression; virucide; antibacterial; analgesic; neuroprotective; nootropic; cerobroprotective; anticonvulsant; hypotensive; cardiant; hypotensive; antidaleratic; antialieratic; antialieratic; antialieratic; antialieratic; antianginal; immunosuppressive; antidepressant; neurodegenerative; ARL.
            skin disorders,
          (osteoarthritis), haematopoietic disorders, inflammatory skin disorders asthma, and various dyslipidaemias. NOV18 comprises a ARL-like protein and maps to chromosome 12q12-q14.
                                                                                                                                                                                                                                                                              2665 -LPILIEDDLEHEKKELQKKQQLSAQLQPAQQQQQQQGHSLLPAPGPAQAMSLPHEGSS
                                                                                                                                                                                                                                                                                                                         198 APRSWKGMNSQVA-----SSLQQPSNLDLPPAPELDWWETGPSLTFIGHQ-----
                                                                                                                                                                                                                                                                                                                                                        2724 P--SLAGSQQQLSLGLAVARQPGLPQPLMPTQPPAHALQ-QRLAPSMAMVSNQGHMLSGQ
                                                                                                                                                                                                                                                                                                                                                                                          ------DIPGVGNIHSGATPPWMIQDEEYIAGNOEIGPSY------EEF
                                                                                                                                                                                    ---EVQMKEKFLVTPQDYAR
                                                                                                                                                                                                                                                      143 FKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEP----QAVPDPEEGSS
                                                                                                                                                   Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; NOVX; Alzheimer's disease; Huntington's; inflammatory;
                                                                                                                   DB 5; Length 4952;
Parkinson's disease, epilepsy, immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NOV18a protein, an ARL like protein SeqID 56.
                                                                                                                                                                                         101 GGLLEHLASPE-----HKKATNKFWWENKA-----
                                                                                                                     5.0%; Score 109; DB 20.9%; Pred. No. 32; ive 51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP68294 standard; protein; 4952 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 -KVLFFGLRGLESSLSIPSTSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2938 QQLLQMQLKVLEEQIGVHRKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JAN-2001; 2001US-0262454P.
23-JAN-2001; 2001US-0263605P.
25-JAN-2001; 2001US-0264159P.
31-JAN-2001; 2001US-026517P.
07-FEB-2001; 2001US-0267057P.
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                                                                                                                 Query Match
Best Local Similarity 20.9
Matches 80; Conservative
                                                                                      Sequence 4952 AA;
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ADP68294
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This invention relates to novel nucleic acid molecules encoding NOVX to polypeptides selected from NOV1 to NOV11 inclusive, as well as variants thereof. Specifically, it refers to vectors, host cells, antibodies, agonists, antagonists and recombinant methods for producing proteins cancluding GPCRs, secretory proteins and dual specificity phosphatases. The present invention describes these proteins as useful for the development of compositions that can be used to treat neurodegenerative diseases such as Alzheimer's and Huntington's, inflammatory conditions including Crohn's disease and rheumarcid arthritis, as well as including Crohn's disease and rheumarcid arthritis, as well as including crohn's disease and rheumarcid arthritis, as well as altopecia, bulina, cancer and manic depression, hypotension, anxiety, allopecia, bulina, cancer and manic depression. As such, they exhibit various activities including vulnerary, virucide, antibacterial, analgesic, neuroprotective, nootropic, cerebroprotective, anticonvulsant, dermatological, osteopathic, antialerary, virucide, antialleraric, hypotensive, cardiant, hypertensive, antiulcer, antialleraric, antiallargic, human NOVX protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                New NOVX polypeptides useful for treating cancers, blood disorders, asthma, psoriasis, vascular disorders, hypertension, viral, bacterial or parasitic infections, allergy, renal disorders and skin disorders.
                                                                                                                                                                                                            Burgess CE, Casman SJ, Colman S, Edinger S;
Gerlach V, Gunther E, Kekuda R, Macdougall JR;
Patturajan M, Rothenberg M, Shimkets RA, Smithson G;
Stone DJ, Vernet CAM, Zerhusen BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 56; 415pp; English.
                                       2001US-0272920P.
2001US-0284549P.
2001US-0285040P.
2001US-0269098P
                                                                                                      24-APR-2001; 2001US-0286287P.
05-JUL-2001; 2001US-0303229P.
                                                                                                                                                                                                                                                                              Stone DJ,
                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                      WPI; 2003-058497/05
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                                          02-MAR-2001;
18-APR-2001;
15-FEB-2001;
27-FEB-2001;
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Ellerman K,
Mehraban F,
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2665 -LPLLIEDLLEHEKKELQKKQQLSAQLQPAQQQQQQQQQQQHSLLPAPGPAQAMSLPHEGSS 2723
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                                                                                                --- EVQMKEKFLVTPQDYAR 142
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                                                                                                                                                                                                                                                                                   198 APRSWKGMNSQVA-----SSLQQPSNLDLPPAPELDWMETGPSLTFIGHQ-----
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    5.0%; Score 109; DB 7; Length 4952;
20.9%; Pred. No. 32;
.tive 51; Mismatches 149; Indels 102; Gaps
                                                                                              101 GGLLEHLASPE-----HKKATNKFWWENKA--
Query Match
Best Local Similarity 20.9
Matches 80; Conservative
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Search completed: June 7, 2005, 11:57:22 Job time : 66.5671 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                    Copyright
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protein search, using sw model OM protein

June Run on:

7, 2005, 11:43:10 ; Search time 14.4085 Seconds (without alignments) 2784.626 Million cell updates/sec

US-09-155-676B-5 Perfect score:

2190 1 IGVTRWRRSRIVDPRAAXNS.....RGLESSLSIPSTSRGGRTHF 417 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues

283416 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 2000000000. Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. SCOr. 113. 13. 110. 13. 110. 13. 110. 10. 10. 10. 10. 10. 10. 10. 10. 1		•				
	ore	Query Match	Length	DB	ID	Description
11 10 10 10 10 10 10 10 10 10 10 10 10 1	134	6.1	423	. 2	T05511	hypothetical prote
11 10 10 10 10 10 10 10 10 10 10 10 10 1	8.5		1479	~	T17401	ᄆ
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.5	5.0	673	~	835335	
10010010010	109	5.0	4957	7	T03455	ALR protein - huma
0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	109	•	5262	7	T03454	ALR protein - huma
01111	6.5	4.9	850	~	T13352	stn-A protein - fr
2222	105	4.8	544	~	AH2494	hypothetical prote
222	3.5	4.7	753	N	S48059	metal-regulatory t
22	3.5	4.7	1980	~	S54307	myosin heavy chain
10	3.5	4.7	3224	٦	S58884	Ran-binding protei
	3.5	4.7	3498	~	T22330	hypothetical prote
	103	4.7	3449	7	T01083	
10	2.5	4.7	1009	~	S60248	-tyros
	102	4.7	762	7	E86373	protein T23E23.10
	101	4.6	359	7	T01275	hypothetical prote
	101	4.6	467	٦	A49377	involucrin - mouse
	101	4.6	260	~	S54093	hypothetical prote
	101	4.6	2101	~	A42184	nuclear mitotic ap
19 100	0.5	4.6	771	н	A33430	h-caldesmon - chic
	0.5	4.6	1277	~	S53043	probable membrane
	100	4.6	810	~	G01252	small GTP binding
	100	4.6	1027	~	T46481	hypothetical prote
. ,	100	4.6	1031		D88912	protein T06A10.1 [
	100	4.6	1031		T33655	hypothetical prote
	100	4.6	1106		T31742	thetical
26	66	4.5	475		A37241	ס
27	66	4.5	1805		A34736	nestin - rat
28 98	8.5	4.5	357		2	MYB-related transc
	8.5	4.5	1009	7	A57434	protein-tyrosine k

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	plasminogen-bindin	nestin - golden ha	hypothetical prote	sensory box sensor	hypothetical prote	calcium-binding pr	hypothetical prote	hypothetical prote	gravin - human	MADS box protein -	junctional sarcopl	DNA-binding protei	SNF2alpha protein	hypothetical prote	hypothetical prote	hypothetical prote	
	843554	T34518	S61015	A82300	T20600	S56142	T22377	C84554	JW0057	T03410	A45990	S52863	845251	T50438	T34247	T34246	
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•	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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C;Accession: T05511
R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.
Bubmitted to the Protein Sequence Database, February 1999
A;Reference number: 215419
A;Accession: T05511
A;Molecule type: DNA
A;Molecule type: DNA
A;Residuaes: 1-423 <BEV>
A;Cross-references: UNIPROT: Q95W36; EMBL: AL035523
A;Experimental source: cultivar Columbia; BAC clone F13M23
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hypothetical protein F13M23.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LEPQAVPDPEEGSSA-----PRSWKG------MNSQVASSLQQPSNLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.1%; Score 134; DB 2; Length 423; Best Local Similarity 18.2%; Pred. No. 0.031; Matches 73; Conservative 58; Mismatches 153; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 4
A;Introns. 88/2, 130/3; 228/1; 253/3; 272/1
A;Note: F13M23.40
C;Superfamily: Arabidopsis thaliana hypothetical protein F13M23.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 LEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYA------
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R;Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano, Oncogene 15, 549-560, 1997
A;Title: Structure and expression pattern of human ALR, a novel gene with strong homolog A;Reference number: Z14954; MUID:97388474; PMID:9247308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-4957 <PRA>
A;Cross-references: UNIPROT:014686; EMBL:AF010404; NID:g2358286; PIDN:AAC51735.1; PID:g2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 GERPFFCPSNGCEKTFSTQYSLKSHMKGHDNKGTAYSALPQHNGSEDTNHSLYLSELGLL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATINKEWWENKAEVOMKEKFLVTPQDYARFKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNSQVASSLQQPSNLDLPPAPELDWMETGP 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLTFIGHQDIPGVGNIHSGA-----TPPWMIQDEEY-IAGNQEIGPSYEEFLKEKEKOK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAP-----PPAPSLGPGSQPAAFGSPPALLQPPEVPVPHSTQFAANHQEFLPHPQAPP 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Spēcies: Homo sapiens (man)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 FKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEP-----QAVPDPEEGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRAHEG--PFFC---GRGTFTAASTQRQLKEAFERLLPQVEAARKAIRAAQVERYVPEH-
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Pred. No. 55;
1; Mismatches 149; Indels 10
                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 12
C;Superfamily: acute lymphoblastic leukemia protein, ALR type
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                         47; Mismatches 134;
R;Radtke, F.
submitted to the EMBL Data Library, May 1993
A;Reference number: 836946
A;Accession: 836946
A;Molecule type: mRNA
A;Residues: 1.61,63-93,'O',94-283,'N',285-673 <RA2>
A;Cross-references: EMBL:X71327
C;Genetics:
A;Gene: MTF-1
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                    Score 110.5;
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 IRTHTGEKPFRCDHDGCGKAFAAS--
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Scott Local Similarity 20.9%; Pre
                                                                                                                                                                                                                                                                                                                                                    5.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                         73; Conservative
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Best Local Similarity
Matches 73; Conserv
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                                                                                             transcription regulator WBSCR9 - mouse

N.Alternate names: Williams-Beuren syndrome deletion transcript 9 homolog
C.Species: Muse musculus (house mouse)
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T17401
R.Peoples, R.J.; Cisco, M.J.; Kaplan, P.; Francke, U.
Cytogenet. Cell Genet. 82, 238-246, 1998
A.Title: Identification of the WBSCR9 gene, encoding a novel transcriptional regulator,
A.Reference number: 218735; MUID:99077764; PMID:985827
A.Accession: T17401
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary;
A.MOLecule type: mRNA
A.Residues: 1-1479 cPEO>
A.Cross-references: UNIPROT:Q92277; EMBL:AF084480; NID:g4165088; PID:g4165089; PIDN:AADG
C.Genetics:
A.Gene: Wbscr0
A.Map position: 5
F;1360-1415/Domain: bromodomain homology <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
35335
transcription factor MTF-1 - mouse
c;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: 835335, 836946
R;Radckke, F.; Heuchel, R.; Georgiev, O.; Hergersberg, M.; Gariglio, M.; Dembic, Z.; Scha EMBO J. 12, 1355-1362, 1993
A;Title: Cloned transcription factor MTF-1 activates the mouse metallothionein I promote A;Reference number: 835335, MuID:93223676; PMID:8467794
A;Recession: 83533
A;Roccule type: mRNA
A;Resiouse: 1-673 «RAD>
A;Cross-references: UNIPROT:Q9JJW8; EMBL:X71327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 ----KGLDS------YEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 VEKKSDGACDSPSSDKENSSQMAQDLQKKETVVKEDEGRRESINDRARRSPRKLPTSLKK 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 FIIPHIQ----EAF-RIRERYE-----ARLERY---SERIWICKSIG-----SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.4%; Score 118.5; DB 2; Best Local Similarity 21.1%; Pred. No. 2.2; Matches 95; Conservative 49; Mismatches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 QLT-
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439

Gaps

2723

Gaps

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hypothetical protein all7136 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120al C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
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A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT: Q24211; EMBL: US4982; NID: 93138877; PID: 93138878; PIDN: AAC166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLTVLYGGILEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSMVKGLDSY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 KDEEDDEFAELAAB-SLTKKEEVTVVSQVVLPVA-QLPTEAFEA-GSWAEFEEQ---SGQ 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 QPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPPWMIQDEEYIAGNQEIGP 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 ---TPKLKLQQXRSSH--IQKKANHALYQLPXGXKPKSTKPLLYLPPKFFIIVFLRKQTY 384
                                                                               stn-A protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T13352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVPIDLSVSL-HLHLIKHKQPVEE---EEELEQKGRENQLLNP-DLSEF-----DSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPGKPKRPPPVRP--PTGPHI-----VPGA-----IYVSEDEENPEDDPLNT
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4.9%; Score 106.5; DB 2;
Best Local Similarity 23.5%; Pred. No. 8.1;
Matches 90; Conservative 52; Mismatches 150;
                                                                                                                                                                                                   whilt, and the EMBL Data Library, May 1998
A;Reference number: Z17660
A;Accession: T13352
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APLAPTLSVDOEAEDFDPFDTSAVSALVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 SFIXFNKVLFFGLRG--LESSLS 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: FlyBase: FBgn0016976
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A;Molecule type: DNA
A;Residues: 1-544 <KUR>
                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-850 <KEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: AH2494
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Caccession: T03454
R;Prasad, R; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano, Oncogene 15, 549-560, 1997
Oncogene 15, 549-560, 1997
A;Title: Structure and expression pattern of human ALR, a novel gene with strong homolog A;Reference number: Z14954; MUID:97388474; PMID:9247308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Mostiques: 1-5262 - SPRA>
A;Cross-references: UNIPROT:014686; EMBL:AP010403; NID:g2358284; PIDN:AAC51734.1; PID:g2
2724 P.-SLAGSQQQLSLGLAVARQPGLPQPLMPTQPPAHALQ-QRLAPSMAWVSNQGHMLSGQ 2780
                                                                                                                            2781 HGGQAGLVPQQSSQPVLSQKPMGTMPPSMCMKPQQLAMQQQLANSFFPDTDLDKFAAEDI 2840
                                                                                                                                                                                                                2914 GGPPAHLLTPSPLSGPGGSSLLEKFELESGALTLPGGPAASGDELDKMESSLVASE---- 2969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3029 P--SLAGSQQQLSLGLAVARQPGLPQPLMPTQPPAHALQ-QRLAPSMAMVSNQGHMLSGQ 3085
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                                                                                                                                                                                 LKEKEKQK-----LKKLPPDRVGANFDHSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKL 333
                                                                                                                                                                                                                                                                                   334 KLQQXRSSHIQKKANHALYQLPXGXKPKSTKPLLYLPPKFF--IIVFLRKQTYSFIXFN- 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --EVQMKEKFLVTPQDYAR 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 ------DIPGVGNIHSGATPPWMIQDEEXIAGNQEIGPSY------EEF 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 LKEKEKQK-----LKKLPPDRVGANFDHSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKL 333
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                                                                               243 -----DIPGVGNIHSGATPPWMIQDEEYIAGNQEIGPSY---
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C;Superfamily: acute lymphoblastic leukemia protein, ALR type
C;Keywords: alternative splicing
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Query Match 4.8%; Score 105; DB 2; Length 544; Best Local Similarity 21.9%; Pred. No. 5.8; 117; Indels 70; Gaps 16; Matches 66; Conservative 48; Mismatches 117; Indels 70; Gaps 16; Qy 88 REHLSHGNLTVLYGGLEHLASPEHKKATNKFWWENKAEV-QMKEKFLVTPODYARPKKS 146	QY 250 IHSGATPPWMIQDEEY-IAGNOEIGPSYEEFLKEKEKQKLKKLPPDRVGANFDHSSRTSA 308 Db 461PPALLQPPEVPHSTQFAANHQEFLPHPQAPQ-PIVFGLSVVAGASASAAAVA 513 QY 309 GWLPSFGPRLEXWTPLAVQTST 330 Db 514 SAVAARAPPOSTTEPLEAWVOT 535
6 B 1 E	RESULT 9 S54307 myosin heavy chain - rat C; Secies: Rattus norvegicus (Norway rat) C; Date: 15-Jul.1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
242 QDIPGVGNIHSGATPPWMIQDEEYIAGNOEIGPSYEE 278	K.Falnata, J.; Socheel, A.A.; Diekmann, D.; Hail, A.; Ruppert, C.; Baehler, M. BNBO J. 14, 697-704, 1995 A.Title: A novel type of myosin implicated in signalling by rho family GTPases. A.Feference number: SS4307; MUID:95188874; PMID:7882973 A.Accession: SS4307
Oy 279 - FLKEKEKQKI.KKI.PPD - RVGANFDHSSRTSAGWI.PSFGPRI.EXWTPI.AVQTSTPKI.KLQ 336 Db 231 GALKQQHQQELERLEQEIRIGIQSEANTKAE EQVQEQLTALQNI.FQQQKEENIRLQ 286	A;Status: preliminary; nucleic acid sequence not shown A;Molcoule type: mRNNA A;Residues: 1-1980 <rei- A;Cross-references: UNIPROT:Q63358; EMBL:X77609; NID:g63999; PIDN:CAA54700.1; PID:g6399.</rei-
287 Q 287	C;Superiamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C zi: C;Reywords: nucleotide binding; P-loop F;149-942/Domain: myosin motor domain homology <mmot> F;289-246(Region: nucleotide-binding motif A (P-loop) F:1593-1641/Domain: profesi kinase C zin-hinding remain remeat homology</mmot>
אטפכ וית־סט פ	Query Match 4.7%; Score 103.5; DB 2; Length 1980; Best Local Similarity 21.4%; Pred. No. 41; Matches 84; Conservative 52; Mismatches 145; Indels 111; Gaps 22;
	Qy 32 RGTFTAASTQRQLKEAFERLLPQ-VEAARKAIRAAQVERYVDEHER 76
A;Reterence number: S48059, MUID:94344782; PMID:8065932 A;Accession: S48059, A;Status: preliminary A;Molecule type: mRNA	QY 77 CCWCLCCGCEVREHLSHGNLTVLYGGLLEHLASPEHKKATNKFWWEN 123 Db 947QALQERLHGEVLRRILLLGSWFRMVLERRHFVQMKHAALTIQACWRSYRVR 997
A;Residues: 1-753 <bru> A;Cross-references: UNIPROT:Q14872; EMBL:X78710; NID:g520933; PIDN:CAA55363.1; PID:g5209 C;Genetics: A;Gene: GDB:MTF1: MTF-1</bru>	QY 124KAEVQMKEKFLVTPQDYARFKKSMVKGLDSYEEKEDKVIKEMAAQIREVE 173
A;Cross-references: GDB:386446; OMIM:600172 A;Map position: 1p34-1p32	QY 174 QSRQEVVRSVLEPQAVPDPEGSSAPRSWKGMNSQVASSLQQPSNLD 220
Query Match Query Match Best Local Similarity 22.0%; Pred. No. 12; Matches 84; Conservative 48; Mismatches 149; Indels 101; Gaps 19;	LPPAPELDWMFTGPSLTFIGHQDIPGVGNIHSGATPPWMIQDEEXIAGNQEIGPSYEE
Qy 19 NSIRAHEGPFFCG-RGTFTAASTQRQLKEAFERLLPQVE 56 	279 FLKEKEKQKLKKLPPDRVGANFDHSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKLKL
Qy 57 AARKAIRAAQVER	OY 336 QQXRSSHIQKKANHALYQLP-XGXKPKSTKPL 366
QY 87 -VREHL-SHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFL 134 1:	Db 1210QVPIVGDPPRSPSFL 1224 RESULT 10
QY 135 VTPQDYARFKKSMVKGLDSYEEKEDKVIKEMAAQIREVEGSRQEVVRSVLEPQAVPDPEE 194 :	SS8884 Ran-binding protein 2 - human N:Alternate names: giant nucleopore protein Nup358; nucleoporin Nup358; RanBP2 protein C;Species: Homo sapiens (man)
QY 195 GSSAPRSWKGMNSQVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGN 249	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: S58884; A57545 R;Yokoyama, N.; Hayashi, N.; Seki, T.; Pante, N.; Ohba, T.; Nishii, K.; Kuma, K.; Hayash Nature 376, 184-188, 1995 A;Title: A giant nucleopore protein that binds Ran/TC4.

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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 96; Conserv
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                                                                            A; Gene: CESP: F47A4.2
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A; Introns: 62/2; 8
A; Note: T10P11.5
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----WENKA----EVOMKEKF 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----KKLPPDRVGA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 NFDHSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSHIQKKANHALYQLPXGX 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGSSAPR--SWKGMNSQVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIH 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPKTPPRWAEDQNSLL--KMICQQVEAIKKEMQELKLNSSNSASPHRWPTENYGPDSVPD 853
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Cispecies: Caenorhabditis elegans
Cipate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
CiAccession: T22330
Rimortimore, B.
submitted to the EMBL Data Library, June 1995
A;Reference number: Z19549
A;Reference number: Z19549
                                                                                                                                                                                                                                                                                                                                                                                                              ---IRAAQVERYVPEHERCCWCLCCGCEVRE
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4.7%; Score 103.5; DB 1; Length 3224;
Best Local Similarity 18.2%; Pred. No. 79;
Matches 74; Conservative 69; Mismatches 132; Indels 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                    606 WKKVLPLLKIIKKKNSIPEPIDPLFKHFHSVDIQASEIVEY------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    894 NVTPTKGPVYGMNRLPPQQHIYAYPQQMTTPPVQSSSACMFSQEMY
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hypothetical protein F47A4.2 - Caenorhabditis elegans
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R;Kaplan, N.; Johnson, D.; Schutz, K.; Gnoj, L.; Hoffman, J.; Till, S.; de la Bastide, M. hi, M.; Martienssen, R.; Chen, E.Y.; Wilson, R.; McCombie, W.R. ubunitted to the EMBL Data Library, November 1998
A;Description: Sequence of A. thaliana BAC TiOP11 from chromosome IV.
A;Reference number: Z14248
A;Molecule type: DNA
A;Residues: 1-3498 «WIL»
A;Cross-references: UNIPROT:Q20497; EMBL:Z49888; PIDN:CAA90064.1; GSPDB:GN00028; CESP:F4
A;Experimental source: clone F47A4
                                                                                                                                                                                                                           A;Introns: 36/3; 72/3; 147/2; 228/3; 261/2; 320/2; 847/3; 881/1; 1317/2; 1500/3; 1653/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2692 EAARQEKERQEQEARMREAREAELSRQRMEQQRRSQQNPYMNQQGQYSQQPPPSYQQSSY 2751
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                                                                                                                                                                                                                                                                                                                                                                                                                         54 QVEAARK-AIRAAQVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLYGGLLEHLASPEH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAVPDPEEGSSA 198
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A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T10P11.5 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 KKATN-----KFWWENKAEVQMKEKFLVTPQDYARFKKSMVKGLDSYEEKEDKV--IKE
                                                                                                                                                                                                                                                                                                                                                        Indels 101; Gaps
                                                                                                                                                                                                                                                                                           Length 3498;
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                                                                                                                                                                                                                                                                                        Query Match
4.7%; Score 103.5; DB 2;
Best Local Similarity 21.6%; Pred. No. 88;
Matches 79; Conservative 47; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.7%; Score 103; DB 2; L 20.1%; Pred. No. 94; rative 46; Mismatches 143;
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2602 EMBAARKEAARRAAEBAYAAEQQR-----
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A;Molecule type: DNA
A;Residues: 1-3449 <KAP>
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	RESULT 14 BRESULT 14 Brocetin T23E23.10 [imported] - Arabidopsis thaliana C;Brecies Arabidopsis thaliana (mouse-car cress) C;Brecies 12 Arabidopsis thaliana (mouse-car cress) C;Brecies 102-Mar.2001 #sequence—revision OZ-Mar.2001 #sext_change 09-Jul-2004 C;Arcession E86379 C;Arcession E86379 C;Arcession E86379 C;Arcession E86379 C;Arcession E86379 C;Arcession E86379 C;Arcession E86370 C;Ar
Qy Qy Qy Qy Qy Qy Qy Qy	RESULT 13 Social Adheriate kinase (EC 2.7.1.112) CAK-beta - human NiAlternate names: cell adhesion kinase-beta CiSpecies Homo sapiens (man) CiSpecies Homo sapiens (man) CiSpecies Homo sapiens (man) CiSpecies Homo sapiens (man) CiSpecies Homo sapiens (man) CiSpecies Homo sapiens (man) Richer 10-Phy-1906 Heacquence revision 27-Feb-1997 #text_change 16-Aug-2004 Riches A. Parelland Homo sapiens (man) Nature 376, 737-745, 1995 A; Fitle: Protein tyrosine kinase PyK2 involved in Ca(2+)-induced regulation of ion ch A; Reference number: 860248; WUID:95379967; PMID:7544443 A; Reference number: 860248; WUID:95379967; PMID:754444 A; Reference number: 860248; WUID:95379967; PMID:7544443 A; Reference number: HONOF A; Reference number: HONOF A; Reference number: HONOF A; Reference number: HONOF A; Reference number: HONOF A; Reference number: HONOF A; Reference number: HONOF A; Reference number: HONOF A; Reference number: HONOF A; Reference number: MAN A; Residues: PERILINIARAY, Dispectable H; Kotani, K.; Sasaki, T. A; Hile: Cloning and characterization of cell adhesion kinase beta, a novel protein-the Norman and Characterization of cell adhesion kinase beta, a novel protein-the Norman and Characterization of cell adhesion kinase beta, a novel protein-the Norman and Characterization of cell adhesion kinase beta, a novel protein-the Norman and Characterization of cell adhesion characterization of cell adhesion kinase beta, a novel protein-the Norman and Characterization of cell adhesion kinase beta, a novel protein-the A; Reference number: A57434; MUID:95403356; PMID:7673154 A; Reference number: A57434; MUID:95403356; PMID:7673154 A; Reference number: A57434; MUID:95403356; PMID:7673154 A; Reference number: A57434; MUID:95403356; PMID:7673154 A; Reference number: A57434; MUID:95403356; PMID:7673154 A; Reference number: A57434; MUID:95403356; PMID:7673154 A; Reference number: A57434; MUID:95403356; PMID:7673154 A; Reference number: A57434; MUID:95403356; PMID:7673154 A; Reference number: A57434

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hypothetical protein At2g19270 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F27F23.7
N;Alternate names: hypothetical protein F27F23.7
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01275; F84574
E;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence.
A;Reference number: 214177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: T01275
A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Status: 1-359 «ROU»
A; Cross-references: UNIPROT: 064560; EMBL: AC003058; NID: 93135250; PID: 93135257
A; Experimental source: cultivar Columbia
B; Lin, X.; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Shen, M.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487; PMID: 10617197
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SAGWLP-SFGPRLEXWTPLAVQTSTPKLKLQQXRSSHIQKKANHALYQL----- 354
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23.8%; Pred. No. 6.6;
tive 30; Mismatches 84; Indels 46;
                                                                                                                                                                                                                                                                  PSGS--SIDCIVHLSRRPARLYL----QQTTRFVQF 735
                                                                                                                                                                                                                           355 PXGXKPKSTKPLLYL---PPKFFIIVFLRKQTYSFIXF 389
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Best Local Similarity 23.8*
Matches 50; Conservative
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A, Map position: 2
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A,Molecule type: DNA
A,Residues: 1-359 <STO>
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Maximum Match 100%
Listing first 45 summaries
                                                            sw model
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1: uniprot_sprot:*
2: uniprot_trembl:*
                                                          protein search, using
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Match Length DB
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xenopus lae
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haemophilus
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plasmid r64
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Q7tni3
Q81220
Q7djm2
O86167
Q79vt6
Q72wk4
Q72wk4
Q72wk4
Q622a2
Q96ru9
Q95r913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 68.4%; Score 1498; DB 2; Length 332; Best Local Similarity 89.1%; Pred. No. 4.3e-95; Matches 286; Conservative 5; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                       [1] — SEQUENCE FROM N.A. Gamou T., Maeno G., Sakiyama T. Kubo T., Arai Y., Ohira M., Gamou T., Maeno G., Sakiyama T. Toyoda A., Hattori M., Sakaki Y., Nakagawara A., Ohki M.; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AB094093; BAC76047.1; -. SEQUENCE 332 AA; 37974 MW; 341209B75BE56349 CRC64;
                                                                                                                                                                                                                                                                                       Last sequence update)
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Q7DJM2
Q8C167
Q79VT6
Q8CUE5
Q7ZWK4
Q719M1
Q6A2A5
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Q54913
Q6GR02
Q8BL65
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Q8C702
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schnefer C.F., Bahat N.K.,

A lopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A papleron M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.B.,

B Expleton M., Soares M.B., Bonaldo M.F., Carnhorl P., Frange C.,

A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carnhorl P., Frange C.,

B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Back S.A., McKwan P.J., McKernan K.J., Maake J.A., Gunsarene P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A. Schnutz J., Nyers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M., Butterfield Y.S.,

A Norley M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 QVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPPWMIQDEEYIA 267
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                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE-Colon;
Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 338 AA; 38244 MW; 8F0858468908CBA1 CRC64;
(TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sci. U.S.A. 99:16899-16903(2002).
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                                                              D630044F24Rik protein (Fragment).
Name=D630044F24Rik;
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VB/N; TISSUE=Colon;
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NON TER 1 1
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                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                   STRAIN=FVB/N;
                     01-OCT-2003
01-OCT-2003
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Arakawa T., Habhizume W.,
Adachi J., Aizawa K., Imagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hirzoka T., Hirzokane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Akach H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Obsato N., Osato N.,
Asito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Asaski D., Shibata K., Shinagwa A., Shiraki T., Sogabe Y., Tagami M.,
Tomaru A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRIN=C57BL/6J; TISSUE=Kidney;
STRAIN=C57BL/6J; TISSUE=Kidney;
STRAIN=C57BL/6J; TISSUE=Kidney;
STRAIN=C903913; Pubmed=11076861; DOI=10.1101/gr.152600;
A MEDLINE=20390913; Pubmed=11076861; DOI=10.1101/gr.152600;
A Konno H., Akiyama K., Nishia K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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of new genes.";
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MEDLINE=9927923; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.,
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                             01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annocation update)
Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched
library, clone:D630044F24 product:hypothetical protein, full insert
                                                                                                                                                                                                                     Craniata, Vertebrata, Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDi
prepare full-length cDNA libraries for rapid discovery of
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; T1SSUE=Kidney;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
194 AA.
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PRT;
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STRAIN=C57BL/6J; TISSUE=Kidney;
The FANTOM CONSOrtium,
                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                       Meth. Enzymol. 303:19-44(1999)
                                      01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
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PRELIMINARY;
                                                                                                                                                                         Name=D630044F24Rik;
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Nature 420:563-573 (2002)
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databases.
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                                                                                                                                                                                                                                 FFCGRGHVYSHKHQRQLKGALERLLPQVEAARRAVRAAQVERYVPEHDRCCWCPCCGCEV
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein F13M23.40 (Hypothetical protein AT4g24900).
Name=F13M23.40; Synonyms=AT4g24900;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                         Length 194;
                                                                                                    34.1%; Score 747; DB 2; Length 19 79.4%; Pred. No. 1.1e-43; ive 12; Mismatches 25; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL035523, CAB36732.1; -.
EMBL, AL161562; CAB79399.1; -.
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Mayer K.F.X., Schueller C.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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423 AA; 47708 MW; 22BDF4C369A70013 CRC64;
                                                             194 AA; 22541 MW; E0C5CBA0F198311C CRC64;
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18.2%; Pred. No. 0.51;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
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EMBL, AK052757; BAC35135.1; -. MGD; MGI. MGI.2685866; D6500044F24Rik. Hypothetical protein. SEQUENCE 194 AA; 22541 MW; E
                                                                                                                                              143; Conservative
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Matches 143
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LSGTSNDIHTKLAFETMDRIKKVPAHHINSYKSND---VMPLQYNTNEYQISLSEIPGVI 208
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REP SECUENCE OF 1-482 FROM WA.

REPAINCE-278L/64; ITSSUB-Thymus;

REPAINCE-278L/64; ITSSUB-Thymus;

REPAINCE-278L/64; ITSSUB-Thymus;

REPAINCE-278L/64; PubMed-12466851; DOI=10.1038/nature01266;

REPAINCE-2784683; PubMed-12466851; DOI=10.1038/nature01266;

REPAINCE-278L/64; PubMed-12466851; DOI=10.1038/nature01266;

REPAINCE-278L/64; PubMed-12466851; DOI=10.1038/nature01266;

REPAINCE-278L/64; PubMed-124, Rondow H., Randanaka I., Kiyosawa H., Radachila R., Mareuda H., Bardaro M., Baldarelli R., Marapin A., Mateude C., Chothia C., Corbani L.E., Cousins S., Radater-1and T., Gariboldi M., Gissi C., Godzik A., Frazer K.S., Radai A., Kawasawa Y., Redzierski R.M., King B.L., A. Kandaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Kandaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Ronagaya A., Kurochkin I.V., Marchionni L., McKenzie L., Miki H., R. Magalott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., R. Radai T., Nummata K., Okido T., Pavan W.J., Pertea G., Pesole G., Radaelina T., Nummata K., Okido T., Pavan W.J., Pertea G., Pesole G., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Wanger L., Wahlestedt C., Wanger L., Wahlestedt C., Wanger L., Wahlestedt C., Wanger L., Wahlestedt C., Wanger L., Wahlestedt C., Wanger L., Wahlestedt C., Wanger L., Wahlestedt C., Wanger L., Wahlestedt C., Wanger L., Wahlestedt C., Wanger L., Wahlestedt C., Samer A., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Shimada K., Sakazume M., Sakazume M., Sakazume N., Sakazume N., Sakazume N., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Hara A., Hashizume W., Imotani K., Ishia K., Sakazume N., Sakazume N., Hara A., Hashizame Y., Walling V., Shinagawa A., Hara A., Hashizawi Y., Waterston R., Indeper E.S., Rogers J.,
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Bromodomain adjacent to zinc finger domain protein 1B (Williams-Beuren
syndrome chromosome region 9 protein homolog) (WBRS9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ĕ
                                                                                                                                                                                                                                                                                                       221 LPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPPWM-IQDEEYIAGNQEIGPSYEEF
                                                                                                                                                                                                                                                                                                                                                          269 NPPG-----VVGMTSISSSHSTDAG-GNVHSGAPPPWLDANDGDF--SSVQLNQSDVAR
                                                                                                  -----LEPQAVPDPEEGSSA-----PRSWKG------MNSQVASSLQQPSNLD
                                                                                                                                                                                          209 HNGSYLNMDDSQFPLCDESGNGFGEHSIPCRSKDYSGNGNYCTQENYQVSQDKKQIDGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peoples R.J., Cisco M.J., Kaplan P., Francke U.; "Identification of the WBSCR9 gene, encoding a novel transcriptional regulator, in the Williams-Beuren syndrome deletion at 7q11.23."; Cytogenet. Cell Genet. 82:238-246(1998).
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"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PLAVQTSTPKLKLQQXRSSHIQKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 ESRKEFEKEKRKLVKTESISTESEPVKIQ----PYISKRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 LKEKEKOKLKKLPPDRVGANFDH-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           092277; 09CU68;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=99077764; PubMed=9858827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Baz1b; Synonyms=Wbscr9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-482 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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us-09-155-676b-5.rup

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Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOC443594 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
      59 QLT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus.
                                     149 ---- KGLDS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse
                                                                                                                                                                   221
                                                                                                                                                                                                                                                                                                 302
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                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 FTAASTQRQLKEAFERLLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEVREHLSHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50827; DDT; 1. PROSITE; PS001359; ZF PHD 1; 1. PROSITE; PS50016; ZF PHD 2; 1. BROSITE; PS50016; ZF PHD 2; 1. Bromodomain; Coiled Coil; Nuclear protein; Transcription regulation;
                                                                                                                              -1- TISSUE SPECIFICITY: Expressed in all tissues examined including heart, brain, spleen, lung, skeletal muscle, kidney and testis.
-!- DEVELOPMENTAL STAGE: Expressed as early as day 7 and in equal
FUNCTION: Forms a chromatin remodeling complex that mobilizes nucleosomes and reconfigures irregular chromatin to a regular nucleosomal array structure (By similarity).

SUBUNIT: Interacts with ISMI (imitation SMI protein) to form the STF-ISMI chromatin remodeling complex (MICH) (By similarity). SUBCELLULAR LOCATION: Nuclear (Potential). Accumulates in pericentromeric heterochromatin during replication (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  led coil (Potential).
DFB5816AE1C0634F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1353499; Bazlb.

GO; GO:0005721; C:centric heterochromatin; IDA.

GO; GO:0000731; C:centric heterochromatin; IDA.

GO; GO:0005513; C:nucleus; IDA.

GO; GO:0005515; P:procein binding; IPI.

GO; GO:0006313; P:chromatin assembly/disassembly; IDA.

GO; GO:0006318; P:chromatin remodeling; IDA.

InterPro; IPR004022; DDT.

InterPro; IPR001965; ZAI_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coiled coil (Potential). Coiled coil (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Mismatches 118;
                                                                                                                                                                           amounts during gestation.
--- SIMILARITY: Belongs to the WAL family.
--- SIMILARITY: Contains 1 bromodomain.
--- SIMILARITY: Contains 1 DPT domain.
--- SIMILARITY: Contains 1 PHD-type zinc finger.
--- SIMILARITY: Contains 1 PHD-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00633; BROMODOMAIN_1; FALSE_NEG.
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DDT.
PHD-type.
Bromodomain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170788 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF084480; AAD08676.1; -. EMBL; AK017894; BAB30992.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00439; Bromodomain; 1.
Pfam; PF00628; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00503; BROMODOMAIN.
SMART; SM00597; BROMO; 1.
SMART; SM00571; DDT; 1.
SMART; SM00249; PHD; 1.
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895
1284
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Matches 95; Conserv
                                                                                                                    similarity)
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189 VPDPEEGS-SAPRSWKGMNSQVASSLQQ------PSNLD- 220
                                                                                                                                                                                                                          --PAPELDWMETGPSLT----FIGHQDIPGVGN 249
                                                                                                                                                                                                                                                                                                                                           ---YEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQA 188
                                                                                                                                                                           148 VEKKSDGACDSPSSDKENSSQMAQDLQKKETVVKEDEGRRESINDRARRSPRKLPTSLKK 207
                                                                                                                                                                                                                                                                                                                 250 IHSGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEK------QKLKKLPPDRVGANFD 301
                                                                                                                                                                                                                                                                                                                                                                                                                                    320 KPKRDSSSLSSPLNPKLWCHVHLEKSLNGPPLKVKNSKNSKSPEEHLEGVMKIMSPNNNK 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE_22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A blatcheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yers R.M., Butterfield Y.S.,
Schnerch A., Schein J.E.,
---HKEA----WEEEQEVAELLKEEF---PNWYEKLVLEMVHHNT
                                                                                                                                                                                                                                                                    208 GERKWAPPKFLPHKYDVKLONEDKIISNVPADSLIRTERPPNKEILRYFIRHNAL---R
                                                                                      ----VDEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                      HSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----HIQKKANHALYQLPXGXKP--KSTKPL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 LHSFHIPKKG-----PAAKKPGKHSDKPL 403
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initiative.";

NLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQ--MKEKFLVTPQDYARFKKSMV---- 148

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Name=ORF5;
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                                                                                                                                                                                                                                            82 CCGC------EVREHLSHGNLTVLY-GGLLE--HLASPEHKKATNKFWMENKA 125
                                                                                                                                                                                                                                                                   60 STGSSQLTHKEAWDEEQEVAELLKE-EFPVWYEKQVLEMVHHNTISLDKLVDQSWMEIMT 118
                                                                                                                                                                                                                                                                                          EVOMKEK--FLVTPQDYARFKKSMVKGLDSYE-------EKEDKVIKEM 165
                                                                                                                                                                                                                                                                                                                119 KYADGEECDFEVGPEKYLRAKIVKVHPLEKEEQASEKKSEGSCDSPSSDKENSNKVAQDI 178
                                                                                                                                                                                                                                                                                                                                        166 AAQIREVEQSRQEVVRSVLE-----PQAVP---DPEGSSAPRSWKGMNSQVASSLQQ 215
                                                                                                                                                                                                                                                                                                                                                      235 DKVISFVPVDSLYRSERPPNKEILRYFIRHNAL----RIGTGENAPWVVEDE--LVKKYT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 LPSKFSDFLLDPHKYMTLNPSSATKRKSLGSPDOKPAKKSKKSPLSPSSWSLANLKKTAV 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 PSNLDLPPAPELDWMETGPSLT----FIGHQDIPGVGNIHSGATPPWMIQDEEYIAGNQE 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SSRISAGMLPSEG-- 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 -PRLEXWTPLAVQTSTPKLKLQQXRSSHIQKKANHALYQLPXGXKPKSTKPLLYLPP 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 SPKLKQMTLLDMAKSTPKVSRAQKGGSNTPR-------SSKPNKYLPP 447
                                                                                                                                                                                                               31 GRGTFTAASTQRQLKEAF----ERLLPQVEAARKAIRA----AQVERYVPEHERCCWCL
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB=Whole body;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                        Indels 171;
                                                                                                                                                  Length 777;
                              TISSUE-Embryo;
Klein S., Gerhard D.S.;
Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072944; AAH72944.1; -
InterPro; IPR004022; DDT.
SWART; SM00571; DDT; 1.
PROSITE; PS50827; DDT; 1.
                                                                                                                          8DBABF7365DE2087 CRC64;
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Last annotation update)
                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                 5.3%; Score 115.5;
21.0%; Pred. No. 21;
ive 55; Mismatches
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                                                                                                                          777 AA; 89051 MW;
Dyn. 225:384-391(2002)
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                                                                                                                                                            Best Local Similarity 21.0
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                       SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 TNEEDDMVEMEEER-----LRMREHVMNEVDSNKDRLV-SLDEFLVATKKKEFLEFD 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., ioquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McErnan K.J., Malek J.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahet J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Shevchenko Y., Rouffard G.G. Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 WWENKAEVQMKEKFLVTPQDYARFKKSMV-----KGLDSYEEKED--KVIKEMAAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDWMETGPSLTFIGHQDIPGVGNIHSGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 DPRAAXNSIRAHEGPFFCGRGTFTAASTQRQLKEAFERLLPQVEAARKAIRAAQVERYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 DPKTFFNLHDTNGDGFF-----YDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 REVEQSRQEVVRSVLEPQAVPDPE----EGSSAPRSWKGMNSQVASSLQQPSNLDLPPAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
Luteovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.2%; Score 113; DB 2; Length 496; 20.8%; Pred. No. 17;
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00018; EF HAND; UNKNOWN 1.
SEQUENCE 496 AA; 58136 MW; 4FD038C12A455AE2 CRC64;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Readthrough protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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ZFIN; ZDB-GENE-030826-14; nuchza.
ZFOX; CO:005509; F:calcium ion binding;
InterPro; IPR002048; EF-hand.
InterPro; IPR010983; EF-hand.
Pfam; PF00036; efhand; Z.
SMART; SM00054; EFh; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Best Local Similarity
Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Whole body;
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                                                                                                                                                                                               107 LASPEHKKATNKF------WWENKAEVQMKEKFLVTPQDYARFKKSMVKGLDSYEEKE 158
                                                                                                                                                                                                                         159 DKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNSQVASSL---- 213
                                                                                                                                                                                                                                        | ::| | | :|
300 NYTIDQSDDVD----PILRDAËVMKFAGFVGAKDRFALQGAKPIGPGDRSIHRFKPSATL 355
                                                                                                                                                                                                                                                                                                                          ----HSGATPPWMIQDEEYIAGNQEIGPSYEEFL---KEKEKQ-----KLKK----LPPD 294
                                                                                                                                                                                                                                                                                                                                                     295 RVGANFDHSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSHIQKKANHALYQL 354
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                    ----QQPSNLDLPPAPELDWMETGPSLTFIGHODI------PGVGNI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Comparison of complete nucleotide sequences of genomic RNAs of four Soybean dwarf virus strains that differ in their vector specificity and symptom production.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           no DNA stage; Luteoviridae;
                                                                                                                                                             97;
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MEDLINE=21578621; PubMed=11722012;
Terauchi H., Kanematsu S., Honda K., Mikoshiba Y., Ishiguro K.,
                                                                                                                                          Length 487;
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           STRAIN=DS;
Terauchi H., Honda K., Yamagishi N., Kanematsu S., Ishiguro
                                                                                                                                                             Indels
                             Hidaka S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB076050; BAC54091.1;
InterPro; IPR000893; Luteo_ORF6.
InterPro; IPR002929; PLMV ORF5.
Pfam: PF01690; PLRV ORF5; IPR015909; PLRV ORF5.
                                                                                                                    70F63DC6BE9B7E9A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                       Query Match 5.1%; Score 112.5; DB 2; Best Local Similarity 23.1%; Pred. No. 18; Matches 74; Conservative 49; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        489 AA
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Pred. No. 18;
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Viruses; ssRNA positive-strand viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                   452 STGTLKGGSLKPKKELPPRF 471
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MRL, ABORDSALSO, BABCSBS.1; --
Pfam, PFO1690; PLRV ORFS; 1.
PRINTS; PRO0910; LVIRUSORF6.
                                                                                                                   487 AA; 54357 MW;
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity
SEQUENCE FROM N.A.
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SEQUENCE
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301 ESYTTDQSDDVEPSPHDADVMKFS---GFVGAKDRFVLQGADPIGPGDRSVRRFKPSATL 357
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                                                                                                                                                                                                                                                                                                                                                               159 DKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNSQVASSLQQPSN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 BESYATDOTDDVE--PILLDADVMKFSGFVGARDRFTLQGAEPIGPGDRTSRRFRPSATL 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354
                                                                                                                                                                                                                                      251 ----HSGATPPWMIQDEEYIAGNQEIGPSYEEFL-KEKEK--------QKLKKLPPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 LVAPAVKK-TAKYNFCVSYGDWTDRDMEFGMVSVVLDEHLEGARSSOYVRKTL----RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 LDLPPAPELDWMETGPSLT-----FIGHQD---IPGVGNI------
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    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soybean dwarf virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
                                                 178 EVVRSVLEP-----QAVP-----DPEEGSSAPRSWKGMNSQVA---
                                                                                                                                             211 SSLQQPSNLDLPPAP-ELDWMETGPSLTFIGHQDI------PGVGNI---
    91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=DS;
Terauchi H., Honda K., Yamagishi N., Kanematsu S., Ishiguro
    Indels
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR000893; Luteo ORF6.
InterPro; IPR002929; PLRV ORF5.
Pfam; PF01690; PLRV ORF5; ...
PRINTS; PR00910; LVIRUSORF6.
1 1 1 SEQÜENCE 489 AA; 54634 MW; PAAE6F4900DBEA77 CRC64;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Readthrough protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.1%; Score 112.5; DB 2;
21.9%; Pred. No. 18;
iive 54; Mismatches 101;
    70;
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    Mismatches
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37;
    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  712 ------GOILERLIEKESQES---------LRSPEEEDQEAGRSLQK 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 663 FPGÅEDÖMLERLVEKEDQSFPRSPEEDQEÅCRPLÖKENQEP------LGYEEAE- 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 GLD---SYEEKEDKVI----KEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSAPRS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   744 GNQEPLGYEEAEGQILERLIEKESQESLRSAEEEDQEACRSL------QKENQEPLG 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WKGMNSQVASSLOOPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPPWMIQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 FTAASTO--ROLKEAFERLLPQ--VEAARKAIRAAQVERYVPEHERCCWCLCCGCEVREH 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22273441; PubMed=12686602;
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                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 XWTPLAVQTSTPKLKL-----QQXRSSHIQKKANHALYQLPXGXKPKSTKPLLYL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the intermediate filament family. EMBL, AF538924; AAN33053.1; -. HSSP; P08670; 1GK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.1%; Score 112; DB 2; Length 189
20.6%; Pred. No. 1.1e+02;
tive 53; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208796 MW; 03AEGB616A1A7623 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chou Y.-H., Herrmann H., Goldman R.D., Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005882; C:intermediate filament; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR011000; Apolp_III_like.
InterPro; IPR001664; IF.
                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                  454 STGTLKGGSLKPKKELPPRF 473
355 PXGX-KPKSTKPLLYLPPKF
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Matches 73; Conservative
                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat)
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

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                                                                                                           Name=stnA; ORFNames=CG40306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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"A product of the Drosophila stoned locus regulates neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: Present at synaptic connections both in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNS and in neuromuscular junctions in the mature embryo (20-22h) and throughout larval development. In the third instar larva, it is expressed in all synaptic boutons types, including I, II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20524362; PubMed=11069931;
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"The products of the Drosophila stoned locus interact with synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        presynatic proteins, are thought to mediate an interaction with Alpha-adaptin (By similarity).
MISCELLANEOUS: StnB, which is involved in the same pathway, is derived from the same dicistronic transcript that encodes these two different proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     III boutons.

DOMAIN: The Asp-Pro-Phe (DPF) motifs, which are found in many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Heterochromatic sequences in a Drosophila whole-genome shotgun
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                                                                                                                                                                                            assembly.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERACTION WITH SYT, AND MUTANT STN-TS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION, AND SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21114085; PubMed=11160392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synaptic boutons
                                                                      STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ramaswami M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endocytosis."
                                                                                                                                                                                                                                                                                                                        release.";
                                                                                                                                                                                                                                                FUNCTION
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVPIDLSVSL-HIHLIKHKQPVEE---EBEBLEQKGRENQLLNP-DLSEF-----DSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 ASTOROLKEAFERLL -- POVEAA-RKAIRAAOVERYVPEHERCCWCLCCGCEVREHLSHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 NLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSMVKGLDSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNSQVASSLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---TPKLKLQQXRSSH--IQKKANHALYQLPXGXKPKSTKPLLYLPPKFFIIVFLRKQTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K->M: In stn-TS2; induce behavioral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91;
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                                                                                                                            EMBL; U54982; AAC16665.1; -.
PIR; T13352; T13352.
FlyBase; FBGH0016976; stnA.
GO; GO:0030139; C:endocytic vesicle; IDA.
GO; GO:000886; C:plasma membrane; IDA.
GO; GO:0008021; C:synaptic vesicle; IGI.
GO; GO:0008015; F:protein binding; IPI.
GO; GO:0008099; P:synaptic vesicle endocytosis; IMP.
Endocytosis; Repeat; Synapse.
DOMAIN
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2773741640B73757 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            536 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.1%; Score 111.5; 23.2%; Pred. No. 44;
non-profit institutions as long and this statement is and
                                                                                                                                                                                                                                                                                                                                                                                     Poly-Lys.
Poly-Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                              Poly-Glu.
Poly-Pro.
DPF 1.
DPF 2.
DPF 4.
DPF 5.
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(TrEMBLrel. 23, 1
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01-MAR-2004
AT11052p.
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                                                                                                                                                                                                                                                                                                                                                                                                          152 DSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLE---PQAVPDPEEGSSAPRSWKGMNSQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                   SEQUENCE FROM N.A.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 LPSDIPPPSQLPSDIPPPSQL-----PS-----DIPPPSQLPSGTPPP 341
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
              Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                  5.1%; Score 111; DB 2; Length 536; 29.7%; Pred. No. 26; rive 21; Mismatches 39; Indels
                                                                                                                                                                                                                                          Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BT001295; AAN71050.1; -.
FlyBase; FBgn0050416; CG30416.
                                                                                                                                                                                                                                                                                                 536 AA; 60593 MW; CE5B462E6E254C0E CRC64;
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Last annotation update)
Name=CG30412; CG30416; ORFNames=CG30416;
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33; Conservative
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NCBI_TaxID=7227;
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Best Local
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
A Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Sylerkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
I'lthe genome sequence of Drosophila melanogaster.";
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Fribe E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 DSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLE---PQAVPDPEEGSSAPRSWKGMNSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patelb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C. Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Gaps
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 VASSLQQPSNL--DLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPP 257
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5.1%; Score 111; DB 2; Length 539;
Best Local Similarity 29.7%; Pred. No. 27;
Matches 33; Conservative 21; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22426065; PubMed=12537568;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -------EDİPEL 1167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SSAPRSWK--GMNSQVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGV 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P. SEQUENCE FROM N.A.

WEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;

WA MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;

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                                                                                                                                                                 01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Kinesin-related protein KIF27.
Macaca fascicularis (Crab earing macaque) (Cynomolgus monkey).
Edwaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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GO; GO:0005875; C:microtubule associated complex; IEA.
GO; GO:0005274; F:AFP binding; IEA.
GO; GO:0003774; F:motor activity; IEA.
R GO; GO:0003774; F:motor activity; IEA.
InterPro; IPR001752; kinesin_motor.
R Pfam; PR00225; Kinesin; 1.
R Pfam; PR00380; KINESINHEAVY.
R ROSITE; PS00411; KINESIN MOTOR DOMAIN1; UNKNOWN_1.
RROSITE; PS0067; KINESIN MOTOR_DOMAIN2; 1.
RAP-binding; Microtubule; Motor protein.
SEQUENCE 1266 AA; 144456 MW; DESBABEEGBSCCEGE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
5.1%; Score 111; DB 2; Length 1266;
Best Local Similarity 21.9%; Pred. No. 80;
Matches 64; Conservative 42; Mismatches 98; Indels 8
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                                                                                                                 PRT; 1266 AA.
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Search completed: June 7, 2005, 12:02:16 Job time : 64.0244 secs

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Sequence 5, Appli
Sequence 4933, A
Sequence 49340, A
Sequence 44039, A
Sequence 105976,
Sequence 32898, A
Sequence 38504, A
Sequence 6063, Ap
Sequence 6063, Ap
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3355, A
101745, Ap
111745, A
35209, A
35828, Ap
6676, Ap
6779, Ap
8705, Ap
8705, Ap
                                                                                                                                   June 7, 2005, 11:57:41; Search time 20.7652 Seconds (without alignments) 2390.553 Million cell updates/sec
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1 IGVTRWRRSRIVDPRAAXNS.....RGLESSLSIPSTSRGGRTHF 417
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Sequence 3
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1: /cgn2 6/ptodata/1/paa/PCT NEW COMB.pep:*

2: /cgn2 6/ptodata/1/paa/USO6 NEW COMB.pep:*

3: /cgn2 6/ptodata/1/paa/USO7 NEW COMB.pep:*

4: /cgn2 6/ptodata/1/paa/USO8 NEW COMB.pep:*

5: /cgn2 6/ptodata/1/paa/USO8 NEW COMB.pep:*

6: /cgn2 6/ptodata/1/paa/USI0_NEW COMB.pep:*

7: /cgn2 6/ptodata/1/paa/USI1_NEW COMB.pep:*

8: /cgn2 6/ptodata/1/paa/USI1_NEW COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-450-763-49939
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US-10-450-763-44039
US-11-097-143-22998
US-11-097-143-22998
US-11-097-143-22998
US-10-940-774A-6063
US-10-940-774A-7037
US-10-940-774A-677
US-11-097-143-3559
US-11-097-143-3559
US-11-097-143-3559
US-11-097-143-3559
US-11-097-143-3773
US-10-940-774A-6779
US-10-940-774A-7759
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PCT-US03-10870-998
US-11-097-143-11865
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Listing first 45 summaries
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					_	RESULT 1
	ALIGNMENTS					
7647,	US-10-940-774A-7647	9	2107	4.6	101	45
764	US-10-940-774A-7646	9	2107	4.6	101	44
21,	US-60-679-970-21	80	2102	4.6	101	43
19.	US-60-679-970-19	0	2102		101	42
Sequence 508, App	119-60-664-936-508	0 0	2101	4.4	101	2 T
585	US-11-085-606-585	7	2101	•	101	39
584	US-11-085-606-584		2101	•	101	38
380,	US-60-679-970-380		1536		101	37
379,	US-60-679-970-379		1536	•	101	36
514,	US-60-664-936-514		1536	•	101	35
513,	US-60-664-936-513		1536	•	101	34
581,	US-11-085-606-581		1536	•	101	33
580,	US-11-085-606-580		1536	•	101	32
355,	US-11-085-606-355		1214	٠	101	31
	US-11-085-606-351		1214	4.6	101	30
357,	US-11-085-606-357		1130	•	101	29
356,	US-11-085-606-356		1130	•	101	28
30390	US-11-097-143-30390		5303	4.6	101.5	27
Sequence 51031, A	US-10-450-763-51031		1717	4.6	101.5	26

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RESULT 1

Sequence 5. Application US/09155676B

Sequence 5. Application US/09155676B

Sequence 5. Application US/09155676B

Sequence 5. Application US/09155676B

Sequence 5. Application US/0915676B

Septicary: WOLDIN, MIXClai

APPLICARY: WALLACH; David

APPLICARY: WALLACH; MANCHAINO, Andrei

APPLICARY: WALLACH; WOULANG, Andrei

APPLICARY: WALLACH; WOULANG, SOF THY RECEPTOR ASSOCIATED FACTOR (TRAP), THEIR

TITLE OF INVENTION: PROJECT OF THE SECRET OF THEIR

TITLE OF INVENTION: PROJECT OF THE SECRET OF THEIR

TITLE OF INVENTION: PROJECT OF THEIR

TITLE OF INVENTION WINDER: 1999-04-01.049/155,676B

CURRENT APPLICATION WINDER: 1999-04-01.11900

PRIOR FILLING DATE: 1999-04-01.11900

PRIOR FILLING DATE: 1999-04-02

PRIOR FILLING DATE: 1996-02-02

SOFTWARE: PROJECT OF THEIR

PRIOR FILLING DATE: 1996-03-02

SOFTWARE: PROJECT OF THEIR

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PROJECT OF THEIR

NUMBER OF SEQ ID NOS: 22

SOFTWARE: MASC-feature

NUMBER OF SEQ ID NOS: 23

SOFTWARE: MASC-feature

NUMBER OF SEQ ID NOS: 23

SOFTWARE: MASC-feature

NUMBER OF SEQ ID NOS: 23

SOFTWARE: MASC-feature

NUMBER OF SEQ ID NOS: 23

SOFTWARE: MASC-feature

NUMBER SINCORATION: As can be any naturally occurring amino acid

SEAURN (130: 1.339)

OTHER INFORMATION: As can be any naturally occurring amino acid

SEAURN (130: 1.339)

OTHER INFORMATION: As can be any naturally occurring amino acid

SEAURN (130: 1.339)

OTHER INFORMATION: As can be any naturally occurring amino acid

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OTHER INFORMATION: As can be any naturally occurring amino acid

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OTHER INFORMATION: As can be any naturally occurring amino acid

SEAURN (130: 1.339)
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US-10-450-763-49940
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US-10-450-763-44039
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                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                  241 HQDIPGVGNIHSGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEKQKLKKLPPDRVGANF 300
                                                                                                                                                                                                                                      61 AIRAAQVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLYGGLLEHLASPEHKKATNKFW 120
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                                                                                                                                                                                                                                                                                                                                                              181 RSVLEPQAVPDPEEGSSAPRSWKGMNSQVASSLQQPSNLDLPPAPPELDWMETGPSLTFIG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 WRRSRIVDPRAAXNSIRAHEGPFFCGRGTFTAASTQRQLKEAFERLLPQVEAARKAIRAA
                                                                                                                                        1 IGVTRWRRSRIVDPRAAXNSIRAHEGPFFCGRGTFTAASTQRQLKEAFERLLPQVEAARK
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                                                                                                                                                                                                                                                                                                            1 IGVTRWRRSRIVDPRAAXNSIRAHEGPFFCGRGTFTAASTQRQLKEAFERLLPQVEAARK
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
; LOCATION: (388)...(388); OTHER INFORMATION: Xaa can be any naturally occurring amino acid US-09-155-676B-5
                                                                                                        ;
0
                                                                       Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
30.6%; Score 670; DB 6; Length 156;
Best Local Similarity 77.9%; Pred. No. 8.2e-43;
Matches 134; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49939, Application US/10450763
; Sequence 49939, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES; FILE REFERENCE: 790CTP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT APPLICATION NUMBER: EQ10/108631
; PRIOR FILING DATE: 2001-03-30
; PRIOR PELING DATE: 2000-03-31
; PRIOR PLING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: CUSTOM
; SEQ ID NO 49999
; ELOUGHH: 156
                                                                                                      Indels

; LOCATION: (1)...(156)
; OTHER INFORMATION: Xaa = X or * as defined in Table
US-10-450-763-49939

                                                                  Query Match
99.5%; Score 2178; DB 5; L
Best Local Similarity 100.0%; Pred. No. 1.9e-155;
Matches 417; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 WSRARL-QPQAPA----AAEGGF--GEAPAPGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (1)...(156)
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US-10-450-763-49939
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LOCATION: (632)..(650)

OTHER INFORMATION: BURKITT'S LYMPHOMA RECEPTOR SIGNATURE domain identified by OTHER INFORMATION: BURKITT'S LYMPHOMA RECEPTOR SIGNATURE domain identified by OTHER INFORMATION: 12.64

FEATURE:
NAME/KEY: DOMAIN

LOCATION: (502)..(736)

OTHER INFORMATION: 7 transmembrane receptor domain identified by PFam, accessioners information: name 7tm_1, E-value=5.2e-81, PFam score of 259.5
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| ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 STGK--WINNG------IVFODEDRI-----IDTYDTDES-------OK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNSQVASSLQOPSNLDLPPAPELDWMETGP 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 ------PG----RRGATPPWMIQDEEXIAGNOEIGPSYEEFLKEKEKQKLKKLPPD 311
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43 QVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLYGGLLEHLASPEHKKATNKFWWENKA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 QVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLYGGLLEHL-----ASPEHKK----
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                                                                                                                                                                                                                                                           Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.3%; Score 554.5; DB 6; Length 741; 40.7%; Pred. No. 2.7e-33; Indels 127; ive 18; Mismatches 52; Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TILE REFERENCE: 190CH29/US
FILE REFERENCE: 790CH29/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-31
PRIOR PLILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDPHTSRSLRIPAEVAPRSKRRCVLERKOPYS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-450-763-49940
; Sequence 49940, Application US/10450763
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 135; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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16;

Gaps

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GENERAL INVORMATION:

APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLBIC ACID
TITLE OF INVENTION: DETECTION EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DETECTION WEBS.
FILE REPRENCE: CLOOG728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-28
PRIOR PLING DATE: 1999-11-2
PRIOR PLING DATE: 1999-11-2
PRIOR PLING DATE: 1999-11-2
PRIOR PLING DATE: 1999-11-2
PRIOR PLING DATE: 1999-11-3
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-24
PRIOR PLING DATE: 2000-01-24
PRIOR PLING DATE: 2000-01-24
PRIOR PLING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 850
                                                                                                                                                                                                                                        147 MVKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGS-SAPRSWKGM 205
                                                                                                                                                                                                                                                                                                                                 206 NSQVASS---LOOPSNLDLPPAPEL--DWMETGPSLTFIGHODIPGV--GNIHSGATP-- 256
                                                                                                                                                                                                                                                                                                                                                                                                                               323 SVPIDLSVSL-HLHLIKHKQPVEE---EEELEQKGRENQLLNP-DLSEF-----DSL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 NLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSMVKGLDSY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 -PWMI------QDEEYI-AGNQEIGPSYE---EFLKEKEKQKLKKLPPDRVGANF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 NLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKK-----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 ASTQRQLKEAFERLL--PQVEAA-RKAIRAAQVERYVPEHERCCWCLCCGCEVREHLSHG
                                                                                                                   35 FTAASTQRQLKEAFERLLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEVREHLSHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91; Gaps
                                                                     81;
                          Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 850;
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                       5.7%; Score 124.5; DB 6; ilarity 23.9%; Pred. No. 0.37; Conservative 46; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32898, Application US/11097143 GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -11-097-143-32898
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APPLICANT: Andersen, Scott E.
APPLICANT: Andersen, Scott E.
APPLICANT: Andersen, Scott E.
APPLICANT: Conner, Timothy W.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Ansucci, James D.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: NUMBER: US/10/703,032
CURRENT APPLICATION NUMBER: 10/020,338
PRIOR PILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 211164
SEG ID NO 105976
LENGTH: 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 SHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARSHLYGTPMG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 ----KKSMVKGL------DSYEEKEDKVIKEMAAQIREVEQSRQEVVRSV-LEPQA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 SAVPSQACLEALLIIVPWGACGVSQEEEES------PAEGSKDEPGEQVELKEEA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 TOROLKEAFERL-----LPOVEAARKAIRAAQVERYVPEHERCCWCLCCGCEVREHL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 SHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 VPDPEEGSSAPRSWKGMNSQVASSLQQPSNLDLPPAPELDWMETGPSLT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 312;
                                                           APPLICANT: Hyeeq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENT POLICATION NUMBER: US/10/450,763

CURRENT PILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: US/10801/08631

PRIOR PILING DATE: 2001-03-30

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CLUSTON

SEQ ID NO 44039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.0%; Score 503; DB 6; Best Local Similarity 49.3%; Pred. No. 6.7e-30; Matches 113; Conservative 14; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(567)
OTHER INFORMATION: unsure at all Xaa locations
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OTHER INFORMATION: Clone ID: PAT_TA_394.pep
US-10-703-032-105976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 105976, Application US/10703032 GENERAL INFORMATION:
                       Sequence 44039, Application US/10450763 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-450-763-44039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :|| |
277 EAPVEDGSQPP-
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSCHILA GENES.

FILE REFERRACE: CLOO728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT APPLICATION NUMBER: US/11/097,143

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-19

PRIOR PLING DATE: 1999-10-28

PRIOR PLING DATE: 1999-11-2

PRIOR PLING DATE: 1999-11-2

PRIOR PLING DATE: 1999-11-2

PRIOR PLING DATE: 1999-11-2

PRIOR PLING DATE: 1999-11-2

PRIOR PLING DATE: 1999-11-2

PRIOR PLING DATE: 1999-11-4

PRIOR PLING DATE: 2090-11-2

PRIOR PLING DATE: 2000-01-12

PRIOR PLING DATE: 2000-02-24

PRIOR PLING DATE: 2000-02-24

PRIOR PLING DATE: 2000-02-24

PRIOR PLING DATE: 2000-03-24

PRIOR PLING DATE: 2000-03-24

PRIOR PLING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 838

LENGTH: BJB
EEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNSQVASSLQ 214
                             152 DSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLE---PQAVPDPEEGSSAPRSWKGMNSQ 208
                                                                                                                                                                          275 SYBEFLKEKEKOKLKKLPPDRVGANFDHSSRTSAGWLPSF-GPRLEXWTPLAVQTS---- 329
                                                                                                                                                                                                                   459 EDDPFNTNYAEQVIKKTTVLEEDDDFDPRAEEHATEPPFLAAPORDLLAGSATDLSQVVP 518
                                                                                                                                                                                                                                                              ---TPKLKLQQXRSSH--IQKKANHALYQLPXGXKPKSTKPLLYLPPKFFIIVFLRKQTY 384
                                                                                                                                                                                                                                                                                                         519 APLAPTLSVDQEAEDFDPFDTSAVSALVQ-----PKSTE------LRFLERELL 561
                                                                                      215 OPSNLDLPPAPELDWMETGPSLTFIGHODIPGVGNIHSGATPPWMIQDEEYIAGNQEIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 LPSDIPPPSQLPSDIPPPSQL-----PS-----DIPPPSQLPSGTPPP 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 VASSLQQPSNL--DLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPP
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Best Local Similarity 29.7%; Pred. No. 6.2;
Matches 33; Conservative 21; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                  385 SFIXFNKVLFFGLRG--LESSLS 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20796, Application US/11097143 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRGANISM: DROSOPHILA US-11-097-143-20796
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RESULT 8 US-10-450-763-38504 : Sequence 38504, Application US/10450763

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Sequence 6663, Application US/10940774A
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
PILE REFERENCE: CLOOJST:
CURRENT APPLICATION NUMBER: US/10/940,774A
CURRENT FILING DATE: 2004-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 HORDGKFCDCCYCEFFGHNAPPAAPTSRNYTEIREKL-RSRLTRRKEBLPMKGGTLGGIP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 ---APELDWMET-GPSLTFIGH------QDIPG-VGNIHSGATPPWMIQDEEYIA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 GNQEIGPSYEEFLKEKEKQKLKKLPPDRVGANFDHSSRTSAGWLPSFGPRLEXWTPLAVQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               598 GH----PSSEE-ASSKEVPSCKQELPEPV-----SSGGKPOKGKROGSQAKKSEA 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 HER-----CCWCLCCG------CEVREHLSHGNLT-----VLYGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LLEHLASPE----HKKATNKFWWENKAEVOMKEKFL--VTPOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAVPDPEEGSSAPRSWKGMNSQVASSLQQPS-NLDDLPP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 YARFKKSMVKGLDSYBEKE-DKVIKEMAAQIREVEQSRQEVVR---SVLE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 830;
APPLICANT: Hyseg, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
                                                                                                                                                                                                                                                                                                                                                                                                 i LOCATION: (1)...(830)
i OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-38504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.0%; Score 108.5; DB 6; 22.8%; Pred. No. 9.4; iive 42; Mismatches 106;
                                                       PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSTPKLKLQQXRSSHIQ 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPAPR-PTSQPRGSQCQ 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 22.8
hes 86; Conservative
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
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19;

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Sequence 7037, Application US/10940774A

Sequence 7037, Application US/10940774A

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISM: METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/10/940,774A

CURRENT FILING DATE: 2004-09-15

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-06

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREUESEQ for Windows Version 4.0
                                                                                                                        88 REHLSHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSM 147
                                                                                                                                                                                                          148 VKGLDSYEEKEDKV---IKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSAPRSWKG 204
                                                                                                                                                                                                                                    ----BGQKDIEDELLTTGLELVDSCIRSLQES-----GILDPQDYSTGERPSLLSQSALQ 165
                                                                                                                                                                                                                                                                                            205 MNSQVASSLQQP----SNLDLP-----PAPELDWMETGPSL----TFIGHQDIPG 246
                                                                                                                                                                                                                                                                                                                                                                          247 VGNIHSGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEKQKLKKLPPDRVGANFDHSSRT 306
                                                                                                                                                                                                                                                                                                                                                                                                                 ----LPDAPPAAAAALYYSSST 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171
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                                                                                                                                                                                                                                                                                                                                   166 LNSKPEGSFÖYPASYHSNOTLALGETTPSQLPARGTQARATGQSFSQGTTSRAGHLAGP- 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LPA-PPR--GGSPLAAPQGGSPTKLQRGSA----PEGATYAAPRGSSPKQS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 PPGAMRSLRA-AGPSAAPRGRPQQPPVPTAAAAMAPLLGRKPFPLVKPLPGEEPLFTIPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 ARKAIRA----AQVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLYGGLLEHLASPEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 TQEAFRTREEYEARLERY---SERIWTCKSTG-----SSQLT------H
                                        GRGTFTAASTQRQLKE---AFERLLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 PRAAXNSIRAHEGPFFCGRG-----TFTAASTQRQL--KEAFERLLP-----QVEA
  Gaps
  Mismatches 111; Indels 119;
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                                                                  ; Score 107.5; DB 6;
; Pred. No. 24;
60; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                        . . . . EPAPPPPPREPFA---PSLGSAFH----
  46;
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ilarity 20.9%;
Conservative 60
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    Conservative
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  81;
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Best Local
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6.63
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                                                                                                                                                                                                                                                                                                                                   88 REHLSHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSM 147
                                                                                                                                                                                                                                                                                                                                                             86 -----GSET----GSMSSMSSAE-----EQPQWQSQ-------107
                                                                                                                                                                                                                                                                                                                                                                                                                                           108 ----DGQKDIEDELTTGLELVDSCIRSLQES-----GILDPQDYSTGERPSLLSQSALQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNSQVASSLQQP----SNLDLP-----PAPELDWMETGPSL----TFIGHQDIPG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 VGNIHSGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEKQKLKKLPPDRVGANFDHSSRT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 VKGLDSYEEKEDKV---IKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSAPRSWKG 204
                                                                                                                                                                                                                                                   31 GRGTFTAASTQRQLKE---AFERLLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 SAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSHIQKKANHALYQLPXGXKPKST 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (224)..(235)
OTHER INFORMATION: VINCULIN SIGNATURE domain identified by eMATRIX,
OTHER INFORMATION: number PR00806A, p-value=7.508e-10, raw score of
                                                                                                                                                               5.0%; Score 108.5; DB 6; Length 1225; 22.7%; Pred. No. 15; tive 46; Mismatches 111; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 1233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION THOSEN INC
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CTP3/US
FILE REFERENCE: 790CTP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 35355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: DOMAIN
LOCATION: (547)...(929)
OTHER INFORMATION: Armadillo/beta-catenin-like repeats
OTHER INFORMATION: Apm, accession name Armadillo_seg,
OTHER INFORMATION: 91.4
                                                                                                                                                                                                                                                                                        42 GSETETTSAILASVKEQELQFERLTRELEÄERQIV-ÄSQLER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.0%; Score 108.5; 22.7%; Pred. No. 15;
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 35355, Application US/10450763; GENERAL INFORMATION:
                                                                                                                                                                                                          81; Conservative
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                                                                                                                                                               Query Match
Best Local Similarity
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Best Local Similarity
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NAME/KEY: DOMAIN
                                                                               TYPE: PRT
ORGANISM: Human
                                                                                                                      US-10-940-774A-6063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-450-763-35355
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                                                            LENGTH: 1225
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Matches
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LOCATION: (4)...(95)
OTHER INFORMATION: Gag P30 core shell protein domain identified by PFam,
OTHER INFORMATION: accession name Gag_D30, E-value=1.4e-27, PFam score of 100.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | : :: | | :: | | : | | ERS--- LEAERASRAERDSALETLQGQLEEKAQELGHSQSALASAQRELAAFRTKVQD-- 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1571 VKOLKEOLAKKEKEHASGSGAQSEAAGRTEPTGPKLEALRAEVSKLEQOCOKOOEQADSL 1630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1686 -----HSKAEDEWKAQ----VARGRQEAERKNSLISSLEEEVSILNRQVLEKEGESKELKR 1737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (434)...(449)
OTHER INFORMATION: POLLEN ALLERGEN FOA PI SIGNATURE domain identified by OTHER INFORMATION: eMATRIX, accession number PR00833H, p-value=3.077e-09, OTHER INFORMATION: 2.30
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                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hyeeq, Inc.
ITILE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES;
FILE REFERENCE: 790CIP3/US;
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PLILING DATE: 2000-03-30
PRIOR PLILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR PLILING DATE: 2000-03-31
PRIOR PLILING DATE: 2000-03-31
PRIOR PLILING DATE: 2000-03-31
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// LOCATION: (1) ... (2246)
// OTHER INFORMATION: Xaa = X or * as defined in Table
US-10-450-763-36209

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                                                  311 LPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSHIQK
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22.1%; Pred. No. 56;
iive 64; Mismatches
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US-10-450-763-36209
; Sequence 36209, Application US/10450763
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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les 98; Conserv
                                                                                                                                 418 LD-----
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NAME/KEY: DOMAIN
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GENERAL INFORMATION:
APPLICANT: Rovalic, David K.
APPLICANT: Andersen, Scott E.
APPLICANT: Angersen, Scott E.
APPLICANT: Angersen, Scott E.
APPLICANT: Byrum, Joseph R.
APPLICANT: Cao, Yongwei I.
APPLICANT: Cao, Yongwei I.
APPLICANT: Cao, Yongwei I.
APPLICANT: Associated With G.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53374)B
CURRENT APPLICATION NUMBER: US/10/703,032
FILE REFERENCE: 2003-11-06
FRIOR FILING DATE: 2003-11-06
FRIOR FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 211164
SEQ ID NO 111745
                                                                                                                                                                                                                                         GNOEIGPSYEEFLKEKEK-----OKLKKLPPDR---VGANFDHSSRISAGWLPSFGP 316
                                                                                                                                                                                                                                                                                       337 KKYSLPSKFSDFLLDPYKYMTLNPSTKRKNTGSPDRKPSKKSKTDNSSLSS-----PLNP 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 LONEDKIISNVPADSLIRTERPPNKEIVRYFIRHNAL----RAGTGENAPWVVEDE--LV 336
                                                                                                                                                                                                                                                                                                                                                                                                   RLEXW-----TPLAVQTS----TPKLKLQQ-----XRSSHIQKKANHAL 351
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                                                                                   ---PAPELDWMETGPSLT----FIGHQDIPGVGNIHSGATPPWMIQDEEYIA 267
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4.9%; Score 106.5; DB 6; Length 605;
Best Local Similarity 21.5%; Pred. No. 8.9;
Matches 85; Conservative 53; Mismatches 132; Indels 125
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US-10-703-032-111745
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APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION OF 1000728

CURRENT FILING DATE: 2005-04-04

FRIOR APPLICATION NUMBER: 60/157,832

FRIOR APPLICATION NUMBER: 60/160,191

FRIOR APPLICATION NUMBER: 60/160,191

FRIOR FILING DATE: 1999-10-19

FRIOR FILING DATE: 1999-10-28

FRIOR FILING DATE: 1999-11-12

FRIOR APPLICATION NUMBER: 60/164,769

FRIOR APPLICATION NUMBER: 60/173,383

FRIOR FILING DATE: 1999-11-12

FRIOR APPLICATION NUMBER: 60/175,693

FRIOR FILING DATE: 2000-01-12

FRIOR APPLICATION NUMBER: 60/175,693

FRIOR FILING DATE: 2000-02-24

FRIOR PILING DATE: 2000-02-24

FRIOR PILING DATE: 2000-02-24

FRIOR APPLICATION NUMBER: 60/194,831

FRIOR FILING DATE: 2000-02-24

FRIOR APPLICATION NUMBER: 60/194,831

FRIOR FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: FASTEEQ FOR WINGOWS VERSION 4.0

SEQ ID NO 35838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518 ------SRILSRKLSPQPP--VVDKK------SAKQKKGKKKQKPQE 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ENKAEVQMKEKFLVTPQDYARFKKSMVKGLDSYEEKEDKVIKEMAAQIR-EVEQSRQEV-
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                                                                                                 ------STQALVSELLPAK 1794
                                                           351 LYQLPXGXKPKSTKPLL--YLPPK 372
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9-10-940-774A-6676
Sequence 6676, Application US/10940774A
GENERAL INFORMATION:
                                                                                                                                                                                                   Sequence 35838, Application US/11097143 GENERAL INFORMATION:
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US-11-097-143-35838
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 GSSAPRS-----WKGMNSQVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 IHSGATPPWMIQDEEY-IAGNQEIGPSYEEFLKEKEKGKLKKLPPDRVGANFDHSSRTSA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 -VREHL-SHGNLTVLYGGLLEHLASPEHKK-----ATNKFWWENKAEVQMKEKFL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 VTPQDYARFKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PPALLQPPEVPVPHSTQFAANHQEFLPHPQAPQ-PIVPGLSVVAGASASAAAVA 513
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                                                                    CURRENT APPLICATION NUMBER: US/10/940,774A
CURRENT APPLICATION NUMBER: US/10/940,774A
CURRENT FILING DATE: 2004-09-15
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 6676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 NSIRAH-----EGPFFCG-RGTFTAASTQRQLK-
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Best Local Similarity 22.0%;
Matches 84; Conservative
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Sequence 36800, A Sequence 9118, Ap Sequence 9118, Ap

Description

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Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 1029, Ap Sequence 49939, A Sequence 49939, A Sequence 49939, A Sequence 1029, A Sequence 17236, A Sequence 17236, A Sequence 17236, A Sequence 17236, A Sequence 17236, A Sequence 2, Appli

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2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 206, App Sequence 206, App Sequence 209186, Sequence 209186, Sequence 20811, Ap Sequence 39251, A Sequence 41619, A Sequence 41619, A Sequence 26189, A Sequence 26189, A Sequence 59765, A Sequence 59765, A Sequence 5927, A Sequence 59227, A Sequence 51821, A Sequence 51821, A Sequence 51821, A Sequence 51821, A Sequence 51821, A Sequence 51821, A Sequence 51821, A Sequence 59966, A Sequence 59966, A

Sequence

-10-425-114-62537 -10-425-114-67550 -10-425-114A-62537

Sequence

TITLE OF INVENTION: FACTOR (TRAF), THEIR PREPARATION AND USE NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSE: RROWNY AND NEIMAR, P.L.L.C. STREET: 624 Ninth Street, N.W., Suite 300 CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 2001 ALIGNMENTS US-09-155-676-5; Application US/09155676; GENERAL INFORMATION: APPLICANT: WALLACH, David
APPLICANT: WALININ, Nikolai
APPLICANT: BOLDIN, Mark
APPLICANT: KOVALENKO, Andrei
APPLICANT: METT, IGOR

SUMMARIES

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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AIRAAQVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLYGGLLEHLASPEHKKATNKFW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 WENKAEVQMKEKFLVTPQDYARFKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 RSVLEPQAVPDPEEGSSAPRSWKGMNSQVASSLQQPSNLDLPPAPELDWMETGPSLTFIG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HQDIPGVGNIHSGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEKQKLKKLPPDRVGANF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 HQDIPGVGNIHSGATPPWMIQDEBYIAGNQEIGPSYEFPLKEKEKQKLKKLPPDRVGANF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 DHSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSHIQKKANHALYQLPXGXKP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IGVTRWRRSRIVDPRAAXNSIRAHEGPFFCGRGTFTAASTQRQLKEAFERLLPQVEAARK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 KSTKPLLYLPPKFFIIVFLRKQTYSFIXFNKVLFFGLRGLESSLSIPSTSRGGRTHF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 KSTKPLLYLPPKFFIIVFLRKQTYSFIXFNKVLFFGLRGLESSLSIPSTSRGGRTHF 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,676
FILING DATE: 04-JAN-1999
CLASSIFICATION NUMBER: PCT/IL97/00117
FILING DATE: 01-APR-1997
PRIOR APPLICATION NUMBER: IL 117800
FILING DATE: 02-APR-1996
PRIOR APPLICATION NUMBER: IL 119133
FILING DATE: 02-APR-1996
PRIOR APPLICATION NUMBER: IL 119133
FILING DATE: 20-APR-1996
ATTORNEY/AGENT INFORMATION:
NAMME: BROWNEY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=21
TELECOMMUNICATION INFORMATION:
NAMME: BROWNEY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 20-62-6197
TELECOMMUNICATION NUMBER: 20-62-6197
TELECOMMUNICATION NUMBER: SIGNED NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.5%; Score 2178; DB 15; Best Local Similarity 100.0%; Pred. No. 2.1e-186; Matches 417; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 417 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-09-155-676-5
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Sequence 5, Application US/09155676A GENERAL INFORMATION:
APPLICANT: WALLACH, David APPLICANT: MALININ, Nikolai

RESULT 2 US-09-155-676A-5

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DHSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSHIQKKANHALYQLPXGXKP 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSVLEPQAVPDPEEGSSAPRSWKGMNSQVASSLQQPSNLDLPPAPELDWMETGPSLTFIG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WENKAEVOMKEKFLVTPQDYARFKKSMVKGLDSYBEKEDKVIKEMAAQIREVEQSRQEVV 180
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0
APPLICANT: KOVALENKO, Andrei
APPLICANT: METT, Igor
TITLE OF INVENTION: MODULATORS OF THE RECEPTOR ASSOCIATED
TITLE OF INVENTION: FACTOR (TRAF), THEIR PREPARATION AND USE
THUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.5%; Score 2178; DB 15; Length 417; 100.0%; Pred. No. 2.1e-186; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPUTER: IEB PC compatible
COMPUTER: IEB PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,676A
FILING DATE: 04-JAN-1999
CLASSIFICATION: DATA:
APPLICATION NUMBER: PCT/IL97/00117
FILING DATE: 01-APR-1997
FILING DATE: 02-APR-1997
FILING DATE: 02-APR-1996
FILING DATE: 02-APR-1996
FILING DATE: 02-APR-1996
FILING DATE: 02-APR-1996
FILING DATE: 02-APR-1996
FILING DATE: 02-APR-1996
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: IL 119133
FILING DATE: 26-AUG-1996
ATORNEY/AGGET L.
NAME: BROWNY, ROGET L.
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: MALLACH=21
TELEPHONE: 202-628-5197
                                                                                                                          ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C. STREET: 624 Ninth Street, N.W., Suite 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 417; Conservative
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TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: protein
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ZIP: 20001
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US-09-155-676A-5
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US-60-453-135-9118

US-GO-453-135-9118

Sequence 9118, Application US/60453135

GENERAL INFORMATION.

APPLICANT: CARGILL, Michele

APPLICANT: CARGUEOVA, Olga

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

TITLE REFERENCE: CL001456

CURRENT APPLICATION NUMBER: US/60/453,135

CURRENT PILING DATE: 2003-03-10

NUMBER OF SEQ ID NOS: 82762

SOCTHARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9118

LENGTH: 212
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                                                                                                                                                                                                                         148 VKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 REHLSHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSM 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 VKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------DIPGVGNIHSGATPPWMIQDEEYIA 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 FFCGRGHVYSRKHQRQLKEALERLLPQVEARKAIRAAQVERYVPEHERCCWCLCCGCEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPPWMIQDEEYIA
                                                                                                               28 FFCGRGTFTAASTQRQLKEAFBRLLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEV
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  DB 37; Length 212;
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                 134 VKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLE-----
Score 972.5; DB 37;
Pred. No. 2.5e-78;
1; Mismatches 7;
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LOCATION: (1)...(212)
COTHER INFORMATION: Xaa = Any Amino Acid
US-60-453-135-9118
  44.4%;
ilarity 74.5%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNQEIGPSYEEFLKE 282
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ORGANISM: Homo sapiens
  Query Match
Best Local Similarity
Matches 190; Conserv
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                                                                                                                                                                                                                                                                                                     APPLICANT: ADAMS, Mark

TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN

TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF

FILE REFERENCE: CL0001381

CURRENT APPLICATION NUMBER: US/10/170,205E

CURRENT FILING DATE: 2002-06-13

NUMBER OF SEQ ID NOS: 40312

SOFTWARE: PATENTIN VETSION 3.2

SEQ ID NO 36800

LENGTH: 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 REHLSHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSM 133
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  DHSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSHIQKKANHALYQLPXGXKP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 VKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNS 207
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Sequence 9118, Application US/60453050

GENERAL INFORMATION:

APPLICANT: CARCILL, Michele

APPLICANT: LUKE, May

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001457

CURRENT APPLICATION NUMBER: US/60/453,050

CURRENT FILING DATE: 2003-03-10

NUMBER OF SEQ ID NOS: 82762

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9118

LENGTH. 212

TAUDE. OF THE REFERENCE: CONTACT OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD OF THE RECORD 
                                                                                     361 KSTKPLLYLPPKFFIIVFLKQTYSFIXFNKVLFFGLRGLESSLSIPSTSRGGRTHF 417
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44.4%; Score 972.5; DB 27; Length
Best Local Similarity 74.5%; Pred. No. 2.5e-78;
Matches 190; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 VKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLE-----
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LOCATION: (1)...(212)
COTHER INFORMATION: Xaa = Any Amino Acid
US-60-453-050-9118
                                                                                                                                                                                              RESULT 3
US-10-170-205E-36800
; Sequence 36800, Application US/10170205E
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-170-205E-36800
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Sequence 17, Application US/10322579
GENERAL INFORMATION:
APPLICANT: BRUNNER, Erich
APPLICANT: BRUNNER, Erich
APPLICANT: REABER, Thomas
APPLICANT: REABER, Thomas
APPLICANT: REABER, Thomas
APPLICANT: PETER, Oliver
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
TITLE OF INVENTION: 105/09/312,579
CURRENT FILING DATE: 2002-12-19
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: US/09/915,543
PRIOR FILING DATE: 2001-07-28
PRIOR FILING DATE: 2000-07-28
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                             Gaps
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                             Indels
55.6%; Pred. NO. 4.3. ...
tive 17; Mismatches 67;
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991 -YALTVRSPAVLSR----
Best Local Similarity 55.6%
Matches 180; Conservative
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SOFTWARE: Patentin versic
SEQ ID NO 17
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US-10-322-579-17
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APPLICANT: BACLER, Konrad
APPLICANT: BACLER, Corrad
APPLICANT: FROESCH, Barbara
APPLICANT: FROESCH, Barbara
APPLICANT: FROESCH, Barbara
APPLICANT: FROESCH, Barbara
APPLICANT: FROESCH, BACTON
APPLICANT: PETER, Oliver
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY
TITLE OF INVENTION: 2001-07-27
CURRENT PELLING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/221,502
PRIOR APPLICATION NUMBER: 60/221,502
PRIOR PETING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VETSION 3.1
                           Sequence 9118, Application US/60466412
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: TAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001466
CURRENT APPLICATION NUMBER: US/60/466,412
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 429241
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9118
LENGTH: 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 972.5; DB 37; Length 212;
Pred. No. 2.5e-78;
1; Mismatches 7; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24; Length 1115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               = Any Amino Acid
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Best Local Similarity 74.5%;
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 GNOEIGPSYEEFLKE 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)...(212)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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ORGANISM: Human lgs-1
                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: VARIANT
              -60-466-412-9118
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61 FFCGRGHVYSRKHQRQLKEALERLLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GUREACH. INFORMATION:

JAPPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRENCE:

CURRENT APPLICATION NUMBER: US/10/217,607

CURRENT PILING DATE: 2002-08-14

FRIOR PEPLICATION NUMBER: 09/758,463

FRIOR APPLICATION NUMBER: 60/179,065

FRIOR APPLICATION NUMBER: 60/179,065

FRIOR FILING DATE: 2000-01-31

FRIOR FILING DATE: 2000-01-31

FRIOR FILING DATE: 2000-01-31

FRIOR FILING DATE: 2000-02-04

NUMBER: OF SEQ ID NOS: 1304

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1029
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PRIOR APPLICATION NUMBER: 60179,065
PRIOR FILING DATE: 2000-01-31
PRIOR PELICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patentin Ver. 2.0
I ENDOR ID 1029
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GENERAL INFORMATION:
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Matches 141; Conservative
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Best Local Similarity 78.8
Matches 141; Conservative
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US-09-758-463-1029
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CRGANISM: Homo sapiens
US-10-217-607-1029
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PCT-US01-08631-49939
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APPLICANT: BASLER, Konrad
APPLICANT: BASLER, Konrad
APPLICANT: BASLER, Erich
APPLICANT: FROBSCH, Barbara
APPLICANT: FROBSCH, Barbara
APPLICANT: FROBSCH, BASLER, Cliver
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
FILE REPERENCE: Q603-69-22
CURRENT FILING DATE: 2003-69-22
CURRENT PILING DATE: 2003-69-22
PRIOR APPLICATION NUMBER: US/09/915,543
PRIOR APPLICATION NUMBER: 60/221,502
PRIOR PILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
SOFTWARE: PATENTING VERSION 3.1
SEQ ID NOS: 22
SOFTWARE: PATENTIN VERSION 3.1
                                                                             1022 ARCLCAPRRGALKPEPPGRTLKLGVPPHTTRKARPHAAKTSP-----RPRCTRQAP--- 1072
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GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM011
CURRENT APPLICATION NUMBER: US/09/758,463
                                                                                                                                                                                        1073 -NKTQSLQLAGKARKTALHLQTKA 1095
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ORGANISM: Human lgs-1
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US-09-758-463-1029
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Sequence 1081, Application PC/TUS0412047
Sequence 1081, Application PC/TUS0412047
Sequence 1081, Application PC/TUS0412047
Sequence 1081, Application PC/TUS0412047
TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: THERE USE
FILE REPERENCE: 08940.0021-00304
CURRENT APPLICATION NUMBER: PCT/US04/12047
CURRENT APPLICATION NUMBER: PCT/US04/12047
NUMBER OF SEQ ID NOS: 1464
SPRIOR APPLICATION NUMBER: US 60/463,708
PRIOR APPLICATION NUMBER: US 60/467,230
PRIOR PRIOR DATE: 2003-04-18
SPRIOR FILING DATE: 2003-05-02
PRIOR PLING DATE: 2003-08-08
PRIOR FILING DATE: 2003-08-08
PRIOR FILING DATE: 2003-08-08
PRIOR FILING DATE: 2003-08-08
PRIOR FILING DATE: 2003-08-08
PRIOR FILING DATE: 2003-08-08
PRIOR FILING DATE: 2003-09-03
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PRIOR PRILICATION NUMBER: US 60/486,480
PRIOR FILING DATE: 2003-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 RVGANFDHSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSHIQKKANHALYQL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 RVGANFDHSSRTSAGWLPSFG---RVWN-----NGRRWQSRAPEGEREVPWSEEQT 359
                                                                                                                                                                                                                                                                                                                                                                                          294
                                            175 KVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLYGGLLEHLARTASLVAAPNWKQFRCL 234
                                                                                                                          115 ATNKFWWENKAEVQMKEKFLVTPQDYARPKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQ 174
                                                                                                                                                                                           -----0K 263
                                                                                                                                                                                                                                                            175 SRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNSQVASSLQQPSNLDLPPAPELDWMETGP 234
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                                                                                                                                                                                                                                                                                                                                                                                          235 SLTFIGHODIPGVGNIHSGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEKQKLKKLPPD
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                                                                                                                                                                                               235 STGK--WINNG-----IVFQDEDRI-----IDTYDTDES-
   66 QVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLYGGLLEHL
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Best Local Similarity
Matches 107; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: DOWAIN
CONTINGUAGES (650)
OTHER INFORMATION: BURKITY'S LYMPHOMA RECEPTOR SIGNATURE domain identified by
OTHER INFORMATION: EMATRIX, accession number PR00564E, p-value=1.918e-23, raw
NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 QVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLYGGLLEHLASPEHKKATNKFWWENKA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 WSRARL-OPOAPA----AAEGGF--GEAPAPGA--------EVEAARKAIRAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.3%; Score 554.5; DB 1; Length 741;
Best Local Similarity 40.7%; Pred. No. 7e-40;
Matches 135; Conservative 18; Mismatches 52; Indels 127; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 WRRSRIVDPRAAXNSIRAHEGPFFCGRGTFTAASTQRQLKEAFERLLPQVEAARKAIRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 EVOMKEKFLVTPQDYARFKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQSRQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 EVQMKEKFLVTPQDYARFKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQSRQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOCKTION: (502)...(736)
OTHER INFORMATION: 7 transmembrane receptor domain identified |
OTHER INFORMATION: name 7tm_1, E-value=5.2e-81, PFam score of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.6%; Score 670; DB 1; Length 156; Best Local Similarity 77.9%; Pred. No. 2.7e-51; Matches 134; Conservative 4; Mismatches 12; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US01-08631-49940

Sequence 49940, Application PC/TUS0108631

GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049

CURRENT APPLICATION NUMBER: PCT/US01/08631

CURRENT APPLICATION NUMBER: 09/540,217

PRIOR PILING DATE: 2000-03-31

PRIOR PILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CUSECM

LENGTH: 741
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES;
FILE REPERENCE: 2127-049
FILE REPERENCE: 2001-03-30
CURRENT APPLICATION NUMBER: 90/540,217
FRICR PILING DATE: 2000-03-31
FRICR APPLICATION NUMBER: 09/649,167
FRICR APPLICATION NUMBER: 09/649,167
FRICR ELING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEX: misc_feature;
; LOCATION: (1)...(156)
; OTHER INFORMATION: Xaa = X or * as defined in Table PCT-US01-08631-49939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US01-08631-49940
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228 SAVPSQACLEALLLIVPWGACGVSQEEEES------PAEGSKDEPGEGVELKEEA 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 ----KKSMVKGL-----DSYEEKEDKVIKEMAAQIREVEQSRQEVVRSV-LEPQA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 TQRQLKEAFERL-----LPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEVREHL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------PPEPKGDATPEGEKAT 303
                                                                     Query Match 23.0%; Score 503; DB 1; Length 312; Best Local Similarity 49.3%; Pred. No. 8.2e-36; Matches 113; Conservative 14; Mismatches 38; Indels
                                                                                                                                                                                                                          APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 2127-049
CURRENT APPLICATION NUMBER: PCT/USO1/08631
CURRENT FILING DATE: 2001-03-30
FRIOR APPLICATION NUMBER: 09/540,217
PRIOR PLING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSCOM
SEQ ID NO 44039
LENGTH: 312
                                                                                                                                                          RESULT 15
PCT-US01-08631-44039
; Sequence 44039, Application PC/TUS0108631
; GENERAL INFORMATION:
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Job time : 188.04 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-08631-44039
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7, 2005, 12:02:31 ; Search time 52.7607 Seconds (without alignments) 2846.907 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpaa/PCT_MRW PUB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1599520 seqs, 360203123 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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DB seq length: 200000000
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Maximum I
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 17, Appl	Sequence 17, Appl	Sequence 17, Appl	Sequence 206, App	Sequence 209186,	Sequence 306861,	Sequence 41619, A	Sequence 69227, A	Sequence 51821, A	Sequence 219898,	Sequence 62537, A	Sequence 67550, A
SUMMARIES	ΩI	US-09-915-543-17	US-10-322-579-17	US-10-664-859-17	US-09-746-783-206	US-10-424-599-209186	US-10-425-115-306861	US-10-425-114-41619	US-10-425-114-69227	US-10-425-114-51821	US-10-425-115-219898	US-10-425-114-62537	US-10-425-114-67550
		6	14	15	10	15	16	15	15	15	16	15	15
	Query Match Length DB	1115	1115					367					
æ	Query	36.3	36.3	36.3	9.0	6.9	5.4	5.3	5.3	5.3	5.1	5.1	5.1
	Score	795	795	795	198	148	117.5	116	116	116	112	112	112
	Result No.	1	71	9	4	co	9	7	œ	O	10	11	12

Sequence 20, Appl	Sequence 133129,	Sequence 56, Appl		Sequence 112, App					Sequence 294295,				Seguence 7554, Ap	H	Sequence 68, Appl	Seguence 69, Appl	Seguence 68, Appl	Sequence 167, App	Sequence 358, App	Sequence 34, Appl	Sequence 825, App	Sequence 127, App	Sequence 30, Appl	Seguence 27, Appl	Sequence 27, Appl	Sequence 27, Appl	Sequence 29, Appl	Sequence 29, Appl	Sequence 29, Appl	Sequence 286927,	Seguence 181208,	Sequence 2, Appli
15 US-10-607-631-20	16 US-10-437-963-133129	LS US-10-051-874-56	LS US-10-051-874-166	15 US-10-085-198-112	15 US-10-051-874-165	16 US-10-425-115-368903	14 US-10-105-021-2	15 US-10-607-631-8	16 US-10-425-115-294295	15 US-10-425-114-62454	14 US-10-171-311-83	15 US-10-094-749-1861	14 US-10-032-585-7554	16 US-10-437-963-128540	9 US-09-839-479-68	15 US-10-376-537-69	15 US-10-702-148-68	15 US-10-051-874-167	16 US-10-755-889-358	10 US-09-315-355-34	9 US-09-925-297-825	l3 US-10-114-893-127	LS US-10-275-595A-30	9 US-09-839-479-27	LS US-10-376-537-27		9 US-09-839-479-29	L5 US-10-376-537-29	15 US-10-702-148-29	L6 US-10-425-115-286927	16 US-10-437-963-181208	3 US-08-987-689A-2
1878	1109	4952	5008	5159	5262	447	270	1879	583	620	2701	526	1094	2093	1525	1525	1525	5262	753	3224	393	905	1056	1527	1527	1527	1531	1531	1531	563	964	1009
5.0	5.0	5.0	5.0	5.0	5.0	4.9	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7
110.5	109.5	109	109	109	109	107	106	105.5	105	105	105	104.5	104.5	104.5	104	104	104	104	103.5	103.5	103	103	. 103	103	103	103	103	103	103	102.5	102.5	102.5
13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: BASLER, KONEAG
APPLICANT: BASLER, KONEAG
APPLICANT: BRUNNER, Erich
APPLICANT: FROSCH, Barbara
APPLICANT: FROSCH, Barbara
APPLICANT: FRAMPS, Thomas
APPLICANT: FRAMPS, Thomas
APPLICANT: FETER, Oliver
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
FILE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
FILE REFERENCE: 060361
CURRENT APPLICATION NUMBER: US/09/915,543
FRICE REPLIAND DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/221,502
PRIOR PELING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   828 FFCGRGHVYSRKHOROLKEALERLLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEV 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 REHLSHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSM 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.3%; Score 795; DB 9; Length 1115; 55.6%; Pred. No. 3.5e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Mismatches
                    Sequence 17, Application US/09915543; Publication No. US20020086986A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 55.6%
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Human lgs-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
US-09-915-543-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-915-543-17
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Best Local
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JAPPLICANT: BASLER, Konrad
APPLICANT: BASLER, Konrad
APPLICANT: BASLER, Barich
APPLICANT: BRINNER, Barich
APPLICANT: FROBSCH, Barbara
APPLICANT: FROBSCH, Barbara
APPLICANT: FROBSCH, Barbara
APPLICANT: FROBSCH, Barbara
APPLICANT: FROBSCH, BASENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
FILE REFERENCE: 060361
CURRENT FAPLICATION NUMBER: US/09/915,543
PRIOR FILING DATE: 2001-07-28
PRIOR PLING DATE: 2000-07-28
NUMBER: OF SEQ ID NOS: 22
NUMBER: OF SEQ ID NOS: 22
SOF ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1072 ARCLCAPRRGALKPEPPGRILKLGVPPHTTRKARPHAAKTSP-----RPRCTRQAP--- 1072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 QVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPPWMIQDEEYIA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 GNQEIGPSYEEFLKEKEKQKIK-KLPPDRVGANFDHSSRTSAGWLPSFGPRLEXWTPLAV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 FFCGRGTFTAASTQRQLKEAFERLLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.6%; Pred. No. 3.5e-58;
Matches 180; Conservative 17; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1073 -NKTOSLOLAGKARKTALHLOTKA 1095
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| YALTVRSPAVLSR--------
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Spaulding, Vikki
Agostino, Michael J.
Howes, Steven H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-09-746-783-206
Sequence 206, Application US/09746783
Publication No. US20030044935A1
CENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
MCCOY, JOHN M.
                                                                         Sequence 17, Application US/10664859
Publication No. US20040038901A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCoy, John M.
LaVallie, Edward
Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Human lgs-1
US-10-664-859-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/10122579
; Sequence 17, Application US/10122579
; Publication No. US20030114413A1
; GENERAL INFORMATION:
APPLICANT: BASLER, Konrad
APPLICANT: BRADER, Eich
APPLICANT: RRAMPS, Thomas
APPLICANT: FROSSCH, Barbara
APPLICANT: FRAMPS, Thomas
APPLICANT: FRAMPS, Thomas
APPLICANT: FRAMPS, Thomas
APPLICANT: RRAMPS, Thomas
APPLICANT: RRAMPS, Thomas
APPLICANT: RAMPS, Thomas
APPLICANT: RAMPS, Thomas
APPLICANT: RAMPS, Thomas
APPLICANT: RAMPS, Thomas
APPLICANT: RAMPS, Thomas
APPLICANT: RAMPS, Thomas
APPLICANT: RAMPS, Thomas
APPLICANT: PETER Oliver: 2002-12-19
CURRENT APPLICATION NUMBER: US/09/915,543
FRIOR PILING DATE: 2000-07-27
FRIOR PILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 1115
LENGTH: 1115
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                                                                                                                                                                            ----RTLKŚĠAFPPQ--TPEAHPQ 1021
                                                                                                                                                                                                                       268 GNQEIGPSYBEFLKEKEKQKLK-KLPPDRVGANFDHSSRTSAGWLPSFGPRLEXWTPLAV 326
                                                                                         ------ TGPPR---- 990
                                                                                                                                208 QVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPPWMIQDEEYIA 267
888 REHLSHGNLIVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSM 947
                                           148 VKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSAPRSWKGMNS 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.3%; Score 795; DB 14; 55.6%; Pred. No. 3.5e-58; ative 17; Mismatches 67;
                                                                                  948 VKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLE--
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                                                                                                                                                                                                                                                                                                                   327 QTSTPKLKL---QQXRSSHIQKKA 347
                                                                                                                                                                       991 -YALTVRSPAVLSR--------
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US-10-322-579-17
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Best Local S
Matches 180
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant: Shou, Vindaa
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
SEQ ID NOS: 369326
                                                                                                                                                      90 WCVFCD----QHIDELNSSFACANAIRHLASAEHVKNLKQFFWKYGGAADQLDAFMVSDD 145
                                                                                                                                                                                                   139 DYARFKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSSA 198
                                                                                                                                                                                                                              --- PAPELDWMETGPSLTFI 239
                                                                                                                                                                                                                                                                                                                                                                                 240 GHQDIPGVGNIHSGAT-----PPWM-IQDEEYIAGNQEIGPSYEEFLKEKEKQKLK 289
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| RAFLESCDFIKASTQWRKVQ 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 NKFWWENKAEVQMKEKFLVTPQDYARFKKSMVKGLDSYEEKEDKVIXEMAAQIREVEQSR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 QEVVRSVLEPQAVPDPEEGS-SAPRSWKGMNSQVASS---LQQPSNLDLPPAPEL--DWM 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 WCLCCGCEVREHLSHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQ
                                                                                                                                                                                                                                                                                                                                  196 SEVCSGANN----FSLQDFAVGRSSLSLPHDGRQRSSNGYSCNKKVRENGRMVSGES----
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                                                                   78;
                       Query Match 6.8%; Score 148; DB 15; Length 3
Best Local Similarity 21.4%; Pred. No. 0.0008;
Matches 60; Conservative 38; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SRTSAGWLPSFG 315
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LOCATION: (1)..(1040)
OTHER INFORWATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 306861, Application US/10425115; Publication No. US20040214272A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        199 PRSWKGMNSQVASSLQQ----PSNLDLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       554 АКААЕЕНККҮ VAE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 KLPPDRVGANFDHS---
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: ADOUGH K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2016-228
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 209186
ILBNGTH: 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 SWKGMNSQVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATPPWMI 260
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                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Barenin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: CURROWALTION:
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 46,931
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_30923C.1.pep
US-10-424-599-209186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.0%; Score 198; DB 10;
62.5%; Pred. No. 7.4e-09;
tive 5; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(389)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-746-783-206
ENCODING THEM
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LENGTH: 104 amino acids
TYPE: amino acid
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                    SEQUENCES: 231
                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
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RSQD 78
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APPLICANT: Cao, Yongwei Tark Barthary Cao, Yongwei Tark District Cao, Yongwei Tark District Cao, Yongwei Tark District Cao, Yongwei Tark District Cao, Yongwei Tark District Cao, Yongwei Tark District Cao, Yongwei Tark District Cao, Yongwei Tark District Cao, Yongwei Tark Cark Cark Cao, 18-21 (53313) B CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 51821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AIRAAQVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLYGGLLEHL----ASPEHKKAT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 ERL--EDDERYSRLEKF-----DRLDIFQEYIRHLEKEEEEQKRVQKD---QVRRQERKN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 QEVVRSVLEPQAVPDPEEGS-SAPRSWKGMNSQVASSLQQPSNLDLPPAPELDWMETGPS 235
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                                                                                                                                                                                                                                                                                                                                                                                         Length 369;
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                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: LIB3076-041-Ell_FLI.pep
US-10-425-114-69227
                                                                                                                                                                                                                                                                                                                                                                                  5.3%; Score 116; DB 15;
20.5%; Pred. No. 0.39;
tive 43; Mismatches 92;
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US-10-425-114-51821
      CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
UNDBER OF SEQ ID NOS: 73128
SEQ ID NO 69227
LENGTH: 369
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; Publication No. US20040034888A1
GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Rovalic, David K.
; APPLICANT: Green, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 TRWSKAILMFEDDER---
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344 AKAAEEHKRYVAE---
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Best Local Similarity
Matches 61; Conserv
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Evoul Yibua

APPLICANT: Avoid K.

APPLICANT: Avoid K.

APPLICANT: Tabaska, Jack E.

APPLICANT: Tabaska, Jack E.

APPLICANT: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILLE REPRENCE: 38-21(531313) B.

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 367
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindgong
APPLICANT: Shou, Yihua
APPLICANT: Sovalic, David K.
APPLICANT: Sovalic, David K.
APPLICANT: Good Steen, Steven E
APPLICANT: Tabaska, Jack E
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                                                                                                                                 275 S--YE---EFLKEKEKQKLKKLPPDRVGANF 300
                                                                                                                                                                       Local Similarity 20.51
les 61; Conservative
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Sequence 62537, Application US/10425114

Publication No. US2004003488811

GENERAL INPORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Sorien, Yihua

APPLICANT: Sorien, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

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117 NKFWWENKAEVQMKEKFLVTPQDYARFKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQSR 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 EMEKQGEIVPATSDSSWLPNFG---SVW----QSGTRKESRKEFEKSHKIHDTKSDHDL 128
                                                    177 QEVVRSVLEPQAVPDPEEGS-SAPRSWKGMNSQVASSLQQPSNLDLPPAPELDWMETGPS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 -----TSAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSH--1QKKANHAL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 NVHTGAPPPHLKANE-----HDPKNLSLKSCGLSSRKGKLRKLNPNRVGAAWAERRRAEM 76
                                                                                                                                                                                                                                                                                                                                  236 LTFIGHQDIPGVGNIHSGATPPWMIQDEEYIAGNQEIGPSY-EEFLKEKEKQKLKKLP 292
                                                                                                                                                                                                                                                                                                                                                                             461 -----QSYLAVASNTSGSTPKELFDDV-----IEELGKQYQEDKIQIKEVVKSGKIP 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.1%; Score 112; DB 16; Length 160; 28.3%; Pred. No. 0.27; tive 17; Mismatches 39; Indels 30
                                                                                                                                                                                                                                           428 RDGFRKMLEEHVA----DGTLNARTRWRDYCAQIKDS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: MRT4577_132134C.1.pep
US-10-425-115-219898
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US-10-425-114-62537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 28.3
1es 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
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Sequence 67550, Application US/10425114

Sequence 67550, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Gao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 67550

LENTH: 253
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                                                                                                                              249 NIHSGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEKQKLKKLPPDRVGANFDHSSR--- 305
                                                                                                                                                                                              115 NVHTGAPPWLKANE-----HDPKNLSLKSCGLSSRKGKLRKLNPNRVGAAWAERRRAEM 169
                                                                                                                                                                                                                                                             -----TSAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSH--IQKKANHAL 351
                                                                                                                                                                                                                                                                                                  170 EMEKQGEIVPATSDSSWLPNFG---SVW-----QSGTRKESRKEPEKSHKIHDTKSDHDL 221
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                                                                      Gaps
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                                                                  30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.1%; Score 112; DB 15; Length 253; Best Local Similarity 28.3%; Pred. No. 0.51; Matches 34; Conservative 17; Mismatches 39; Indels 30
Length 253;
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Sequence 20, Application US/10607631

Sequence 20, Application US/10607631

GENERAL INFORMATION:

APPLICANT: Minion, F. Chris

APPLICANT: Minion, F. Chris

TITLE OF INVENTION: Immunogenic Mycoplasma Hyopneumoniae

TITLE OF INVENTION: Immunogenic Mycoplasma Hyopneumoniae

TITLE OF INVENTION: UNMURBER: US/10/607,631

CURRENT PELICATION NUMBER: 60/392,632

PRIOR FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 20

LENGTH: 1878

TYPE: PRIOR Mycoplasma hyopneumoniae

US-10-607-631-20
                                                               39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: LIB3060-078-C12_FLI.pep
US-10-425-114-67550
Query Match 5.1%; Score 112; DB 15; Best Local Similarity 28.3%; Pred. No. 0.51; Matches 34; Conservative 17; Mismatches 39;
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APPLICANT: BURGES, Catherine E
TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: USING THE SAME
FILE REFERENCE: 21402-245
CURRENT APPLICATION NUMBER: US/10/051,874
CURRENT PILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 60/268,595
PRIOR APPLICATION NUMBER: 60/265,587
PRIOR FILING DATE: 2001-09-27
PRIOR PILING DATE: 2001-09-27
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
307 SAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSHIQKKANHALYQLPXGXKPKSTKPL 366
                                   367 LYLPPKFFIIVFLRKOTYSFIXFNKVLFFGLRGL-ESSLSIP 407
                                                                                                                                      ----TVLFDSGATHSFISKK---FVGMHGLVREELSTP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feynor Gorman, Linua Gorman, Linua Mezes, Peter D : Kekuda, Ramesh f: Taupier Jr, Raymond J T: Gerlach, Valerie Trage, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2001-05-17
APPLICATION NUMBER: 60/330,336
FILING DATE: 2001-10-18
APPLICATION NUMBER: 60/265,530
FILING DATE: 2001-01-31
                                                                                                                                                                                                                                                      Sequence 56, Application US/10051874
Publication No. US20040005557A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guo, Xiaojia Sasha
Bdinger, Shlomit R
MacDougall, John R
Malyankar, Uriel M
Patturajan, Meera
Shimkets, Richard A
Pena, Carol BA
Tchernev, Velizar T
                                                                                                                                                                                                                                                                                                                       APPLICANT: Padigaru, Muralidhara APPLICANT: Alsobrook II, John P
                                                                                                                                                                                                                                                                                                                                                              Colman, Steven D
Spytek, Kimberly A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Millet, Isabelle
Miller, Charles E
Lepley, Denise M
Smithson, Glennda
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Herrman, John L
Peyman, John A
                                                                                                                                                                                                                                                                                                                                                                                                                                             Vernet, Corine AM
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Casman, Stacie J
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Rothenberg, Mark
Stone, David J
                                                                                                                                                                                                                                                                                                                                                                                               Spytek,
Boldog,
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US-10-051-874-56
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APPLICANT:
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APPLICANT:
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APPLICANT:
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                     14;
                                                                                                    92 SHGNLTVLYGGLLEHL-----ASPEHKKATNKFWWENKAEVOMKEKFL--VTPQDYA 141
                                                                                                                                               414 SLGKYNFLFDDLASHLDYTFLVSKAKIKQSSITKKLFIELPIKISLKSSILGDQEPNIKT 473
                                                                                                                                                                                             142 RFKKSMVKGLDSYEEKE-DKVIKEMAAQI-REVEQSRQEVVRSVLEPQAVPDPEEGS-SA 198
                                                                                                                                                                                                                          199 PRSWKGMNSQVASSLQQPSNLD--LPPAPELDWMETGPSLTFIGHQDIPGVGNIHSGATP 256
                                                                                                                                                                                                                                                                                                                                 534 DENLKAINNQ--DGLEEDDNITERLPENSPIQY-----QEKAGLG---SSPDK 577
                                                                                                                                                                                                                                                                                                                                                                                 PWMIQDEE----YIAGNQEIGPSYEEFLKEKEKQKLKKLPPDRVGANFDHSSRTSAGWLP 312
                                                                                                                                                                                                                                                                                                                                                                                                                            578 PYMIKDVQNQRYYLAKSQ----IQELIKAKDYTKLAKLLSNRHTYNISLRLKEQ---LF 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 --VTPQ----DYARFKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 DELINQLISGDYADFERLVDKAIRQEDQRNKMDRKRKAAQFRAHQGSHQ------RPRF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 VPDPEEGSSA--PRSWKGMNSQVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 SFGPRLEXWTPLA----VQTSTPKLKLQQXRSS----HIQKKANHALYQLPXGXKPKST 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----KAEVQMKEKFL---- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TPGQCGGPTTMIVRQYRPFN------PSN-----FHQGAS----GSQDQHG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 VGNIHSGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEKQKLKKLPPDRVGANFDHSSRT 306
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                                                                51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                   DB 15; Length 1878;
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                                                              Indels
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US-10-437-963-133129
           5.0%; Score 110.5; DB 15;
23.7%; Pred. No. 11;
tive 45; Mismatches 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Bukharov, Andrey A.
APPLICANT: Bukharov, Andrey A.
APPLICANT: Li, Ping
         Query Match
Best Local Similarity 23.74
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Oryza sativa
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US-10-437-963-133129
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LENGTH: 1109
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Query Match 5.0%; Score 109; DB 15; Length 4952; Best Local Similarity 20.9%; Pred. No. 54; Matches 80; Conservative 51; Mismatches 149; Indels 102; Gaps 15;
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PRIOR APPLICATION NUMBER: 60/261,376
PRIOR FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 269
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 56
LENGTH: 4952
                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 10, Appl
Sequence 9709, Ap
Sequence 8, Appli
Sequence 8, Appli
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11205, A
2, Appli
15814, A
32, Appl
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US-09-159-469-50
US-09-693-542-50
US-09-693-542-50
US-09-949-016-11205
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US-09-949-016-11205
US-09-949-016-9199
US-09-949-016-9109
US-09-949-016-9109
US-09-949-016-9709
US-08-949-016-9709
US-08-949-016-9709
US-08-59-214A-8
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ALIGNMENTS

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158 LNSKPEGSFÖYPASYHSNOTLALGETTPSQLPARGTQARATGOSFSQGTTSRAGHLAGP- 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REHLSHGNLTVLYGGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSM
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                                                                                          APPLICANT: St. George-Hyslop, Peter H.
APPLICANT: St. George-Hyslop, Peter H.
TITLE OF INVENTION: Proteins Related to Neoronal
TITLE OF INVENTION: Regeneration and Uses Thereof
FILE REFERENCE: 1034/1F811
CURRENT APPLICATION NUMBER: US/09/501,171
CURRENT APPLICATION NUMBER: 2000-02-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 4.
; Sequence 4, Application US/09501171; Patent No. 6783982; GENERAL INFORMATION:
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30;

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222

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392 KL--WCHVHLKKSLSGSPLKVKNSKNSKSPBEHLEEMMKMMSPNKLHTNFHIPKKG---- 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 SSQIAQDHQKKETVVKEDEGRRESINDRARRSPRKLPISLKKGERKWAPPKFLPHKYDVK 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -------PAPELDWMETGPSLT----FIGHQDIPGVGNIHSGATPPWMIQDEEYIA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 LONEDKIISNVPADSLIRTERPPNKEIVRYFIRHNAL----RAGTGENAPWVVEDE--LV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLEXW-----XRSSHIQKKANHAL 351
                                                                                                                                                                                                                                                                                                                                   58 ARKAIRA-----AQVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLYGGLLEHLASPEH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                             KKATNKFWWENKAEVQ--MKEKFLVTPQDYARFKKSMV-----KGLDS----- 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 AVGEECDFEVGKERMLKVKIVKIHPLEK------VDEEATEKKSDGACDSPSSDKEN 222
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4.7%; Score 104; DB 4; Length 1525;
Best Local Similarity 21.3%; Pred. No. 1.5;
Matches 99; Conservative 53; Mismatches 109; Indels 204;
                                                                                                                                                                           207;
                                                                                                                     DB 4; Length 1540;
                                                                                                                                                                                                                                                                                                                                                                            Indels
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4.9%; Score 107.5; DB 4;
Best Local Similarity 20.9%; Pred. No. 0.72;
Matches 104; Conservative 60; Mismatches 126;
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Patent No. 6596482

GENERAL INFORMATION:
PAPLICANT:
TILE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042001

CURRENT APPLICATION NUMBER: US/09/418,710

CURRENT APPLICATION NUMBER: US/09/418,710

CURRENT APPLICATION NUMBER: BCT/JP98/01783

PRIOR FILING DATE: 1999-10-15

PRIOR PLING DATE: 1999-10-24

PRIOR APPLICATION NUMBER: JP 9/310027

PRIOR PLING DATE: 1997-04-18

PRIOR PLING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 73

SOFTWARE: FastSEQ for Windows Version 4.0

SEMENT 15-26
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                      ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7037
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TYPE: PRT
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LENGTH: 1540
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| Sequence 7037, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWIER: VEWI
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Best Local Similarity 22.7%; Pred. No. 0.41;
Matches 81; Conservative 46; Mismatches 111; Indels
                                  Sequence 6063, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-016-6063
                    US-09-949-016-6063
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REFERENCE/DOCKET NUMBER: 106.941.155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
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STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09066046A; Patent No. 6204252; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Superko, Colleen
REGISTRATION NUMBER: 39,
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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APPLICANT: MURPHY, Cheryl
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Best Local Similarity
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                                                                                                                                                          143 FKKSMV-----KGLDS-----KGLDS-118
                                                                                                                                                                                     143 ----VDEEATEKKSDGACDSPSSDKENSSQIAQDHQKKETVVKEDEGRRESINDRARRS 197
                                                                                                                                                                                                                                                                                                                                                               198 PRKLPTSLKKGERKWAPPKFLPHKYDVKLQNEDKIISNVPADSLIRTERPPNKEIVRYFI 257
                                                                                                                                                                                                                                                                                                                                                                                                                             258 RHNAL----RAGTGENAPWVVEDE--LVKKYSLPSKFSDFLLDPYKYMTLNPSTKRKNTG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 SPDRKPSKKSKTDNSSLSS----PLNPKL--WCHVHLKKSLSGSPLKVKNSNSKSPEE 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 FKKSMV-----KGLDS------KGLDS-178
                                                                                                                                                                                                                                                                                                                                                                                                    240 GHQDIPGVGNIHSGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEK------QKLKKL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 PPDR----VGANFDHSSRTSAGWLPSFGPRLEXW-------TPLAVQTS----TPKL 333
                               BEPF-----PTIPHTQ----BAF-RTREEYE-----ARLERY---SERIWTCKSTG 56
                                                                                                      EEPF-----PTIPHTQ----EAF-RTREEYE-----ARLERY---SERIWTCKSTG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----HKEA----WEEGEVAELLKEEF---PAWYEK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 EGPFFCGRGTFTAASTQRQLKEAFERLLPQVEAARKAIRAAQVERYVPEHERCCWCLCCG 84
EGPFFCGRGTFTAASTQRQLKEAFERLLPQVEAARKAIRAAQVERYVPEHERCCWCLCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 KLQQ-----XRSSHIQKKANHALYQLPXGXKP--KSTKPL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 HLEEMMKAMSPNKLHTNPHIPKKG------PPAKKPGKHSDKPL 402
                                                                                                                                                                                                                                       179 VVRSVLEPQAVPDPEEGS-SAPRSWKGMNSQVASSLQQ-----
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; Patent No. 6727222
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 06501-042002
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US/09/819,479
; CURRENT FILING DATE: 1999-10-15
; PRIOR FILING DATE: 1999-10-15
; PRIOR FILING DATE: 1999-04-17
; PRIOR FILING DATE: 1999-04-17
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR FILING DATE: 1997-10-24
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 68
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US-09-839-479-68
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                                                                                                                                                                                                                                                                                         198 PRKLPTSLKKGERKWAPPKFLPHKYDVKLQNEDKIISNVPADSLIRTERPPNKEIVRYFI 257
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216 ----PSNLD-----LP-----FI
                                                                                              VVRSVLEPQAVPDPEEGS-SAPRSWKGMNSQVASSLQQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 KLQQ------XRSSHIQKKANHALYQLPXGXKP--KSTKPL 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATIOG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,046A
FILING DATE: 24 Apr-1998
CLASSIFICATION: VUNKNOWN-)
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us-09-155-676b-5.rai

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250 IHSGATPPWMIQDEEY-IAGNQEIGPSYEBFLKEKEKQKLKKLPPDRVGANFDHSSRTSA 308
                                                                           -----PALLQPPEVPVPHSTQFAANHQEFLPHPQAPQ-PIVPGLSVVAGASASAAVA 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 HLSHGNLTVLYGGLLEHLASPEHKKATNKFW------WENKA----EVQMKEKF 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 LVTPQDYARFKKSMVKGLDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              651 HITFALLDAVNGNIEDAVTAFESIKSVVSYWNLALIFHRKAEDIENDALSPEEQEECKNY
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                                                                                                                                                                                                                                   Sequence 34, Application US/08705660
; Patent No. 5858683
; GENERAL INFORMATION:
    APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF CERVICAL CANCER
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC comparible
OPERATER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Pred. No. 5.3;
9; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GREENHALGH, DUNCAN A
REGISTRATION NUMBER: 38,678
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
TELECOMMUNICATION INFORMATION:
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125 High St.
                                                                                                                          309 GWLPSFGPRLEXWTPLAVQTST 330
                                                                                                                                                        SAVAAPAPPOSTTEPLPAMVQT 535
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APPLICATION NUMBER: US/08/705,660
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18.2%; Pred
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 18.2,
T4; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boston
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Sequence 6676, Application US/09949016

Retent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-14-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PELING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FEASESEQ for Windows Version 4.0

SEQ ID NO 6676
   13,
                                                                                                                           -TPQ--DYARFKKSMVKGLDSYEEKEDK 160
                                                                                                                                                                                              ----VLYGGLLEHLASPEHK 113
                                                                                                                                                                                                                                         161 VIKEMAAQIREVEQSRQEVVRSVLEPQAVPDPEEGSS----APRSWKGMNS--QVASSL 213
                                                                                                                                                                                                                                                                                                           214 QQPSNLDLPPAPELDWMETGPSLTF-----IGHQDIPGVGNIHSGATPPWMIQDE 263
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                                DPRAAXNSIRAHEGPFFCGRGTFTAASTOROLKEAFERLLPOVEAARKAIRAAOVERYV- 71
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                                                                    -----KCRVVRGTWRPSELVLYVG
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   79; Gaps
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 51; Mismatches 114; Indels
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22.0%; Pred. No. 0.59;
tive 48; Mismatches 149;
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                                                                                                    PEHERCCWCLCCGCEVREHLSHGNLT-----
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Conservative
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Best Local Similarity
Matches 84; Conserv
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                                                                                                                                                                                                                       854 GY-QGSQTFHG------APLTVATTGPSV-----YYSQSPAYNSQYLLRPAA 893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KKLPPDRVGA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPKTPPRWAEDQNSLL--KMICQQVEAIKKEMQELKLNSSNSASPHRWPTENYGPDSVPD 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 NFDHSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSHIQKKANHALYQLPXGX 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           854 GY-QGSQTFHG------APLTVATTGPSV-----YYSQSPAYNSQYLLRPAA 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGSSAPR -- SWKGMNSQVASSLQQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIH 251
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1161, Application US/09538092

Sequence 1161, Application US/09538092

Patent No. 6753314

GENERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION Protein-Protein Complexes and Method of Using Same;

TITLE OF INVENTION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR PLING DATE: 1999-04-01

PRIOR PLING DATE: 1999-04-01

PRIOR PLING DATE: 1387-04-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CURAPALSEGFORMATHER VERSION 0.9
                 EGSSAPR -- SWKGMNSQVASSLOQPSNLDLPPAPELDWMETGPSLTFIGHQDIPGVGNIH 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----IRAAQVERYVPEHERCCWCLCCGCEVRE 89
                                                                                                                                                  796 SPKTPPRWAEDONSLL--KMICQQVEAIKKEMQELKLNSSNSASPHRWPTENYGPDSVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3224;
                                                                                                                                                                                                                                                                                                           359 KPKSTKPLLY----LPPKFFIIVFLRK-----QTYSFIXFNKVLF 394
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OTHER INFORMATION: Polypeptide Accession Number P49792
                                               Query Match 4.7%; Score 103.5; DB 4; Best Local Similarity 18.2%; Pred. No. 5.3; Matches 74; Conservative 69; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 SGATPPWMIQDEEYIAGNQEIGPSYEEFLKEKEKQKL
                                                                                                         SGATPPWMIQDEEYIAGNOEIGPSYEEFLKEKEKOKL
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ORGANISM: Homo sapiens
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                                          -----KKLPPDRVGA 298
                                                                                                                           299 NFDHSSRTSAGWLPSFGPRLEXWTPLAVQTSTPKLKLQQXRSSHIQKKANHALYQLPXGX 358
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                                                                                                                                                                                                                                                                                                                                                            Sequence 34, Application US/08989045
Patent No. 6027905
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WEESEE, SUSAN
APPLICANT: OBAR, ROBERT
TILLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DETECTION OF CERVICAL CANCER
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy Size
COMPUTER: PatentIn PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.7%; Score 103.5; DB 3;
18.2%; Pred. No. 5.3;
iive 69; Mismatches 132;
EGGPLYKNGSLRNADSEIKRSTPSPTRYSLSPSKSYK---
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NAME: GREENHALGH, DUNCAN A
REGISTRATION NUMBER: 38,679
REGISTRATION NUMBER: 38,679
RELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3224 amino acids
                                          SGATPPWMIQDEEYIAGNOEIGPSYEEFLKEKEKQKL-
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Best Local Similarity
Matches 74; Conserv
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STREET: 12.
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131;
                                                                                                                                                                                                                    Cervical Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 3224;
                        894 NVTPTKGPVYGMNRLPPQQHIYAYPQQMHTPPVQSSSACMFSQEMY 939
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359 KPKSTKPLLY----LPPKFFIIVFLRK-----QTYSFIXFNKVLF 394
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                                                                                                                                          GENERAL INTERNATION:
APPLICANT: Keesee, Susan
APPLICANT: Keesee, Susan
APPLICANT: Wolar, Kobert
APPLICANT: Wolar, Ving-Jye
TITLE OF INVENTION: Methods for the Detection of Cerr
FILE REFERENCE: WTP-023DV2
CURRENT APPLICATION NUMBER: US/09/315,355A
CURRENT APPLICATION NUMBER: US 08/989,045
PRIOR APPLICATION NUMBER: US 08/989,045
PRIOR APPLICATION NUMBER: US 08/705,660
PRIOR FILING DATE: 1999-030
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENGTH: 3224
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18.2%; Pred. No. 5.3;
tive 69; Mismatches 132;
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Patent No. 6596482
GENERAL INFORMATION:
APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042001
CURRENT PAPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP99/01783
                                                                               RESULT 11
US-09-315-355A-34
Sequence 34, Application US/09315355A
Patent No. 6803189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 18.2
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----VDEEATEKKSDGACDSPSSDKENSSOIAQDHOKKETVVKEDEGRRESINDRARRS 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 EEPF-----FIIPHIQ----EAF-RIREEYE-----ARLERY---SERIWICKSIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.7%; Score 103; DB 4; Length 1527;
Best Local Similarity 21.3%; Pred. No. 1.9;
Matches 99; Conservative 53; Mismatches 109; Indels 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 KLQQ------XRSSHIQKKANHALYQLPXGXKP--KSTKPL 366
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TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REPERENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/839,479
CURRENT FILING DATE: 2001-04-20
RIOR PELICATION NUMBER: US 09/418,710
PRIOR APPLICATION NUMBER: US 09/418,710
PRIOR APPLICATION NUMBER: US 09/418,710
PRIOR APPLICATION NUMBER: US 09/418,710
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-14
PRIOR FILING DATE: 1999-10-14
PRIOR PILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-04-18
NUMBER: OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR FILING DATE: 1997-04-18
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                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
US-09-418-710-27
                                                                                                                                                                                                                                      LENGTH: 1527
TYPE: PRT
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US-09-839-479-27
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4.7%; Score 103; DB 4; Length 1531;
Best Local Similarity 21.3%; Pred. No. 1.9;
Matches 99; Conservative 53; Mismatches 109; Indels, 204;
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TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/839,479
CURRENT FILING DATE: 2001-04-20
PRIOR PLILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: US/09/18,710
PRIOR PLILING DATE: 1999-04-17
PRIOR PLILING DATE: 1999-04-17
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-04-18
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
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Patent No. 6727222
GENERAL INFORMATION:
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                                                                            ch 4.7%; Score 103; DB 4; Length 1527; Similarity 21.3%; Pred. No. 1.9; 99; Conservative 53; Mismatches 109; Indels 204;
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21.3%; Pred. No. 1.9;
tive 53; Mismatches 109; Indels 20
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CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT PILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FABSESQ for Windows Version 4.0
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; ORGANISM: Homo sapiens
US-09-839-479-27
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APPLICANT: Jones, 1
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Search completed: June 7, 2005, 12:04:51 Job time: 19.3155 secs

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l Labaes I to 4596)
Wallach,D., Malinin,N., Boldin,M., Kovalenko,A. and Mett,I.
MODULATORS OF TWF RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR
PREPARATION AND USE
Patent: WO 9737016-A 6 09-OCT-1997;
YEDA RES & DEV (IL)
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Location/Qualifiers
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100.0%; Pred. No. 0;
iive 0; Mismatches
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AC136172
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Matches 4596; Conservative
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AUTHORS
TITLE
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ACO03963 Homo sapi
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ACO87298 Homo sapi
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AR062290 Sequence
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                                                         8, 2005, 23:18:24 ; Search time 13067.6 Seconds (without alignments) 17042.190 Million cell updates/sec
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AX774978 Sequence
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15.64 GUGGGGGGGGGGGGGGGCCCAGGGGGGCGCGGGGGGCGCGGGGGG	CCCGGGTCACAGTGCCTCCTGAAAACACGGCTCAGCCGTTCCCAGGGGATTGCCAGCCCCCCGGGGCTCAGCGCTCCAGGGGCAGCATTGCCAGCCCCCCGGGGCAGCATTGCCAGCCCCCCGGGGCAGCAGCGCCAGCCCCCCGGGGCAGCA
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1084 GGCMANCTIGGCCTGTGTMARCAGCCAGAMACCCTTGCCTGACCCACACCTGACGAMACTG 1144 1161	2044 TGCCTCAAGATTGCCAGGAGCCTCCGCCTGTGAGGGAGATCCCACCTCCTGCGCCCCT 2103 2045 TGCCTCAAGATTGCCAGCGGAGCCTCTGGGGGAGATCCCACCCTCTGCGCCCCT 2104 2045 TGCCTCAAGATTGCCAGCGCTCCGGCCTCTGGGGCCCCT 2104 2104 CTCACAGCCCAGGCCATCCAAGAGGGCTGAGGAAAGAGCCCATCCACCGGTGTCTGCA 2163 11111111111111111111111111111111111

Db 4325 ACGTAGCATTAAATCAGCTGTGAATCGTCAGGGGGTGT Qy 4384 GCAGGGGACGCCGAGACTCCGTGGGAAAGCTCATTCC Db 4385 GCAGGGGACGCCGAGACTCCGTGGGAAAGCTCATTCC Qy 4444 TGTCCAGCTGTCCACATTGAGTCAGACTCCCTGGGG Qy 4504 ATAAAGAACTGCACATTGAGTCAGACTCCCGGGG Qy 4504 ATAAAGAACTGCACATTGAGTCAGACTCCCGGGG Qy 4505 ATAAAGAACTGCAGCCTTGGTACTGCAGAGTCTGGGTT Db 4565 TAAAGTTTGGGGTGATGACAAATGTTAAAAAA 4595 Db 4565 TAAAGTTTGGGGTGATGACAAATGTTAAAAAA 4596	AL RS AL RS AL AL AL AL AL AL AL AL AL AL AL AL AL	COMMENT NIX is a serine trianse (MAPSK), that bind adapter proteins associated, either direction with other adapter proteins, with severing the content of anning. NIX overexpression in cells actifactor NF kappa B. Cellular expression two TNF-metants blocks NF kappa B induction two TNF receptors, by CD95 (Fas/Apo-1) anning NORTI/FADD, adapter proteins that bind blocks NF kappa B induction by IL-1. FEATURES Location/Qualifiers 14596	/organism="Homo saplens" /mol_type="mRNA" /db_xref="taxon:9606" /cell_type="B cells" /cell_type="B cells" /ince="lysin-rich region" /codon start=//codon sta	/procein id="CAA'1306 1" /db xref="G1:184134" /db xref="G1:184134" /db xref="G1:184134" /db xref="G1:184134" /db xref="G0A:099558" /db xref="Uniprot/Swiss-Prot:0 /db xref="Uniprot/Swiss-Prot:0 /translation="MAVMEMACPGAPGSRA VEKSPYCGKWEILINDVITACTAKEGSERA AGSKQYSGSESLDQIPNNVAHATEGKWARV LAKPLPRTPEGESCTIPVQEDESPLGAPVV PALPRSELHKLISPLQCINHVWKLHPQDG PHPLESFLGKLACVDSQKPLPDPHLSKLAC
			CGCCCCACTTGCACCTCTGATGACCTCTAAGCACTTTCATGGCTGCCCTCTGGCAGGGC CGACGCCACTTTGCATTGATGACCTCAAAGCACTTTCATGGCTGCCCTCTGGCAGGGC GGCCGCCACTTTTGCACTCTGATGACCTCAAAGCACTTTCATGGCTGCCCTCTGGCAGGGC AGGGCAGGGC	4204 GTCTTGAGCTGTCCACATGCATGTGACTCCTCAAACCTCTTCCAGATTTCTCTAAGAATA 4263 [
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The Weizmann Institute, Dept of yout 76100, ISRAEL.

Insee, resembling several MAP binds specifically to TRAR2, an directly or through interaction averal receptors of the TNF/MGF activates the transcription ion of kinase-deficient ion by TNF, by either of the ion by TNF, by either of the ion to these receptors. It also
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                                          CCCACATCTTGCCAAGACAGCCTT 4443
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RI I'RLYGAVREEWWNI FRELLEGGSCLDEDRALYYLGQQALEGLBSTHS
RI ILHDVKADNVLLSSDGSFGEVHRAEDCOLVEGGCLDEDRALYYLGQQALEGLBSTHS
RI ILHDVKADNVLLSSDGSMALCDFGHAVCLQPGLGKSLLTGDY I PGTETHMAPE
VVLGRSCDAKUDVWSSCCMMLHALCDFGHAVCLQPGLGKSLLTGDY I PGTETHMAPE
LTAQAI QEGLRKEPIHRVSACCMCHAMTQPFRGPLCLKI ASEPPPVREI PPSCAP
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YFNGVKVQIOSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFSLVTKDGQPVRYDME
VPDSGIDLQCTLAPDGSFAWSWRVKHGQLENRP"
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HQTLHAQPRELSPRAPGPRPAEETTGRAPKLQPPLPPBPPEPPNKSPPLTLSKEESGWW
EPLPLSSLEPAPARNPSSPERKATVPBQELQQLBIELFLNSLSQPFSLEBQBGILSCL
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                            Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAR Plate: 69 Row: f Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCCTGTGTTCTGCGGAAAGTGGGAGATCCTGAATGACGTGATTACCAAGGGCACAGCCA
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/clone="MGC:45335 IMAGE:5497185"

/clone_lise="NTH MGC_85"

/lab_host="NHH MGC_85"

/note="Yector: pCMV-SPORT6"
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/db_xref="Locusin:9020"
/db_xref="Locusin:9020"
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/gene="MAP3K14"
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Rothe, M. and Wu, L.
Nucleic acids encoding human NIK protein
Patent: US 5843721-A 1 01-DEC-1998;
Location/Qualifiers
                                                                                         DB
                                                                                       Score 3149.6;
Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 3152; Conservative (
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                                                             CTGCTGGCTACCACTCTTCCCCAGAGCAGCAGCCCCGAGGCCCCTTCAGGCCCAGCAGCATG
                                                                                          CCCCAGACTCGCTGGCACTCCAGTTCCCTCATATAAAGGTGAAGGGTGATGCAGGATAT
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Qy 3052 GGCCAGCTGGAGAACAGGCCCTAACCCTGCCCTCCACCGGCCGG	RESULT 9 AR068515 LOCUS LOCUS BETINITION Sequence 1 from patent US 5854003. ACCESSION AR068515.1 GI:6000722 KEYWORDS SOURCE Unknown. ORGANISM Unknown. ORGANISM Unknown. ORGANISM Corening method for agents that modulate human NIK activity JUNNAL Patent: US 5854003-A 129-DEC-1998; FRATURES SOURCE 1. 3156 AUTHORS SOURCE 1. 3156 AUTHORS SOURCE 1. 3156 AUTHORS SOURCE 1. 3156 AUTHORS SOURCE AUTHORS SOURCE AUTHORS SOURCE AUTHORS SOURCE AUTHORS SOURCE AUTHORS SOURCE AUTHORS AUTHORS AUTHORS SOURCE AUTHORS AUTHORS SOURCE AUTHORS A	Query Match 68.5%; Score 3149.6; DB 6; Length 3156; Best Local Similarity 99.9%; Pred. No. 0; 0; 0; Gaps 0;	Qy 292 GAACTCCCCAAGGAGAAGAAGACGCCGCACTGGGGAAGAAACAGAGCTCCGTCTAC 351	Oy 412 GTGATTACCAAGGCCAAGGAAGGCTCCGAGGCAGCCAGCTGCCATCTTATC 471
1972 AGCAGCTGCTGTATGATGCTGCACAGGCTGCCACCCCTGGACTCTTTC	2332 CGGCCAGCTGAGGAGACAACAGCCCCTAAGCTCCAGCCTCCTCCCACCAGAG 2391 2101 CGGCCAGCTGAGGAGACAACAGCCAGAGCCCCTAAGCTCCAGCCTCCTCCCCACCAGAG 2160 2392 CCCCCAGAGCCAAACAACACTCCTCCTCTTTGAGCTAGGCTCTCTCT	2632 GACAGCCTCTCCCTGTCGGATGACAGTGAGAAGAACCCATCAAAGGCCTCTCAAAGCCTCG 2691 [2752 AGCTGGAACATGGTGGCCCGGGGGGCCCACCGACACCCCAAGCTATTTCAATGGT 2811	2872 GTCAAAGTGGGAGATCGCCACTGGCATCAGCAGCTGCCGGCTGCAGCTTCAGC 2931 [

	1912 ACCCACNTGGCTCCGGAGGTGGTGGGGAGGTGCCGACGCCAAGGTGGATGTCTGG 1971	2032 CGAGGGCCGCTCTGCCTCAGGTTGCCAGCGGCTCCGCCTGTGAGGAGATCCCACCC 2091 [2152 CGCGTGTCTGCAGCGGAGCTAGAACCGGGCACTACAGCAAGTGGGAGGT 2211	2272 AATTACCACCAGCCCAGCCCAGCCCAGGGGGTTTCGCCAAGGCCCCAGGGCCC 2331 2041 AATTACCACCACCCTCCATGCCCAGGCGAGAGGTTTCGCCAAGGCCCCAGGGCCC 2100 2332 CGGCCAGCTGAGGAACAACAGGCAGAGAGCTCCAAAGCTCCTCCCAGGGCCC 2100		GAACCCTTACCTCTGTCCTCCGAGCCAGCCCTGCCAGAAACCCCAGCTCAACAGG [2632 GACAGCCTCTCCTGTCGGATGACAGTAAGAAGAACCCATCAAAGACCTCTCAAAGCTCG 2931 2401 GACAGCCTCTCCTCTCTGTAAGATGACAGAACCCCATCAAAGCCTCTCAAAGCTCG 2460 2692 CGGGAACCCTGTCGGGATGACAGTCAGAAGCCCATCAAAGCCTCTCAAAGCTCC 2751	2461 CGGGACACCCTGAGGCGTACACTCCTGGAGCAGCCGAGGCCGAGGCTCGAAGCTCC 2520 2752 AGCTGGAACATGGTGCTGGCCCGGGGGCCCACCGACACCCCAAGCTATTTCAATGGT 2811
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DB
                                                             Score 3149.6;
Pred. No. 0;
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 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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I (bases 1 to 3156)

Rothe, M. and Wu.L.

NIK proteins, nucleic acids and methods
Patent: JP 2001510348-A 1 31-JUL-2001;

PN JP 2001510348-A/1

PD 31-JUL-2001

PP 02-JUL-1997 US 08/887518

PI MIKE ROTHE, LIN WU
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PF 02-JUL-1998 JP 1999507409
PR 03-JUL-1997 US 08/887518
PI MIKE ROTHE, LIN WU
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C07K7/06, C07K7/08, C07K14/47, C12N1/00, C12N5/10, C12N15/12, C12N15/
                       GACCTGCAGTGCACACTGGCCCCTGATGGCTCGCCTGGAGCTGGAGGGTCAAGCTT
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Strandedness: Double;
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Location/Qualifiers
1.2844
/organism="unknown"
/mol_type="genomic DNA"
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AR429673
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RESULT 12 CQ845924 LOCUS DBFINITION Sequence 4571 from Patent EP1440981. ACCESSION CQ845924.1 GI:50895523 VERSION VERSION CQ845924.1 GI:50895523 CQ845924.1 GI:50895523 KEYWORDS SOURCE ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) Ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Nammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. TITLE AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Makamatsu,A., Sato,H., Ishii,S., TITLE Full-length human cdna JOURNAL Research Association for Biotechnology (JP) FEATURES 1. 3152 Course //Mollifers ORIGIN ORIGIN	Query Match 58.2%; Score 2673.4; DB 6; Length 3152; Best Local Similarity 98.4%; Pred. No. 0; Matches 2775; Conservative 0; Mismatches 36; Indels 10; Gaps 7; Ov 1764 TCTGCATGGGACGTCAAAGGTGACAAGGTGATGGGAGCCAGGAGG 1823	340 TCCCGGGGCGGCGTGGCGGGGGGGGGGGGGGGGGGGGG	OY 1884 CACAGGGGACTACATCCCTGGCACAAGAGACCCCCATGGCTCCGGAGGTGCTGGGCAG 1943 Db 460 CACAGGGGACTACATCCCTGGCACAGAGACCCACATGGCTCCGGAGGTGCTGGTGCTGGGCAG 519	1944 GAGCTGCGAGGTGGTGTCTGGAGCTGCTGTTGATGTTGATGCTGAGTGTCAA 2003	Db S80 GGCTGCCCTGGACTCAGTTCTTCGAGGGCCGTCTGCTCTAAGATTGCCAGGGA 639 Qy 2064 GCCTCCGCCTGTGAGGGAGATCCCACCCTCTGCGCCTCTCACAGCCCAGGCCATCCA 2123	Oy 2124 AGAGGGGCTGAGGAAAGAGCCCATCCACCGCGTGTCTGCAGCGGAGCTGGGAAGGT 2183	QY 2184 GAACCGGGCACTACAGCAAGTGGAAGAGCCCTTGGAAGAGAGAG	Oy 2244 ACCAAGACATCCACGCCAAATCAAGCCAATTACCACAGACCTCCATGCCGAGG 2303	AY 2304 AGAGCTTTCGCCAAGGCCCCAGGCCCCGGCCAGCTGAGAACAACAGGCAGCCCC 2363	Qy 2364 TAAGCTCCAGCCAGCAGAGCCCCAGAGCCAAACAACAACTCCTCCCTTGAC 2423
1741 AGCAGCTGCTGTATGATGCTGCACGGCTGCCCCCTGGACTCCTTTC 1800 2032 CGAGGGCCGCTCTGCCTCAGATTGCCAGCGCTGCCCCTGTGAGGAGATCCCACC 2091 1801 CGAGGGCCGCTCTGCCTCAAGATTGCCAGCGAGCCTCTGCGCTGTGAGGAATCCCACC 2091 1801 CGAGGGCCGCTCTCAAGATTGCCAGCGAGCCTCCGCCTGTGAGGAATCCCACC 1860 2092 TCCTGCGCCCTCTCAAGATTGCCAGGAGCCTCCAGCCTGTGAGGAGTCCCACCC 1860 2092 TCCTGCGCCCTCTCAAGATTGCCAGGCATCCAAGAGAGATCCCACCA 1920 2152 CGCGTGTCTGCAGGCCAGGCCATCCAAGAGAGCCTACAGCAATCCAC 1920 2152 CGCGTGTCTGCAGGAGGAGAGATCAACAGCACTACAGCAATCAGGAGGT 1980 2212 CTGAAGAGCCCTTGGAGGGAAATATAAGAACCAGGACATCCACCGCCAAATCAAGCC 2040 2212 CTGAAGAGCCCTTGGAGGGAAATATAAAGAACCAAGAACCACCACAAATCAAGCC 2040 2212 AATTACCACCAGACCTTGGAGGGAAATATAAAGAACCAAAACAACACCAAATCAAGCC 2040 2272 AATTACCACCAGACCCTCCATGCCCAGAGAGCTTTCGCCAAAGGGCCCCAAGGGCCC 2100 2332 CGGCCAGCTGAGGAGAAATATAAAGAACCCAAAACACACCCCCAAGGGCCCCAAGGGCCC 2100 2332 CGGCCAGCTGAGGAGAAATATAAAGAACCCAAAACACACCCCCAAGGGCCCCCAAGGGCCCCAAGGGCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCAAGGGCCCCAAGGGCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCCAAGGGCCCCAAGGGCCCCCC	2392 CCCCCAGAGCCAAAGTCTCCTCCCTTGACTTTGAGCAGGAGGAGTCTGGGATGTGG 2451 [AGCCTGTCCCAGCCATTTCTCTGGAGGAGCAGGAGCAAATTCTCTCGTGCCTCATATATAT	2632 GACAGCCTCTCCCTGTCGGATGACAGTGAGAACAACCCTTCAAAGCCTCG 2691	2461 GGGACACCCTGAGCTCAGGCGTACACTCCTGGAGCCGAGGCCGAGGCTCGAAGCTCC 2520 2752 AGCTGGAACATGGTGCTGGCCCGGGGCGCCCCCCGACCCCCAAGCTATTTCAATGGT 2811 2521 AGCTGGAACATGGTGGTGGCCGGGGGGGGCGCCCACCGACCCCAAGCTATTTCAATGGT 2810 2521 AGCTGGAACATGGTGGTGGCCCGGGGGGGGCGCCCCCCCACCCCAAGCTATTTCAATGGT 2580	2812 GTGAAAGTCCAAATACAGTCTCTTAATGGTGAACCCTGCACATCCGGGAGTTCCACCGG 2871 	2872 GTCAAAGTGGGAGACATCGCCACTGGCATCAGCAGCTCCCAGCTGCAGCTTCAGC 2931	2932 TIGGICACCAAAGACGGGCAGCTGTICGCTACGACAIGGAGGIGCCAGACTCGGGCAIC 2991 	2992 GACCTGCAGTGCACACTGGCCCCTGATGGCTTCGCCTGGAGCTGGAGGGTCAAGCAT 3051	3052 GGCCAGCTGGAGAACAGGCCCTAA 3075

3503 CAAGTGTGTAAGGGCCCAAACTCAGGTTCAGTGGAGAACCAGGTCAGCAGGTATGCCCGC 3562 	3563 CCGTAGGTTAAGGGGGCCCTCTAAACCCCTTGCCTGGCCTCACCCTGGCCAGCTCACCCCT 3622	w 0	a actiticaggiigiigiigiigiigiigiigiigiigiigiigiigi	43 GAAGGTGTGAGTGATGGTTCTCAGTCCCCAGACATGTGCCCCTTTGCTGCTGGTGGTTGT 38	803 CCACTCTTCCCCAGAGCACCAGGCCCCGAGCCCTTCAGGCCCAGCACCCCGGGCTC 38	scaggatatge 	3923 AACAGTCTGTGGATGGACATGATCAGTGCTAAGGAAAGCAGCAGAGAGAG	TCAGCATCAC 40 CAGCATCAC 26	42 ACTGACACTCACCCTGCCCTGGCCAGAGGTACTGCCGACGGCACTTTCCACTC 41 	SCAGTGACAC 41 SCAGTGACAC 27	T 42	2 GCAIGIGACTCCTCAAACCTCTTCCAGATTTCTCTAAGAATAGCACCCCCTTCCCCATIG 4	82 CCCCAGCTTAGCCTCTTCTCCCAGGGGAGCTACTCAGGACTCACGTAGGATTAAATCAGC 43	4342 TGTGAATCGTCAGGGGTGTCTGCTAGCTTCAACCTCCTGGGGCAGGGGACGCCGAGAT 4401 	4402 CCGTGGGAGAAGCTCATTCCCACATCTTGCCAAGACAGCCTTTGTCCAGCTGTCCACATT 4461	4462 GAGTCAGACTGCTCCCGGGGAGAGAGCCCCGGCCCCCAGCATAAAGAACTGCAGCCTT 4521	22 GGTAC 92 GGTAC	4582 C 4582
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              CCTCTGTGACTTTGGCCATGCTGTGTGTCTTCAACCTGATGGCCTGGGAAAGTCCTTGCT
                                                                                                                       CACAGGGGACTACATCCCTGGCACAGAGACCCACATGGCTCCGGAGGTGGTGCTGGCAG
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Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M.,
Sugiyama, T., Irie, F., Otsuki, T., Sato, H., Wakamatu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Satio, K., Mishikawa, T.,
Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Wagatusuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A.,
Rawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K.
NEDO human cDNA sequencing project
Unpublished
Unpublished
Isogai, T. and Yamamoto, J.
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Submitted (01-MAR-2004) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisazazu, Chiba 292-0818, Japan
Kazusa-Kamatari, Kisazazu, Chiba 292-0818, Japan
Kazusa-Kamatari, Kisazazu, Chiba 292-0818, Japan
Kemail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
                                                                                                                                         AK131438 3152 bp mRNA linear PRI 07-MAY-2004 Homo sapiens cDNA FLJ16568 fis, clone TESOP2000390, highly similar to Mitogen-activated protein kinase kinase kinase 14 (EC 2.7.1.37).
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AK131438.1 GI:47077391
Oligo capping; fis (full insert sequence).
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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	Qy 4102 TGATGACCTCAAAGCACTTTCATGGCTGCCTCTGGCAGGGCAGGGCAGGGCAGTGACAC 4161 D 2672 TGATGACCTCAAAGCACTTTCATGGCTGCCCTCTGGCAGGGCAGGGCAGGGCAGTGACAC 2731 Qy 4162 TGTAGGAGGATAGCAGGAGATGGGGTGAAGGGACAGGACCTCTCACAT 4221	2732 TGTAGGAGCATAGCAAGCCAGGAGATGGGGTGAAGGACACACAC	4282 CCCCAGCTTAGCCTCTTCTCCCAGGGGGGTACTCAGGACTCACGTTAAATCAGG [Qy 4402 CGGGGGAGAGCTCATTCCCACATTGCCAACATTGCCAACATTGTCCACATT 4401 Db 2972 CGGGGGAGAGCTCATTCCCACATCTTGCCAAGACCATTGTCCAGCTGCACATT 3031 Qy 4462 GAGTCAGACTGCTCCGGGGAGAGAGACCCCGGGCCCCAGCACATAAAGAACTGCAGCCT 4521 Db 3032 GAGTCAGACTGCTCCAGGGAGAGAGAGACCCCGGCCCCCAGCACATAAAAGAACCGCAGCCTT 3091	Qy 4522 GGTACTGCAGAGTCTGGGTTGTAGAGAACTCTTTGTAAGCAATAAAGTTTGGGGTGATGA 4581	RESULT 14 AF143094 LOCUS LOCUS DEFINITION MUS musculus NF-kappaB inducing kinase (Nik) mRNA, complete cds. ACCESSION AF143094.1 GI:4877962 VERSION AF143094.1 GI:4877962	SOURCE Mus musculus (house mouse) ORGANISM Mus musculus Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCE 1 (bases 1 to 2829) AUTHORS Shinkura,R., Kitada,K., Matsuda,F., Tashiro,K., Ikuta,K., Suzuki,M., Kogishi,K., Serikawa,T. and Honjo,T. TITLE Alymphoplasia is caused by a point mutation in the mouse gene	ACURNAL Nat. Genet. 22 (1), 74-77 (1999) MEDLINE 99251583 PUBMED 10319865 REFERENCE 2 (bases 1 to 2829) AUTHORS Shinkura,R., Kitada,K., Matsuda,F., Tashiro,K., Ikuta,K., TITLE Direct Submission	AL S urce
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Oy 2986 GGCATCGACCTGCAGTGCACTGGCCCTGATGGCAGCTTCGCCTGGAGGGTC 3045	RESULT 15 A66647 LOCUS DEFINITION Sequence 3 from Patent W09737016. ACCESSION A6647 ACCESSION A6647 ACCESSION A6647 ACCESSION KEYWORDS SOURCE Unidentified ORGANISM Unidentified ORGANISM Unidentified ORGANISM AUTHORS AUTHOR	Query Match Query Match Best Local Similarity 90.5%; Pred. No. 0; Matches 2335; Conservative 4; Mismatches 159; Indels 81; Gaps 34;	QY 2099 CCCTCTCACAGCCATCCAAGAGGGGCTGAGGAAAGAGCCCATCCACCGCGTGT 2158	Oy 2159 CTGCAGCGGAGCTGGGAGGGAACCGGGCACTACAGCAAGTGGGAGCTCTGAAGA 2218		Oy 2339 CTGAGGAGACAGCAGAGCCCCTAAGCTCCAGCCTCTCCCACCAGGCCCCAG 2398	Oy 2399 AGCCAAACTCTCCTCCCTTGACTTTGAGCAAGAAGAGTCTGGGATGTGGGAACCCT 2458	Oy 2459 TACCTCTGGAGCCAGCCCCTGCCAGAAACCCCAGCTCACCAGCTCAGCGGAAAG 2518	Oy 2519 CAACCGTCCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	QY 2579 CCCAGCCATTTTCTCTGGAGGAGCAAATTCTCTCTGTGCCTCAGCATCGACAGCC 2638
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ALIGNMENTS

AAV03326 standard; DNA; 4596 BP.

AAV03326

(first entry)

15-APR-1998

AAV03326;

Human tumour necrosis factor receptor-associated factor 2; TRAF2; TRAF-2 binding protein; NF-kappaB activity; NF-kappaB induction; intracellular signalling activity; acute hepatitis; autoimmune-induced call death; 88. Boldin M, Kovalenko A, Mett I; DNA sequence of NF-kappaB inducing kinase. Location/Qualifiers 232. .3075 /*tag= a (YEDA) YEDA RES & DEV CO LTD. 97WO-IL000117. 96IL-00117800. 96IL-00119133. Wallach D, Malinin N, WPI; 1997-503101/46. P-PSDB; AAW42402. 01-APR-1997; 02-APR-1996; 26-AUG-1996; sapiens WO9737016-A1 09-OCT-1997. Homo Key

DNA encoding tumour necrosis factor receptor-associated factor binding molecule - used for modulation or mediation in cells of the activity of NF-kB.

Claim 11; Fig 6; 127pp; English.

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The present sequence encodes a NF-kappa inducing kinase (NIK). The full conditions as obtained by PCR using clone 10 (AAV03324). NIK was cound to induce NF-kappaB even more effectively than TRAF2. Proteins capable of binding to TRAF2 and NIK were identified. The NIK or TRAF-2 conditions are signaling activity modulated or mediated by TRAF2. TRAF-binding proteins are especially used for con mediated by TRAF2. TRAF-binding proteins are especially used for prevention or treatment of pathological conditions associated with NF-CC prevention or treatment of pathological conditions associated with NF-CC kappaB induction, e.g. acute hepatitis, autoimmune-induced cell death, c.g. death of the beta Langerhans cells or the pancreas that results in clidenates, the death of cells in graft rejection, the death of cells in graft rejection, the death of cells in graft rejection, the death of cells in graft rejection, the death of cells in graft rejection, the death of cells in graft rejection, the death of cells in graft rejection, the death of cells in graft rejection of the AIDS virus and AIDS sinhibited T cell suicide which causes proliferation of the AIDS virus and hence the AIDS disease. The proteins are also useful for screening of ligands compable of binding to a protein, which are useful for modulating cellular
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed construction of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed construction of (II) or to treat disease states involving (II). (II) is activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a copylypeptide in tissue, as molecular weight markers and as a food complement. (II) and its binding pattners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of involving aberrant protein espression or biological activity. The copyreptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations or responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this coding sequences of the printed specification, but was obtained in celectronic format directly from WIPO at
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food supplement; medical imaging; diagnostic; genetic disorder;
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The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-[amino(4-chlorophenyl) (1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl) -1-methyl-2-(lH)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be modulated in the presence of FTI.
                                                                                                                                                                                                         Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
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10	RESULT 5 ADR25114 ID ADR25114 standard; DNA; 4596 BP. XX AC ADR25114; XX DT 21-OCT-2004 (first entry) XX XX DX ABs; breast cancer; prognosis; gene expression; diagnosis. XX XX XX XX XX XX XX XX YX YX YX YX YX
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4590; Conservative 0; Mismatches
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                                                                                                                                                                                                                          are associated with carcinomes. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (GAP); (iii) for screening of a bioactive agent capable of modulating the activity of GAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of GAP; (vi) for treating carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA gene sequence. Note: This parent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
                                                           carcinoma
                                                                                                                                                                                                             present invention relates to novel DNA and protein sequences which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGATGTTTGGAGGATGAGTATGTGTGGCGAGGGCACACATAAAACAGGCAGAGACCCTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGACCTGCTCTGTTTTGGTCTCTCTCAGGATGAGCACAAGCCTGGGAGATGGCAGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGGGGGACTGTGCCGTGTGGAACGTGTAGCTGTTGA-AGGTGGACTCTGTTACCATTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4684 BP; 1057 A; 1434 C; 1328 G; 865 T; 0 U; 0 Other;
                                                           treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 96.6%; Score 4440; DB 11; Length Best Local Similarity 99.1%; Pred. No. 0; Matches 4549; Conservative 0; Mismatches 30; Indels
                                                        Recombinant nucleic acid useful for diagnosis and
                                                                                                                                                  Claim 1; SEQ ID NO 887; Opp; English.
                                                                                          nucleotide sequence.
2003-328604/31
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CTGAGTGTGAGAATAGCCAAGAGTTCAGCCCCACCTTTTCAGAACGCATTTTCATCGCTG

CTACAGAGGCAAAATGGCCCGTGTGTGTTGGAAGGGAAAGCGTCGCAGCAAAGCCCGGA 712

CTACAGAGGGCAAAATGGCCCGTGTGTGTTGGAAGGGAAAGCGTCGCAGCAAAGGCCCGGA

GGTCCAAACAGTACAGTCCGAGAGTCTTGATCAGATCCCCAACAATGTGGCCCATG

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1933 ANTIACTICOACTICAGAGGATTCTGCAAGGGGATCTGAACTGACGAGGGTCTGAACTGT 1852 1853 CCAGCGAAGGGACCACCACTGTTGAACTTGGCACACTGTGAACTTCAACCTG 1812 1854 CCAGCGAAGGGACCACCACCACTGTTGAACTTGGCACACTGTGAACTTCAACCTG 1812 1855 CCAGCGAAGGGACCACCACCACTGTTGAACTTGGCACACACTGTGAACTTCAACCTG 1812 1856 ATTGCTCCAAAGGGACCACCACCACTGTGAACTTCAACCACACTGCAACTGGAACACACTGCAACTGTGAACTTCAACCACACTGTGAACTGTGAACTGCAACACACTGCAACTGCAACACACTGCAACACACAC
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100	RESULT 7 AAV73917 ID AAV73917 ID AAV73917 XX AC AAV73917; XX DT 04-MAR-1999 (first entry) XX DE Human NIK CDNA. XX NIK; Nuclear factor-kappa B; NF-kB; signal transduction; TNF; human; tumour necrosis factor; NF-kB-inducing kinase; screening; interaction; KW diagnostic; therapy; ds. XX NIK; Nuclear factor; NF-kB-inducing kinase; screening; interaction; KW diagnostic; therapy; ds. XX Homo sapiens. XX CS Homo sapiens. XX PN USS854003-A. XX PP 29-DEC-1998. XX PP 26-FEB-1998; 98US-00032475. XX PP X
2812 AAATACAGTCTCTTAATGGTGAACACCTGCACATCGGGAGTTCCACGGGGTCAACGTGG 2912 2813 GAGACATCGCCACTGGCATCAGCACACACACTCGGGAGTTCCACCTGGTCACCC 2914 2813 GAGACATCGCCACTGGCATCAGCACACACTCCAGCTGCACCTTCAGCTTGGTCACCA 2912 2814 AAGACGGGCACTGCATTCGCTACACACACTCCAGCTTCAGCTTGGTCACCA 2912 2815 GAGACGGCCACTGCACTTCGCTACACACTCGAGCTTCAGCTTGGTCACCTTGGTCACCA 2912 2816 AAGACGGGCACCTGTTCGCTACACACACTCGAGCATCAACACTCGACACTCGACACTTGGTCACACTTGGTCACCTTGGTCA	

Σ Rothe Wu L,

WPI; 1999-094902/08

Screening agents for modulating interaction of nuclear factor kappab inducing kinase - with kinase-binding target, useful for controlling levels of the kinase, for treatment and diagnosis of conditions associated with e.g. inhibition of signal transduction by tumour necrosis

Disclosure; Col 11-14; 16pp; English.

This sequence encodes a novel human nuclear factor-kappaB (NFkB)-inducing kinase (NIK) which is used in a method for screening for agents that modulate the interaction of NIK with a NIK-binding target. The encoded protein can be used as a modulator of cellular functions at the NIK level, or for development of such compounds. NFkB is involved in expression of many immune and inflammatory responses and of some important viral genes. The protein may be used diagnostically and therapeutically, in conditions associated with abnormal utilisation of pathways that involve NFkB, e.g. inhibition of signal transduction by tumour necrosis factor (TNF)

ö 291 351 411 471 531 ATCGCCCAGGCTGAGTGTGAGAATAGCCAAGAGTTCAGCCCCACCTTTTCAGAACGCATT 300 TTCATCGCTGGGTCCAAACAGCAGTCCGAGAGTCTTGATCAGATCCCCAACAAT 360 651 831 600 GAACTCCCCAAGCCAAGGAGAGACGCCCCCCCCGGGAGAAAACAGAGCTCCGTCTAC 120 AAGCTTGAGGCCGTGGAGAGAGCCCTGTGTTCTGCGGAAAGTGGGAGATCCTGAATGAC 180 591 AAAGCCCGGAAGAAACGCAAGAAGAAGAGCTCAAAGTCCCTGGCTCATGCAGGAGTGGCC 711 TTGGCCAAACCCCTCCCCAGGACCCCTGAGCAGGAGGAGCTGCCACCATCCCAGTGCAGGAG 771 891 999 9 232 ATGGCAGTGATGGAAATGGCCTGCCCAGGTGCCCCTGGCTCAGCAGTGGGGCCAGCAGAAG GAACTCCCCAAGCCAAAGGAGAAGACGCCGCCACTGGGGAAGAAACAGAGCTCCGTCTAC AAGCTTGAGGCCCGTGGAGAAGAGCCCCTGTTCTGCGGAAAGTGGGAAGATCCTGAATGAC GTGATTACCAAGGCACAGCCAAGGAAGGCTCCGAGGCCAGGCCCAGCTGCCATCTTATC ATCGCCCAGGCTGAGTGTGAGAATAGCCAAGAGTTCAGCCCCACCTTTTCAGAACGCATT TTCATCGCTGGGTCCAAACAGTACAGCCAGTCCGAGAGTCTTGATCAGATCCCCAACAAT GTGGCCCATGCTACAGAGGGCAAAATGGCCCGTGTGTGTTGGAAGGGAAAGCGTCGCAGC TTGGCCAAACCCCTCCCCAGGACCCCTGAGCAGGAGAGCTGCACCATCCCAGTGCAGGAG GATGAGTCTCCACTCGGCGCCCCATATGTTAGAAACACCCCGCAGTTCACCAAGCCTCTG GATGAGTCTCCACTCGGCGCCCCATATGTTAGAAACACCCCGCAGTTCACCCAAGCCTCTG AAGGAACCAGGCCTTGGCCAACTCTGTTTTAAGCAGCTTGGCGAGGGCCTACGGCGG Gaps DB 2; Length 3156; .. 0 T; 0 U; 0 Other; 4; Indels Query Match 68.5%; Score 3149.6; Best Local Similarity 99.9%; Pred. No. 0; Matches 3152; Conservative 0; Mismatches Sequence 3156 BP; 736 A; 991 C; 895 G; 534 241 ч 292 121 652 61 352 181 472 532 592 421 712 772 412 301 361 481 832 541 601 ઠે ઠે 셤 ઠે a ò g ò a ò g ઠે qq & g ઠે g ò 임

à	892	CTGCCTCGATCAGAACTCCACAAACTGATCAGCCCCTTGCAATGTCTGAACCACGTGTGG 951
ch Ch	661	
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සු	721	AAACTGCACCCCCCAGGACGGAGGCCCCCTGCCCTGCCC
જે દ	1012	12 AGCAGACTGCCTCATCCCATTCCACTCTCCAGCCCTGGAAACCTCACCCTCTG 1071
3 8	1072	CASCHICCHICCHICCHICCHICCHICCHICCHICCHICCHI
8 8	841	
λ̈́o	1132	CTGAGGAAGTGGCGTGTAGACAGTCCAAAGCCCCTGCCTG
q	901	CHGAGGAAACTGGCCTGTGTAGACAGTCCAAAGCCCCTGCCTG
à	1192	AGCTGCCTGTCTCGTGGTGCCCATGAGAAGTTTTCTGTGGAGGAATACCTAGTGCATGCT 1251
Db	961	-
à	1252	CTGCAAGGCAGGTGAGCTCAAGCCAGGCCCACAGCTGACCAGCCTGGCCAAGACCTGG 1311
qq	1021	
ò	1312	-
ОР	1081	-
δ	1372	-
QQ	1141	CTGCTCACTGAGAACTCAAGCCAGTGGATTATGAGTACCGAGAAGAAGTCCACTGGGCC 1200
ò	1432	ACGCACCAGCTCCGCCTGGGCAGAGGCTCCTTCGGAGAGGTGCACAGGATGGAGGACAAG 1491
qq	1201	ACGCACCAGCTCCGCCTGGGCAGAGGCTCCTTCGGAGAGGTGCACAGGATGGAGGACAAG 1260
ò	1492	CAGACTGGCTTCCAGTGCGCTGTCAAAAGGTGCGCCTGGAAGTATTTCGGGCAGAGGA 1551
qq	1261	CAGACTGGCTTCCAGTGCGCTGTCAAAAGGTGCGCCTGGAAGTATTTCGGGCAGAGGAG 1320
ò	1552	CTGATGGCATGTGCAGGATTGACCTCACCAGAATTGTCCTTTGTATGGAGCTGTGAGA 1611
DP	1321	CTGATGGCATGTGCAGGATTGACCTCACCCAGAATTGTCCCTTTGTATGGAGCTGTGAGA 1380
ò	1612	
Ор	1381	daadggcciitgggicaacaicricaiggagcigcicgaadgrggcicccigggccagcig 1440
ò	1672	GTCAAGGAGCAGGCTGTCTCCCAGAGGACCGGGCCCTGTACTACTAGGGCCAGGCCCTG 1731
Db	1441	drcaaddaddaddcrorccadaddaccdddcroracraddccaddcc
ý	1732	
Db	1501	GAGGGTCTGGAATACCTCCACTCACGAAGGATTCTGCATGGGGACGTCAAAGCTGACAAC
λ̈	1792	GTGCTCCTGTCCAGCGATGGGAGCCACGCAGCCCTCTGTGACTTTGGCCATGCTGTGT 1851
DP	1561	GIGCTCCTGTCCAGCGATGGGAGCCACGCAGCCCTCTGTGACTTTGGCCATGCTGTGTGT 1620
λŏ	1852	7
Db	1621	-
δ	1912	Н
QQ	1681	SACATGGCTCCGGAGGTGGTGCTGGGCAGGAGCTGCGACGCCAAGGTGGATGTCTGG
ò	1972	AGCAGCTGCTGTATGATGCTGCACATGCTCAACGGCTGCCACCCCTGGACTCAGTTCTTC 2031

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GGCCAGCTGGAGAACAGGCCCTAACCCTGCCCTCCACGCCGGCTCCACACTGCCGGAAA 2880
                                                                                                                                                                                                                                                                         CCGCCACGTGAAGAGACAGAAGGAGGATGGCAGGAGTTACCTGGGGAAACAAAAAACAGGA 3351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This cDNA encodes a nuclear factor kappa B (NF-kB)-inducing kinase (NIK) polypeptide or its fragment has one or more activities selected from kinase activity and inhibitory activity; IkB kinase-alpha and beta binding activity and binding inhibitory activity; tumour necrosis factor (TNF) receptor-associated factor 2 binding activity and binding inhibitory activity; IkB binding activity and binding inhibitory activity; IkB binding activity and binding inhibitory activity. NF-kB activating and inhibitory activity. A vector containing the NIK nucleic acid can be used to transform host
                                                                                                                                                                                              AAGCAGAATGCCTCCCAGGATTTCACACCTGAGCCCTGCCCCACCCTGCTGAAAAAAATA
                                      GCAGCCTTCCTGCTCCACGATGCTGCCCTGAAAACACAGGCTCAGCCGTTCCCCAGG
                                                                            GGATTGCCAGCCCCCCGGGCTCACAGTGGGAACCAGGGCCTCGCAGCAAGGTGGGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIK; IKB; NF-KB; TNF; kinase; nuclear factor kappa B; inhibition; tumour necrosis factor; binding; genetic hybridisation; screening; signal transduction; biopharmaceutical; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe, vector or recombinant nucleic acid encoding a polypeptide, especially human nuclear factor kappa-B-inducing kinase protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide encoding cDNA
                                                                                                                                                                                                                                                                                                                                                      TCTTTTTCTGCCCCTGCTCCAGTCGAGTTGGCCTGA 3387
                                                                                                                                                                                                                                                                                                                                                                              TCTTTTTCTGCCCCTGCTCCAGTCGAGTTGGCCTGA 3156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "NIK polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .2844
/*tag= a
/product= "NIK polype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for producing recombinant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Col 11-14; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NF-kB-inducing kinase (NIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV71603 standard; cDNA; 3156
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P-PSDB; AAW81564.
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cells for the recombinant production of the protein. The NIK nucleic acid and the polypeptide may be used in diagnosis (e.g. genetic hybridisation screen for NIK transcripts), therapy (e.g. NIK kinase inhibitors to inhibit TNF signal transduction), and in the biopharmaceutical industry
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                                                              2101 CGGCCAGCTGAGGAGACAACAGGCAGAGCCCCTAAGCTCCAGCCTCCTCCCCTCCCACCAGAG
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AATTACCACCAGACCCTCCATGCCCAGCCGAGAGCTTTCGCCAAGGGCCCCAGGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This cDNA encodes a nuclear factor kappa B (NF-kB)-inducing kinase (NIK) polypeptide. The NIK polypeptide or its fragment has one or more activity activities selected from kinase activity and inhibitory activity; IKB kinase-alpha and beta binding activity and binding inhibitory activity, tumour necrosis factor (TNF) receptor-associated factor 2 binding activity and binding inhibitory activity, IKB binding activity and binding inhibitory activity, NF-kB activity, IRB binding activity and binding inhibitory activity, NF-kB activity and binding inhibitory activity. The NIK nucleic acid and the polypeptide may be used in diagnosis (e.g. genetic hybridisation screen for NIK transcripts), therapy (e.g. NIK kinase inhibitors to inhibit TNF signal transduction), and in the biopharmaceutical industry (e.g. as immunogens, reagents for isolating other transcription regulators, and reagents for screening chemical
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                                                                                                                                                                                                                                                                                                                                                                                                                          NIK; IkB; NF-kB; TNF; kinase; nuclear factor kappa B; inhibition; tumour necrosis factor; binding; genetic hybridisation; screening; signal transduction; biopharmaceutical; immunogen; pharmacological; transcription regulator; human; ds.
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0
                                                                                                                                                                                                                                                                                                                                                                          Human NF-kB-inducing kinase (NIK) polypeptide encoding cDNA
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3387
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                             TCTTTTTCTGCCCCTGCTCCAGTCGAGTTGGCCTGA
  TCTTTTTCTGCCCCCGGTCCAGTCGAGTTGGCCTGA
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Pred. No. 0;
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1. .2844
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/product= "NIK polype
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99.9%;
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Best Local Similarity 99.9
Matches 3152; Conservative
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This DNA sequence codes for human wild-type NIK (see AAY31665), a NF-kB inducing kinase having serine/threonine kinase activity. The invention relates to: (a) an N-terminus deletion mutant NIK protein (see AAY31666); and (b) a kinase deficient NIK mutant protein (see AAY31666); that inhibits auto-phosphorylation or transphosphorylation. The invention provides the molecular basis for cytokine induction of N-kB-dependent immune and inflammatory responses, emphasising a role for both NIK-NIK and NIK-IKK (IkB-specific kinase) interactions. A novel and highly specific method for modulating NF-kB-dependent immune, inflammatory and anti-apoptotic responses is based on interruption of the critical protein interaction of NIK and IKK. The mutant NIK proteins are used in claimed methods for inhibiting NF-kB-dependent gene expression. The kinase-deficient NIK mutant proteins hinbit activation of IKK. The N-terminal deletion NIK mutant proteins bind to IKK, thus inhibiting NIK/IKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACTCCCCAAGCCAAAGGAGAAGACGCCGCCACTGGGGAAGAAGAACAGAGCTCCGTCTAC 120
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                                                                                                                                                                                                                                                                                           New NF-kB inducing kinase proteins, used for inhibiting a kB-dependent immune response, e.g. an inflammatory response or an anti-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCGCCCAGGCTGAGTGTGAGAATAGCCAAGAGTTCAGCCCCACCTTTTCAGAACGATT
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interleukin-1; cytokine; inhibitor; antiinflammatory; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2844 BP; 665 A; 887 C; 809 G; 483 T; 0 U; 0 Other;
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Pred. No. 0;
0; Mismatches
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ilarity 99.9%;
Conservative (
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Score 2673.4;
Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
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                                      GTGAAAGTCCAAATACAGTCTCTTAATGGTGAACACCTGCACATCCGGGAGTTCCACCGG
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                    GTGAAAGTCCAAATACAGTCTCTTAATGGTGAACACCTGCACATCCGGGAGTTCCACCGG
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Irie R;
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PA (SAGR-) SAGRES DISCOVERY.

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Morris DW;

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WFI; 2003-328604/31.

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Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.

PT comprises a nucleotide sequence.

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Claim 1; SEQ ID NO 884; Opp; English.

XX

The present invention relates to novel DNA and protein sequences which care associated with carcinomas. The sequences are useful for: (i) for screening of bioactive agent capable of continuous Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iii) for carcinoma; (vii) for inhibiting the activity of CAP; (iii) for treating carcinoma; (vii) for inhibiting the activity of CAP; (ix) sa a biochip; (c) for diagnosing carcinoma Associated (CA) gene copy number. In addition, the carcinoma are useful as DNA vaccines and the CAP; (ix) as a biochip; (c) for diagnosing carcinoma Associated (CA) gene copy number. In addition, the carcinoma including lymphoma. The present sequence is one such CA gene sequence. Note: This patent is an equivalent to basic patent

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Sequence 2828 BP; 688 A; 880 C; 790 G; 470 T; 0 U; 0 Other;
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Sequence 2828 BP; 688 A; 880 C; 790 G; 470 T; 0 U; 0 Other; sry Match 44.4%; Score 2042.6; DB 11; Length 28:

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1128 1185 1245 1305 1080 1365 1425 1725 1499 1785 1545 ACAGAGACCCACATGGCTCCGGAGGTGCTGGCCAGGAGCTGCGACGCCAAGGTGGAT 1965 1011 1071 840 960 gegegeccaegecricecriciscriritaagaaacaagargageccrecearcegra CTGCCTCGACCAGAACTCCACAACTGATCAGCCCCCTTGCAATGTCTAAACCACGTGTGG GACTCTGCCGTCCTGGACAAACTAGCCGGTGTCAGCGGCCAGCGGCCTCTGCCTGGCCCA CCGCATCTAAGCCAACTGGCCCATGGAGACAGTCAGAAGCCGCTGCCTGGCCCACACTG GACAAGCAGACAGGCTTCCAGTGTGTGTCTAAAAAAGGTACGACTCGAGGTGTTTCGGGTA TIGIGCCTGCAACCTGACGGCCTAGGGAAATCCTTGCTCACAGGGGACTACATTCCTGGC AGCAGACTGCCTCATCCCTTCCCATTCCACCTCTCCAGCCCTGGAAACCTCACCCTCTG GAGT----CCTTCCTGGGCAAACTGGCCTGTGTAGACAGCCAGAAACCCTTGCCTGACCCA GAGCCCAGCTGCCTGTCTCGTGGTGCCCATGAGAAGTTTTCTGTGGAGGAATACCTAGTG CATGCTCTGCAAGGCAGCGTGAGCTCAAGCCAGGCCCACAGGCCTGACCAGGCCTGGCCAAG CATGCGCTCCAAGGAAGTGTGAGCTCAGGCCAAGGCCCACAGCCTGGCCTGGCTAAG ACATGGTCCTCGGGAAGCGCCAAGCTGCAGAGGCTCGGCCCCGAAACTGAGGACAACGAG GACAAGCAGACTGGCTTCCAGTGCGCTGTCAAAAAGGTGCGCCTGGAAGTATTTCGGGCA GTGAGAGAGGGCCTTGGGTCAACATCTTCATGGAGCTGCTGGAAGGTGGCTCCCTGGGC GTGAGAAGGCCCGTGGGTGAACATCTTCATGGAACTGCTAGAAGGTGGCTCGCTGGCT CAGCTGGTCAAGGAGCAGGGCTGTCTCCCAGAGGACCGGGCCCTGTACTACCTGGGCCAG GACAACGTGCTCCTGTCCAGTGATGGAAGCCGAGCGGCCCTCTGCGACTTTGGCCACGCC **ACCTGGGCAGCACGGGGCTCCAGATCCCGGGAGCCCAGCCCCCAAAACTGAGGACAACGAG** GGTGTCCTGCTCACTGAGAAACTCAAGCCAGTGGATTATGAGTACCGAGAAGAAGTCCAC TGGGCCACGCACCACCTCCCCTGGGCAGAGGCTCCTTCGGAGGAGGTGCACAGGATGGAG GAGGAGCTGATGGCATGTGCAGGATTGACCTCACCCCAGAATTGTCCCTTTGTATGGAGCT GCCCTGGAGGGTCTGGAATACCTCCACTCACGAAGGATTCTGCATGGGGACGTCAAAGCT GCCCTGGAGGGCTGGAGTACCTCCACACACGCAGGATTCTGCATGGCGATGTCAAAGCT GACAACGTGCTCCTGTCCAGCGATGGGAGCCACGCAGCCCTCTGTGACTTTGGCCATGCT GTGTGTCTTCAACCTGATGGCCTGGGAAAGTCCTTGCTCACAGGGGGACTACATCCCTGGC 1012 1072 1129 1186 1246 1021 1260 1546 1320 1606 1380 1440 1500 1560 661 721 781 841 901 1306 1426 1201 1486 1726 1786 1846 1906 601 892 952 196 1081 1620 1366 1666 Š 원 8 a 8 g 8 g ∂ P ò g ò g δ 셤 ò 셤 ò g ð a ò Dp ò d ò g ò g δ 요 ð g $\stackrel{>}{\circ}$

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                                                                                                              CCACCCTCCTGCGCCCCTCTCACAGCCCAGGCCATCCAAGAGGGGGCTGAGGAAAAGAGCCC 2145
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The present sequence encodes a protein designated NWP1, a TRAF2 binding protein. This protein contains Ser/Thr protein kinase motifs. A full length CDNA clone encoding NF-kappa8 (NIK) was obtained by PCR using the present clone, clone 10. The clone 10 protein is capable of binding to at class amino acids 222-501 of TRAF2. The TRAF2-2 binding proteins can be used for modulation or mediation in cells of the activity of NF-kappa8 or TRAF2. TRAF2-binding proteins are especially used for prevention or treatment of pathological conditions associated with NF-k8 induction, the transpersant cells or the pancreas that results in diabetes, the death of cells in graft rejection, the death of coligodendrocytes in the brain in multiple sclerosis, and AIDS inhibited T cell suicide which causes proliferation of the AIDS virtus and hence the AIDS disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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llarity 90.5%; Pred. No. 0;
Conservative 4; Mismatches
2799 AAGCATGGTCAGCTGGAGAACCGACCCTA 2827
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                                                                                                                                                                                                            standard; cDNA; 2631
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Matches 2335; Conserv
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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for carcinoma; (vi) for inhibiting the activity of CAP; (vi) for diagnosing carcinoma; (vi) for inhibiting the effect of CAP; (vi) for tracting carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma and propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent
                                                                                                                                                                                                            4477
                                                                                                                         TGTCTGCTAGCCTCAACCTCCTGGGGCAGGGACGCCGAGACTCCGTGGGAGAAGCTCAT 2400
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DB 11; Length 73967;

33.9%; Score 1556.2;

Query Match

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sequence tags for identifying expressed cartivity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in capposition for generating or other types of data and products dependent on DNA and and to acid sequences. Abs64197-Abs94564 represent novel human diagnostic coding sequences. Abs64197-Abs94564 represent novel human diagnostic coding sequences. Abs64197-Abs94564 represent novel human diagnostic coding sequences. Abseator from the printed specification, but was obtained in abectronic format directly from WIPO at the very sequences.
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                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2760;
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                                    AGCCCCACTATCAGTGTCCAGCGTGCTGGTTCCCCCAGAGCACAGCTCAGCATCACAGA
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AAS79491 standard; cDNA; 2760 BP.
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2968 ATGGAGGTGCCAGACTCGGGGATCGACTGCACTGGCCCTGATGGCAGCTTC 3027
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BM543747 BE276256

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BMO48296 BIJ61002 BHI61002 BHI61002 CN409540 CN579910 CN579910 CN579910 BMS47747 BMS47747 BMS47747 BMS47747 BMS47747 BMS47747 BMS47747 BMS474747 BMS474747 BMS474747 BMS4748591 AM178916 BMS4748591 AM178916 AM178916 AM178916

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BE391253 CA748591

BI554785 AI956650

BE388034

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ALIGNMENTS

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BI489907

BQ923823 BM550076

BI489907

BM048296 BI161002

AGENCOUR

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CR749592 3971 bp mRNA linear HTC 19-AUG-2004
Homo sapiens mRNA; cDNA DKFZp686J04131 (from clone DKFZp686J04131).
CR749592
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/clone lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfiIA + SfiIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERWANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKRZ); Email 8. Wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                German Genome Project.

This clone (DKRZp686J04111) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomicoschung GmbH in Berlin, Germany. Please contact RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKRZp686J04131
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3971)
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The German cDNA Consortium
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differentially spliced"
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                                                                                                               CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
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kinase kinase kinase 14 (MGD|MGI:1858204, GB|NM_016896,
evidence: BLASTN, 100%, match=2829)
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/db xref="taxon:10090"
/clone="9630045G21"
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/dov stage="l6 days neonate"
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                                                    Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) USA Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Organism="Pan troglodytes"
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/db_xref="taxon:9598"
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/gene="MAP3K14"
/locus_tag="HCM4937"
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AY413579

2829 bp DNA linear GSS 17-DEC-2003
Mus musculus MAP1XI4 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY413579.1 GI:39769541

DEFINITION ACCESSION VERSION

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                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 2829)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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/mol type="genomic DNA"
/db_xref="taxon:10090"
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/gene="MAP3K14"
/locus_tag="HCM4937"
(house mouse)
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/mol_type="manAA"
/db_zref="taxon:9606"
/db_zref="taxon:9606"
/clone="CSOBKOLIYM14"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/cell_line="HELA"
/clone_lib="HOMO sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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AL578455 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens cDNA clone CSODKOllYM14 3-PRIME, mRNA sequence.

AL578455.3 GI:46257344
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Similarity 94.1%; Pred. No. 2.9e-226;
16; Conservative 13; Mismatches 44;
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1. (Dases 1 to 1140)

NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                          CAAAACAGGGATCTTTTCTGCCCCTGCTCCAGTCGAGTTGGCCTGACCGCTTGGATCA
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSDORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
ALS56130 appiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDNA clone CSODK011YM14 5-PRIME, mRNA sequence.
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                        Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODK011BG07QP1&c=8426.r. Location/Qualifiers
                                                                                                                                                                                                                                 1 (bases 1 to 1133)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31277934.
Contact: Genoscope
                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                          Homo sapiens (human)
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AGENCOURT_10326204 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:6572558
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BU541005
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArCc
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2764 row: n column: 14
High quality sequence start: 31
High quality sequence stop: 630.
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1 (Dases 1 to 955)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
  CCTGCTGAGAAAACACTCCGCCACGTGAAGAGACAG-AGGAGGATGGCAGGAGTTACCTC
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1116 GGAAGGGGAAAAGAA 1130
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Site_Z: SalI; Cloned unidirectionally; oligo-dff primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 GGCCTCTCAAAGCTCGGGGACACCCTGAGCTCAGGCGTACACTCCTGGAGCAGCCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2796 AAGCTATTTCAATGGTGTGAAAGTCCAAATACAGTCTCTTAATGGTGAACACCCTGCACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 AAGCTATTTCAATGGTGTGAAAGTCCAAATACAGTCTCTTAATGGTGAACACCTGCACAT
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12128 row: c column: 03
High quality sequence stop: 724.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2556 AGAATTATTCCTCAACAGCCTGTCCCAGCCATTTT
                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                     AAGAAGGTGTGTAAGTGAAGTGGTTCTCAGTCCCCAGACATGTGCCCCTTTGCTGCTGGC 3800
                                                                                                                                                                                        TACCACTCTTCCCCAGAGCAGCCCCCGAGCCCCTTCAGGCCCAGGCTTGCAGAC 3860
                                                                                                                                                                                                                                        TCGCTGGCACTCAGTTCCCTCATCTGTAAAGGTGAAGGGTGATGCAGGATATGCCTGACA 3920
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                                    Score 811.4; DB 5;
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_08"
/note="Grgan: lymph, Vector: pCMV-SPORT6; Site 1: Not!;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                      Conteact: Robert Strausberg, Ph.D.

Conteact: Rober Témail nih.gov

Tissue Procurement: Lou Staudt

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12127 row: p column: 01

High quality sequence stop: 595.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1038)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/clone="IMAGE:5497584"
                                                                                                          BM454415
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 909)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 1, 2003 this sequence version replaced gi:30307969.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was diagested with Not I and cloned
into the Not I and Ecof V sites of the pCMVSPORT 6 vector. Library
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/db_xref="taxon:9606"
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/cell_line="HELA"
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               GCCCTGGAAACCTCACCCTCTGGAGTCCTTCCTGGGCAAACTGGCCTGTGAAACAGCCA
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BX331085 GI:46263202
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Matches 889; Conservative
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602726122F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4865789 5',
mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 774)

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Email: cgapbs-romail.nih.gov
Tissue Procurement: ATC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intramural Sequencing Center

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1731 row: k column: 06

High quality sequence stop: 748.

Location/Qualifiers
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3945 TCAGTGCTAAGGAAAGCAGCAG-AGAGAAGG-TCCGGCGCCCCCAGCCCCAATCAGTG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayaseu, W., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, T., Miyazaki, A., Ohno, M., Ohsato, N., Okazaki, S., Saito, R., Sakai, K., Sakai, K., Sakazume, N., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagabe, Y., Tangami, M., Tagawa, A., Takaku-Akahira, S., Takamasu, M., and Hayashizaki, Y., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
                                                                                   AKUJBB28
Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230066D12 product:mitogen-activated protein kinase kinase kinase kinase 14, full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2964)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
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HTC; CAP trapper.
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/do_type="mRNA"
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/clone lib="NIH MGC 15"
/clone lib="NIH MGC 15"
/clone lib="NIH Made by objeo-dr priming. Directionally
ECORT, CDNA made by objeo-dr priming. Directionally
cloned into ECORI/Khol sites using the following 5,
adaptor: GGCACGAG(G). Size-selected >500bp for average
inser size I BRb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2160 TGCAGCGGAGCTGGGAGGGAAGGTGAACCGGGCACTACAGCAAGTGGGAGGTCTGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2280 CCAGACCCTCCATGCCCAGCCGAGAGGTTTCGCCAAGGGCCCCAGGGCCCCGGCCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.2%; Score 745; DB 4; L. 98.6%; Pred. No. 2.5e-176; ive 0; Mismatches 10;
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Matches 762; Conserv
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1. .294
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Pax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse Lissues.
Division of Experimental Animal Research in Riken contributed to
prepare mouse Lissues.
URL:http://genome.gsc.riken.jp/
URL:http://fentom.gsc.riken.jp/.
Location/Qualifiers
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82.6%; Pred. No. 2.7e-175;
ive 0; Mismatches 179;
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601 TGCAATGTCTAAACCACGTGTGGAAACTCCACCACCCCCAGGCCACAGGCCCCCGGCCCC
                                                                    TGCCC-ACGCACCCTTCCCCTATAGCAGACTGCCTCATCCCTTCCCATTCCACCCTCTC
                                                                                                      CACCGGACTCACCCCTTCCCCTACAGCGGAATGCCCCATCCTTCCCATTCTACCCCTG
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Search completed: June 10, 2005, 20:27:55 Job time : 9696.08 secs THIS PAGE BLANK (USPTO)

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GenCore version 5.1.6
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Maximum Match 100%
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		97A-	18-9,	87-9,	75A-	92-86	9-2	US-10-087-192-884
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UMMA		6-60	10-1	10-3	10-2	10-0	9-87	10-0
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13 US-10-087-192-886 18 US-10-296-115-97 13 US-10-087-192-883 17 US-10-108-260A-1754 19 US-10-433-793-141 10 US-09-918-995-2585	0 US-10-433-793-1425 US-00-783-590-1185 US-10-029-386-863 US-10-380-127A-3 US-10-357-930-229 US-10-357-930-123 US-10-357-930-1334 US-10-357-930-1334 US-10-357-930-1334 US-10-357-930-1334 US-10-357-930-1334 US-10-000-864-11	US-10-357-930-315 US-10-425-115-111 US-10-369-493-268 US-10-369-493-268 US-10-416-477-2 US-10-754-829A-2 US-10-754-829A-2 US-10-425-114-262 US-10-425-114-262	17 US-10-108-260A-974 18 US-10-433-794-32 18 US-10-263-929-4 9 US-09-858-754-1 19 US-10-728-019-1 19 US-10-728-019-1 13 US-10-728-019-13 14 US-110-425-114-19039 18 US-110-425-114-19039
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APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong

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APPLICANT: Sernards, Rene
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665 AAACGGAAGAAGAACTCAAAGTCCCTCGCTCATGCAGGAGTGGCCTTGGCCAAACCC 724 724 CTCCCCAGGACACCCTGAGCAGGAGAGCTGCACCAATGCAGGAGGATGAGTTCCA 783 [CTCGGCGCCCCATATGTTAGAAACACCCGGAGTTCACCAAGCCTCTGAAGGAACCAGGCCTCGGCGCCCAGGCCTCGGCGCGCGC	CTTGGGCAACTCTGTTTTAAGCAGCTTGGCGAGGGCCTACGGCCGGC	904 GAACTCCACAAACTGATCAGCCCCTTGCAATGTCTGAACCACGTGTGGAACTGCACCAC 963 	964 CCCCAGGAGGCCCCCTGCCCTGCCCAGGCACCCCTTCCCCTATAGCAGACTGCCT 1023	1024 CATCCCTTCCCATTCCACCTCTCCAGCCTGGAAACCTCACCCTCTGGAGTCCTTCCT	1084 GGCAAACTGGCCTGTGTAGACAGCCAGAAACCCTTGCCTGACCCTGAGCAAACTG 1143 	1144 GCCTGTGTAGACAGTCCAAAGCCCTGCCTGGCCCACACTGGAGCCCAGGCTGCTT 1203 	CGTGGTGCCCATGAGAAGTTTTCTGTGGAGGAATACCTAGTGCATGCTCTGCAAGGCAGC 	GGGGC 1 GGGGC 1	CTGAG CTGAG	AAACTCAAGGCAGTGGATTATGAGTACGAGAAGAAGTCCACTGGGCCACGCACCAGCTC		1504 CAGTGCGCTGTCAAAAAGGGCCCTGGAAGTATTTCGGGCAGAGGAGCTGATGGCATGT 1563 	1564 GCAGGATTGACCTCACCAGAATTGTCCCTTTGTATGGAGCTGTGAGAGAGGCCCTTGG 1623 	GTCAACATCTTCATGGAGCTGCTGGAAGGTGGCTCCCTGGGCCAGCTGGTCAAGGAGCAG 1 	1684 GGCTGTCTCCCAGAGGACCGGGCCCTGTACTACTGGGCCAGGCCCTGGAGGGTCTGGAA 1743 	1744 TACCTCCACTCACGAAGGATTCTGCATGGGGACGTCAAAGCTGACAACGTGCTCCTGTCC 1803

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S GGGGACTGTGCCGTGTGGAACGTGTAGA-AGGTGGACTCTGTTACCATTGAGG 63 [185 GACCTGCTCTCTTTTGGTCTCTCTCAGGATGGCAAAGCCTGGGAATGGTGTGTG 24 GAAATGGCCTCCCCAGGATGGCACAAGCCAGGAAAGCAACCAGGATGTG 245 GAAATGGCCTCCCCAGGTCGCTCAGCAGAGGAACTCCCCAGG 303 (365 GTGGAGAAGGCCTGTGTTCTGCGGAAAGTGGGAGATCCTGAATGACGTGATTACCAAG 424 424 GGCACAGCCAAGGAAGGCTCCGAGGCCAGCTGCCATCTCTTATCATGCCAGGCT 483 425 GGCACAGCCAAGGAAGGCTCCGAGGCCAGCTGCCATCTCTATCATCGCCCAGGCT 484 484 GAGTGTGAGAATAGCCAAGAGTTCAGCCCCACCTTTTCAGAACGATTTTCATCGCTGGG 543		CTCCCCAGGACCCCTGAGCAGGAGGAGCACCATCCCAGTGCAGGAGGATGAGTCTCCA 7 CTCGGCGCCCCATATGTTAGAAACACCCCGCAGTTCACCAAGCCTCTGAAGGAACCAGGC 8 [905 GAACTCCACAAACTGATCAGCCCTTGCAATGTCTGAACCCACGTGGGAAACTGCACCC 964 964 CCCCAGGACGGAGGCCCCTGCCCACGCACCCCTTCCCCTATAGCAGACTGCCT 1023

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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 5.2945200122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PRIOR PLICATION NUMBER: US 09/798,586
PRIOR PRIOR DATE: 2001-03-02
NUMBER OF SEQ 1D NOS: 2019
SOFTWARE: PASELSEQ for Windows Version 4.0
SEQ ID NO 887
                                                                                                                                                  TAAAGTTTGGGGTGATGACAAATGTTAAAAA 4595
                                                                                                                                                               Score 4440; DB
Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.1%;
Matches 4549; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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US-10-087-192-887
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Pred. No. 0;
0; Mismatches
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                         US/09/871,889
FILE REFERENCE: 30448.61USU1
CURRENT APPLICATION NUMBER: US/09/871,8
CURRENT FILING DATE: 2001-06-01
PRIOR FILING DATE: 1999-02-25
PRIOR PLING DATE: 1999-02-25
PRIOR PLING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 2844
                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: NF-KAPPA B INDUCING
US-09-871-889-2
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Best Local Similarity 99.9%;
Matches 2840; Conservative
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     GCTCCCTGGTAGAATACACCACACTTTTCAGGTTGTTGCAACACAGGTCCTGAGTTGACC 3764
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Patent No. US20020042499A1
GENERAL INFORMATION:
APPLICANT: Greene, Warner C.
APPLICANT: Lin, Xin
APPLICANT: Geleatinas, Romas
APPLICANT: Geleatinas, NOVEL INHIBITOR OF THE INFAMMATORY RESPONSE INDUCED
TITLE OF INVENTION: BY TNF-ALPHA AND IL-1
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                                                           TGTGCCCCTTTGCTGCTGGCTACCACTCTTCCCCAGAGCAGCAGGCCCCGAGCCCCTTCA
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10.72 AGCAGACTGCCTCTCCCATTCCACCCTCTCGGAAACCTCACCCTCTG 840 10.72 GAGTCCTTCCTGGGCAAACTGGCCTGTGTGTGAAACCCTTGCCTGACCCACAC 1131 11	AGCAGGGGCTCCAGGGGCCCACAGGCCCACAGGCTTTTCTGTGGAGAATACCTAGTGCTGCTCTGTGCTGCTGCTGCTGCTGGTGCTGCTGGTGCTGGTGCTGGTGCTGGTGCTGGTGCTGGTGG	CTGCTCACTGGAAACTCCAGCGGATTATGGGTACGAGAAGAACTCCACTGGGCCCTGCTCACTGGCCCTGGGCCCTGGGCCTGGGGCTTTATGGGTACCGAGAAGATCCACTGGGCCTGGGCCTCGGGCAGAAGAACTCCAGGGCCTGGGATTATGAGTACCGAGAAGAAGTCCACTGGGCCTGGGCCTGGGCATGGGCACAGGGCCTCGGCCTGGGCACAGGCTCCTTCGGAGAGGTGCACAGGATGGAGACAAGACAGCTCCTTCGGAGAGGTGCACAGGATGGAGACAAGAGGCTCCTTCGGAGAGGTGCACAGGATGGAGGACAAGAGGTGCACCAGGCTCCGCCTGGGCAGAGGCTCCTTCGGAGAGGTGCACAGGATGGAGGACAAGACAGGACAAGGTGCCACAGGATGGAGGACAAGAAAAAAAA	CAGACTGGCTTCCAGTGCGCTCCAAAAAGGTGCGGCTGGAAGTTTCGGGCAGAGGAG 132 CTGATGGCATGTGCAGGATTGACCTCACCCAGAATTGTCCCTTTTGTATGAGCTGTGAGA 161 CTGATGGCATGTGCAGGATTGACCTCACCCAGAATTGTCCCTTTTGTATGGAGCTGTGAGA 161 CTGATGGCATGTGCAGGATTGACCTCACCCAGAATTGTCCCTTTTGTATGGAGCTGTGAGA 138 GAAGGCCTTGGGTCAACATCTTCATGGAGCTGCTGGAAGGTGGCTCCCTGGAGCTGTGAGA 167	1841 CARAGGAGGCTGTCTCCAGAGGCCGGCCTGTACTGCGCGGCCCTG	1792 GTGCTCCTGTCCAGCGATGGGAGCCACCAGCAGCCTTGTGCCATGCTGTGTT 1851	1912 ACCCACATGGCTCCGGAGGTGGTGGTGGCAGGAGCTGCGAGGTGGATGTCTGG	

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     FOR
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER; FILE OF INVENTION: CANCER; CURRENT APPLICATION NUMBER: US/10/087,192; CURRENT FILING DATE: 2002-03-01; PRIOR APPLICATION NUMBER: US 09/747,377; PRIOR FILING DATE: 2000-12-22; PRIOR FILING DATE: 2000-12-22; PRIOR RAPLICATION NUMBER: US 09/798,586; PRIOR FILING DATE: 2001-03-02; NUMBER OF SEQ ID NOS: 2059; SOFTWARE: FREESEQ for Mindows Version 4.0
                                                                                                                                                                                                                 ; Score 2042.6;
; Pred. No. 0;
0; Mismatches
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Best Local Similarity 83.4%;
Matches 2377; Conservative
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APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR RILING DATE: 2000-012-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 886
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Sequence 886, Application US/10087192 Publication No. US20020182586A1 GENERAL INFORMATION:

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Sequence 97, Application US/10296115; Publication No. US20040053248A1; GENERAL INFORMATION:

3276 3335 3395 3455 3515 3575 3635 3698 3755 3815 3875 3935 3994 780 124 180 240 300 360 420 480 540 600 9 720 9 TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides FLB REFERENCE: 784PCT CURRENT APPLICATION NUMBER: US/10/296,115 CURRENT FILING DATE: 2002-11-18 PRIOR APPLICATION NUMBER: US09/488,725 PRIOR PELLING DATE: 2000-01-21 PRIOR PILLING DATE: 2000-01-21 PRIOR APPLICATION NUMBER: US09/552,317 PRIOR APPLICATION NUMBER: US09/552,317 NUMBER OF SEQ ID NOS: 1478 CTGCTGAGAAAACACTCCGCCACGTGAAGAGACAG-AGGAGGATGGCAGGAGTTACCTCG GATCAGTGACCATTTGCTGGCAGACAGGGGAGAGCAGCTTCCAGCCTGGGTCAGGTCAGGGGG TGGGCGAGCCCCTCGGCCCTCACCCTCCAGGCTGCTGAGAGTGTCAAGTGTGAAGG 361 GGGCCCTCTAAACCCCTTGCCTGGCCTCACCTGGCCCACCCCTTTTGGGTGTAGGG GAAAAGAATGCCTGACCCTGGGAAGGCTCCCTGGTAGAATACACCACACTTTTCAGGTTG TGAAGTGGTTCTCAGTCCCCAGACATGTGCCCCTTTGCTGCTGGCTACCACTCTTCCCCA TCCCTCATCTGTAAAGGTGAAGGGTGATGCAGGATATGCCTGACAGGAACAGTCTGTGGA TGGACATGATCAGTGCTAAGGAAAGCAGCAGAGAGAGAGGCG-TCCGGCGCCCCAGCCCCAC CAGCAAGGTGGGGCAAGCAAATGCCTCCCAGGATTTCACACCTGAGCCCTGCCCCACC caddaadgreededaadcaaareccreededarrreacaeerreadecereeceaee CTGCTGAAAAAAA-TCCGCCACGTGAAGAGACAGAGGAGGAGGATGGCAGGAGTTACCTGG GGAAACAAAACAGGGATCTTTTTCTGCCCCTGCTCCAGTCGAGTTGGCCTGACCCCGCTTG GATCAGTGACCATTTGTTGGCAGACAGGGGAGAGCAGCTTCCAGCCTGGGTCAGAAGGGG TGGGCGAGCCCTTCGGCCCCTCACCCTCCAGGCTGCTGTGAGAGTGTCAAGTGTGTAAAGG GGGCCCTCTAAACCCCTTGCCTGGCCTCACCTGGCCAGCTCACCCCTTTTGGGTGTAGGG GAAAAGAATGCCTGACCCTGGGAAGGCTCCCTGGTAGAATACACCACACTTTTCAGGTTG TTGCAACACACGTCCTGAGTTGACCTCTGGTTCAGCCAAGGACCAAAGAAGGTGTGTAAG TIGCAACACAGGICCIGAGITIGACCICTGGITCAGCCAAGGACCAAAGAAGAGGIGIGIAAG GAGCAGCAGCCCCGAGCCCCTTCAGGCCCAGCACTGCCCCAGACTCGCTGGCACTCAGT aagcagcagcccccagccccrrcaggccccagcacrgccccagacrcgcrgccacrcagr TCCCTCATCTGTAAAGGTGAAGGTGATGCAGGATATGCCTGACAGGAACAGTCTGTGGA TGAAGTGGTTCTCAGTCCCCAGACATGTGCCCCTTTGCTGCTGCTACCACTCTTCCCCCA Gaps 7; 1385; Length Indela 15; DB 18; 0; Mismatches Score 1304; Pred. No. 0; 3995 721 ò 8 à

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Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
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US-10-108-260A-1754/c
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Pred. No. 1.6e-132;
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Publication No. US20020182586A1

GENERAL INFORMATION:
APPLICANT: Morris, David W.
TITLE OF INVENTION: CANCER
FILE REFERENCE: 5294500122
CURRENT APPLICATION NUMBER: US/10/087,192

CURRENT FILING DATE: 2002-03-01

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR PLICATION NUMBER: US 09/747,377

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

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PRIOR PLING DATE: 2001-03-02

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; OTHER INFORMATION: n = A,T,C or
US-10-087-192-883
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ORGANISM: Mus musculus
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NAME/KEY: misc_feature
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Best Local Similarity
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LENGTH: 42566
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US-10-087-192-883
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                                                                        GACCTGCTCTGTGTTTGGTCTCTCTCAGGATGAGCACAAGCCTGGGAGATGGCAGTGATG
                                                                                                                 5185 GATTTGTTTTGTGTTTTGGTTTTTTAGGATGAGTATAAGTTTTGGGAAGATGGTAGTGATG
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; Sequence 2585, Application US/09918995
; Publication No. US/0030073623A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: RROM VARIOUS CDNA LIBRARIES
; TITLE REFERENCE: 20411-756
; CURRENT FILICATION NUMBER: US/09/918,995
; CURRENT FILICATION NUMBER: US/09/235,076
; PRIOR RPLICATION NUMBER: US/09/235,076
; ROWER OF SEQ ID NOS: 38054
; SOFTWARE: PastSEQ for Windows Version 3.0
; SEQ ID NO 2885
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; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2585
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US-09-918-995-2585
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TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/433,793
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 141
LENGTH: 6673
                                                                                                                                                                                                                                                                                                                                                                                   2179 CTAGTGGGAGGTCTGAAGACCCTTGGAGGGGAGAATATAAAGAACCAAGACATCCACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1879 AGCTCACCAGAGCGGAAAGCAACCGTCCCGGAGCAGGAACTGCAGCAGCTG 1829
                                                                                                                                                                                                                                                                     Query Match 7.6%; Score 349.4; DB 17; Length 2475; Best Local Similarity 99.7%; Pred. No. 1.1e-93; Matches 350; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.3%; Score 291.6; DB 19; Length 6673; Best Local Similarity 76.3%; Pred. No. 3.7e-76; Matches 371; Conservative 0; Mismatches 114; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-433-793-141
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA FILE REFERENCE: H1-A0106 CURRENT APPLICATION NUMBER: US/10/108,260A CURRENT APPLICATION NUMBER: US/10/108,260A NUMBER OF SEQ ID NOS: 5458 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1754 LENGTH: 2475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 141, Application US/10433793
Publication No. US20040142334A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-1754
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US-10-433-793-141
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NAME/KEY:
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3149 ACACAGGCTCAGCCGTTCCCAGGGGATTGCCAGCCCCCCGGGTCACAGGGAACCAGGG 3208
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                                                                                                                                                                                                             Sequence 142, Application US/10433793
Publication No. US20040142334A1
GENERAL INFORMATION No. US20040142334A1
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/433,793
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
LENGTH: 6673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 GGCCTGCCCAGGTGCCCCTGGCTCAGCAGTGGGGAGCAGGAACTCCCCAAGCCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.3%; Score 243.6; DB 19; Length 6673; Best Local Similarity 70.2%; Pred. No. 9.8e-62; Matches 341; Conservative 0; Mismatches 144: ThAble 1
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; Sequence 11852, Application US/09783590
; Patent No. US20020110850A1
                                                                                CCTCGCAGCAGGTGGGG 3229
                                                                                                    CCTCGCAGCAGGAGGTGGAG 499
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US-10-433-793-142/c
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APPLICANT: Li, Haodong
APPLICANT: Rosen, Craid, A.
APPLICANT: Rosen, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
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                                                                                                  FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR PRILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
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NAME/KEY: misc feature
TOCATION: (100)
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (195)
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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INFORMATION: n equals a,t,g,
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:INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: mlsc feature
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INFORMATION: n equals a,t,g,
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APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
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OTHER INFORMATION: n equals
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                                                                                                                                                                                                                                                                                                                                                      misc feature
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Best Local Similarity
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                                                                                                                                                                                                                                                              SEQ ID NO 11852
LENGTH: 296
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4; Gaps	AAGAAT	AAGAAC	SCAACA	SCAACA	-AAGTG	AAAGTG	SAGCAG	SAGNAG		
4	GGGAA	GGNAA	TIGIL	TTGTT	AAGTG	AAGTG	CCCCAC	CCCCAC	1867	96
16; Indels	TGGGTGTAC	TGGGTGTAC	CTTTTCAG	CTTTTAAGG	AAGGTGTGT	AAGGTGTGT	ACCACTCT	ACCACTCT	TCGCTGG	TCGNTGG 2
	CCCTTT	CCCTTT	ACCACA	ACCACA	CCAAAG	CCAAAG	CTGGCT	CTGGNT	CCAGAC	CCANAT
0; Mismatches	TGGCCAGCTCAC	TGGCCAGCTCAC	rgg-ragaatacaccacactr		FTCAGCCAAGGA	FTCAGCCAAGGA	CCCAGACATGTGCCCCTTTG-CTGCTGGCTACCACT	CCCTTTGCCTG	CCAGCACTGCC	CCAGNACTGCC
0,	TCACC	TNACC	CTCCC	CTCCC	TCTGG	101111	ATGTG	ATGTG	TCAGG	TNAGG
267; Conservative	AAACCCCTTGCCTGGCCTCACCTGGCCACCTCTTTTGGGTGTAGGGGAAAAGAAT 3644	10 AAACCCCTTGCCTNACCTGGCCAGCTCACCCCTTTTGGGTGTAGGGGNAAAAGAAC	3645 GCCTGACCCTGGGAAGGCTCCCTGG-TAGAATACACCACACTTTTCAGGTTGTTGCAACA 3703	70 GCCTGACCCTGGGAAGGCTCCCTGGNTAGANTACACCACACTTTTAAGGTTGTTGCAACA 129	CAGGICCTGAGTTGACCTCTGGTTCAGCCAAAGACGAAGGTGTGTAAGTG-AAGTG 3762	130 NAGGTCCTGAGTTGACTTCAGCCAAGGACCAAAGGAGGTGTGTGT	GTTCTCAGTC	190 GITCINAGICCCCAGACAIGIGCCCCCTTTGCCTGGNTACCACTCTTCCCCAGAGNAG 249	CAGGCCCCGAGCCCC-TTCAGGCCCAGCACTGCCCCAGACTCGCTGG 3867	250 NAGGCCCCGAGCCCCTTTNAGGCCCAGNACTGCCCCANATTCGNTGG 296
8 267	3585	10	3645	70	3704	130	3763	190	3822	250
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Search completed: June 11, 2005, 06:13:18 Job time : 1756.62 secs

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1590, Ap 1591, Ap 1454, Ap

Sequence 1 Sequence 1 Sequence 1

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Title: Perfect score:

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Minimum DB seq Maximum DB seq

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292 GAACTCCCCAAGCCAAAGGAGAAGACGCCGCCACTGGGGAAGAACAGAGCTCCGTCTAC 351
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                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08887518

Patent No. 5843721

GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
TITLE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
                                                                                                                                                                    US-09-270-767-15818
US-09-949-016-1590
US-09-949-016-1591
US-09-016-434-1454
US-08-878-989-12
US-09-691-861A-1
US-08-16-434-1147
US-08-459-448A-26
US-08-459-595A-26
US-08-459-504B-26
US-08-459-444-26
US-09-547-422-26
US-09-988-462-26
US-09-988-462-26
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US-09-230-896C-5
US-09-270-767-536
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99.9%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                  ALIGNMENTS
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSNAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-008
TELEPHONE: (415) 343-4341
TELEPRAY: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
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Matches 3152;
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Compugen Ltd.
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US-09-257-703-2

US-09-257-703-2

US-09-513-999C-2583

US-09-513-999C-2583

US-09-688-688A-3

US-08-471-146C-5

US-08-471-146C-5

US-08-461-146C-5

US-08-421-890-11

US-08-421-890-11

US-08-421-890-5

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US-08-461-146C-11

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               GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                nucleic search, using sw model
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length: 2000000000
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Match Length
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                                                                                               ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION AND ATA:
APPLICATION NUMBER: US/08/887,518
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REPERENCE/DOCKET NUMBER: 197-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3156 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TANDOLARY: linear
268 BUSH STREET, SUITE 3200
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99.9%;
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Best Local Similarity 99.9
Matches 3152; Conservative
                      SAN FRANCISCO
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US-09-023-321-1
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US-09-023-321-1
Sequence 1, Application US/09023321
Sequence 1, E44073
GENERAL INFORMATION:
APPLICANT: W. Lin
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
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772 GATGAGTCTCCACTCGGCGCCCCATATGTTAGAAACACCCCGCAGTTCACCAAGCCTCTG 831	CTGCCTCGATCAGAACTCCACAAACTGATCAGCCCCTTGCAATGTCTGAACCACGTGTGG	1011	1012 AGCAGACTGCCTCATCCCTTCCACCTCTCCAGCCTGGAAACCTCACCTCTG 1071	1072 GAGTCCTTCCTGGGCAAACTGGCCTGTGTAGACAGCCAGAAACCCTTGCCTGACCACAC 1131	AGCCC 1191	ATGCT 1251 ATGCT 1020	CCTGG 1311 	CCAGCACGGGGCTTCCAGATCCCGGGAGCCCCAAAACTGAGACAACGGGGTGTC 1371	CTGCTCACTGAGAAACTCAAGCCAGTGGATTATGAGTACCGAGAAGAAGTCCACTGGGCC 1431	ACGCACCAGCTCCGCCTGGGCAGAGGCTCCTTCGGAGAGGTGCACAGGATGGAGGACAAG 1491	AGGAG 1551 	CTGATGGCATGTGCAGATTGACCTCACCCAGATTGTCCCTTTGTATGGAGCTGTGAGA 1611	GAAGGCCTTGGGTCAACATCTTCATGGAGCTGCTGGAAGGTGGCTCCCTGGGCCAGCTG 1671	22 CHICAGGAGCAGGCTGTCTCCCAGAGCGGCCTGTACTACTACTACGGCCAGGCCTG 1731	GAGGGTCTGGAATACCTCCACACAGGATTCTGCATGGGGACGTCAACAGGCCCIG 1500	192 GRGCTCCTGTCCACGATGGGAGCCACGCACCCTCTGTGACTTTGGCCATGCTGTGTT 1851	CAACCTGATGGCCTGGGAAAGTCCTTGCTCACAGGGGACTACATCCCTGGCACAGAG 1911

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2701 TTGGTCACCAAAGACGGGCAGCCTGTTCGCTACGACATGGAGGTGCCAGACTCGGGCATC 2760
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                                                                                                                                                                    GCAGCCTTCCTGCTCGGTGCACGATGCTGCCCTGAAAACACAGGCTCAGCCGTTCCCAGG
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                                                                                                 GGCCAGCTGGAGAACAGGCCCTAACCCTTGCCGCCGCCGGCTCCACACTGCCGGAAA
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ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
FILING DATE:
PILING DATE:
PILING DATE: 08/887,518
FILING DATE: 08/887,518
FILING DATE: 36,627
FILING DATE: 36,627
FILING DATE: 343-4341
TELECOMMUNICATION INFORMATION:
TELEBHONE: (415) 343-4341
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEBHONE: (415) 343-4341
TELEBTA: 3156 dase pairs
TYPE: nucleic acid
STRANDEDMESS: double
STRANDEDMESS: double
TYPE: DONA
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; Sequence 1, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
APPLICANT: Wo. Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and
NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS: 4
; CORRESPONDENCE BORNESS: 4
; TREET: 268 BUSH STREET, SUITE 3200
; STREET: 268 BUSH STREET, SUITE 3200
; STATE: CALIFORNIA
; COUNTRY: USA
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                                                                   INFAMMATORY RESPONSE INDUCED
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Pred. No. 0;
0; Mismatches
          SQUENCE 2, Application US/09257703
Patent No. 626538
GENERAL INFORMATION:
APPLICANT: Greene, Warner C.
APPLICANT: Gleene, Warner C.
APPLICANT: Lin, Xin
TITLE OF INVENTION: BY THE ALPHA AND IL-1
FILE REFERENCE: 30448.61USUI
CURRENT APPLICATION UNDRER: US/09/257,703
CURRENT APPLICATION NUMBER: 60/076,299
EARLIER FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 2
SCOTTWARRE
                                                                                                                                                                        KINASE (NIK)
                                                                                                                                                              ; TYPE: DNA
; ORGANISM: NF-KAPPA B INDUCING
US-09-257-703-2
                                                                                                                                                                                               Query Match 61.7%;
Best Local Similarity 99.9%;
Matches 2840; Conservative (
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1140 1260 1020 1371 1200 1380 1440 1500 101 1131 1191 1251 1311 1431 1491 1551 1611 1731 1791 1851 1620 1911 1680 1971 2031 1800 840 900 960 1021 CTGCAAGGCAGCGTGAAGCTCAAGCCCAGGCCCACAGCCTGACCAGCCTGGCCAAGACCTGG GCAGCACCACCACCACCCCACCCCACCCCAAAACTGAGAACACAGCGTGTC 1201 ACGCACCAGCTCCGCCTGGGCAGAGGCTCCTTCGGAGAGGTGCACAGGATGGAGGACAAG CAGACTGGCTTCCAGTGCGCTGTCAAAAAGGTGCGGCTGGAAGTTTTCGGGCAGAAG GAAGGCCTTGGGTCAACATCTTCATGGAGCTGCTGGAAGGTGGCTCCCTGGGCCAGCTG 1741 AGCAGCTGCTGTATGATGCTGCACATGCTCAACGGCTGCCACCCCTGGACTCATTCTTC CTGCCTCGATCAGAACTCCACAAACTGATCAGCCCCTTGCAATGTCTGAACCACGTGTGG AGCAGACTGCCTCATCCCTTCCCATTCCACCTCTCCAGCCCTGGAAACCTCACCCTCTG GAGTCCTTCCTGGGCAAACTGGCCTGTGTAGACAGCCAGAAACCCTTGCCTGACCCACAC GAGTCCTTCCTGGGCAAACTGGCCTGTGTAGACAGCCAGAAACCCTTGCCTGACCCACACA 961 AGCTGCCTGTCTCGTGGTGCCCATGAGAAGTTTTCTGTGGAGGAATACCTAGTGCATGCT CTGCAAGGCAGCGTGAGCTCAAGCCCACAGCCTGACCAGGCCTGGCCAAGGCCTGG 1081 GCAGCACGGGGCTCTAGATCCCGGGAGCCCAGGCCCCAAAACTGAGGACAACGAGGGTGTC CAGACTGGCTTCCAGTGCGCTGTCAAAAGGTGCGCCTGGAAGTATTTCGGGCAGAGGAG 1612 GAAGGGCCTTGGGTCAACATCTTCATGGAGCTGCTGGAAGGTGGCTCCCTGGGCCAGCTG GTCAAGGAGCAGGCTGTCTCCCAGAGGACCGGGCCCTGTACTACCTGGGCCAGGCCCTG GTCAAGGAGCAGGCTGTCTCCCCAGAGGACCGGGCCCTGTACTACCTGGGCCCAGGCCCTG GAGGGTCTGGAATACCTCCACTCACGAAGGATTCTGCATGGGGACGTCAAAGCTGACAAC GAGGICTGGAATACCTCCACTCACGAAGGATTCTGCATGGGGACGTCAAAGCTGAAAC 1681 ACCCACATGGCTCCGGAGGTGCTGGGCAGGAGCTGCGACGACGACGTCTGG AGCAGCTGCTGTATGATGCTGCACATGCTCAACGGCTGCCACCCCTGGACTCATTCTTC AGCTGCCTGTCTCGTGGTGCCCATGAGAAGTTTTCTGTGGAGGAATACCTAGTGCATGCT CTGCTCACTGAGAAACTCAAGCCAGTGGATTATGAGTACCGAGAAGAAGTCCACTGGGCC ACGCACCAGCTCCGCCTGGGCAGAGGCTCCTTCGGAGAGGTGCACAGGATGGAGGACAAG GTGCTCCTGTCCAGCGATGGGAGCCACGCAGCCCTCTGTGACTTTGGCCCATGCTGTGTGT Greencereceaeceareceaeceaeceaecerererereaerringecearecrererer

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Sequence 2, Application US/09871889A

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Factoric 2, Application US/09871889A

Factoric No. 645728

GENERAL INFORMATION:

APPLICANT: General Warner C.

APPLICANT: General Response Involution of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion of the Inversion o
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: NF-KAPPA B INDUCING KINASE (NIK)
US-09-871-889A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.9%;
Matches 2840; Conservative
       RESULT 5
US-09-871-889A-2
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APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATCHE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATCHE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATCHE OF TAGE 1990-02-24
CURRENT FILING DATE: 1990-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTHARE: Patent.pm
SEQ ID NO 2583
LENGTH: 362
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Pred. No. 3.2e-70;
0; Mismatches 13;
2821 GGCCAGCTGGAGACAGGCCCTAA 2844
                                                                                                     Sequence 2583, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
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Sequence 5071, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
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Best Local Similarity 95.9%;
Matches 306; Conservative
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US-09-513-999C-2583
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 19 OTHER INFORMATION: 8=9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: CDS
LOCATION: 79..360
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-010-03
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 207012
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| Patent No. 6498035
| GENERAL INFORMATION T. Ward
| APPLICANT: William Gaarde
| APPLICANT: Brett P. Monia |
| APPLICANT: Brett P. Monia |
| APPLICANT: Jacqueline Wyatt |
| TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK3 EXPRESSION |
| FILE REFERENCE: RTS-0143 |
| FILE REFERENCE: 2000-09-08 |
| CURRENT FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 88 |
| SEQ ID NO 3 |
| LENGTH: 2348 |
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53.4%; Pred. No. 2.8e-13;
vative 0; Mismatches 197; Indels
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Best Local Similarity 53.4
Matches 236; Conservative
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; Sequence 5, Application US/08323460A; Patent No. 5854043
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US-08-323-460A-5
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US-08-472-934-5
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                                                                                                                            DB 4; Length 2348;
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Patent No. 5753446

GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield
STREET: 60 State Street
                                                                                                                        Query Match 1.9%; Score 88.8; DB 4; Length 2
Best Local Similarity 53.4%; Pred. No. 2.9e-13;
Matches 236; Conservative 0; Mismatches 197; Indels
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APPLICATION NUMBER: US/08/472,934
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,421
FILING DATE: 15-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/354,516
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
                                     NAME/KEY: CDS
LOCATION: (84)...(1964)
ORGANISM: Homo sapiens
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                                                               , LOCATION: (84
US-09-658-688A-3
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US-08-472-934-5
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1835 ACCTGCACACCAACATGATTGTGCATCGGGACATCAAGGGAGCCAATATCCTCCGAGACT 1894
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1.8%; Score 83.8; DB 1;
Best Local Similarity 52.6%; Pred. No. 7.4e-12;
Matches 234; Conservative 0; Mismatches 202;
                                                                                                                                                                                                                 PFILING DATE: 12-1993

PFILING DATE: 12-1993

APPLICATION NUMBER: 08/323,460

FILING DATE: 14-0ct-1994

PRIOR APPLICATION DATE: 14-0ct-1994

PRIOR APPLICATION DATE: PCT/US94/11690

FILING DATE: 14-0cT-1994

PRIOR APPLICATION DATE: PCT/US94/04178

PRIOR APPLICATION NUMBER: PCT/US94/04178

FILING DATE: 15-ARP-1994

ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 31,503

REGISTRATION NUMBER: 31,503

REGISTRATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFAX: (617) 227-7400

INFORMATION FOR SEO ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: DATE: LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH: 2019 agirs LENGTH
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FILING DATE: 21-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5,405,941
FILING DATE: 15-Apr-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3089 base pai
TYPE: nucleic acid
STRANDEDNESS: double
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400..2280
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2066 CTGTGGTGGAAATGCTGACAGAGAAACCACCTTGGGCAGAGTATGAAGCTATGGCTGCCA 2125
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,146C
FILING DATE: OS-JUN-1995
CLASSIFICATION: 435
                                                                                                         2126 TTTTCAAGATTGCCACCCAGCCTAC 2150
                                                        2045 GCCTCAAGATTGCCAGCGAGCCTCC 2069
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APPLICATION NUMBER: US 08/354,516

FILING DATE: 21-FEB-1995

FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254

FILING DATE: 15-APR-1993

FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,460

FILING DATE: 14-0CT-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PROTAURED DATA:
APPLICATION NUMBER: PROTAURED DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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60 State Street
                                                                                                                                                                                 RESULT 11
US-08-461-146C-5
Sequence 5, Application US/08461146C
Patent No. 5991265
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REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CPI
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 227-7400 TELEPAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: ME
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400..2280
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Best Local Similarity
Matches 234; Conserv
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: JOHNSO
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CITY: Boston
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FEATURE:
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US-08-461-146C-5
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                         , GARY L.
METHOD AND PRODUCT FOR REGULATING CELL
RESPONSIVENESS TO EXTERNAL SIGNALS
1.0
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,460A
FILING DATE: 14-0CT-1994
CLASSIFICATION 530
PRIOR APPLICATION NUMBER: US/08/9254
FILING DATE: 14-APR-1993
ATTONNEY/AGENT INFORMATION:
NAME: KOVARIK, JOSEPH E.
REGISTRATION NUMBER: 33,005
REGISTRATION NUMBER: 33,005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 303/663-9700
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1.8%; Score 83.8; DB 2; 1
Best Local Similarity 52.6%; Pred. No. 7.4e-12;
Matches 234; Conservative 0; Mismatches 202;
                       APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: METHOD AND PRODUCT FOR
TITLE OF INVENTION: RESPONSIVENESS TO EXTE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: SHERIDAN ROSS & MCINTOSH
STREET: 1700 LINCOLN STREET, SUITE 3500
CITY: DENVER
                                                                                                                                                                                                                                                                      ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: single
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GENERAL INFORMATION:
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USA
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; LOCATION: 400.
US-08-323-460A-5
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1625 TCAACATCTTCATGGAGCTGCTGGAAGGTGGCTCCTGGGCCAGCTGGTCAAGGAGCAGG 1684
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GARY L. METHODS FOR REGULATING MEKK PROTEIN ACTIVITY
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FEATURE
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                                                                                                                                                                                           1895 CAGCTGGGA---ATGTGAAGCTTGGGGATTTTGGGGCCAGCAAACGCCTACAGAACCATCT 1951
                                                                                                                                                                                                                                                                                              1952 GCATGTCAGGGACAGGCAT----TCGCTCTGTCACTGGCACACCCTACTGGATGAGTC 2005
                                                                                                                                                                                                                                                                                                                                                                                1985 TGATGCTGCACATGCTCAACGGCTGCCACCCCTGGACTCAGTTCTTCCGAGGGCCGCTCT 2044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2066 CTGTGGTGGAAATGCTGACAGAGAAACCACCTTGGGCAGAGTATGAAGCTATGGCTGCCA 2125
1685 GCTGTCTCCCAGAGGACCGGGCCCTGTACTACCTGGGCCCAGGCCCTGGAGGGTCTGGAAT 1744
                                     1775 GAGCTCTGACAGAGAGTGTGACCCGCAAGTACACCCGGCAGATTCTGGAGGGCATGTCAT 1834
                                                                                 1745 ACCTCCACTCACGAAGGATTCTGCATGGGGACGTCAAAGCTGACAACGTGCTCCTGTCCA 1804
                                                                                                                       1835 accrecacacarcardarrerecarcededacarcaadeaccaararecrecedagaer 1894
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                                                                                                                                                                                                                                                      GCCTGGGAAAGTCCTTGCTCACAGGGACTACATCCCTGGCACAGAGACCCACATGGCTC 1924
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,145C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: NOVEL MEKK PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield, LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 11-APR-1993
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/323,460
FILING DATE: 14-0CT-1994
PRICE APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-0CT-1994
PRICE APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/354,516
APPLICATION NUMBER: US 08/354,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2045 GCCTCAAGATTGCCAGCGAGCCTCC 2069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08461145C Patent No. 6074861 GENERAL INFORMATION:
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REGISTRATION UNDBER: P-41,106
REFERENCE/DOCKET NUMBER: CPI-0
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CLASSIFICATION:
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US-08-461-145C-5
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GENERAL IN CYRAILON;
TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To External
TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To External
FILE REPERIORS: CPI-004DVCP3
CURRENT APPLICATION NUMBER: US/08/628,829A
CURRENT FILING DATE: 1995-04-05
EARLIER APPLICATION NUMBER: 08/440,421
EARLIER FILING DATE: 1994-10-14
EARLIER FILING DATE: 1994-10-14
EARLIER FILING DATE: 1994-05-15
EARLIER FILING DATE: 1995-06-05
EARLIER FILING DATE: 1995-04-24
EARLIER FILING DATE: 1995-04-24
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATCHON OF : 2.0
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1.8%; Score 83.8; DB 3;
Best Local Similarity 52.6%; Pred. No. 7.4e-12;
Matches 234; Conservative 0; Mismatches 202;
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                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
(617) 227-7400
                                                                 'n
                        TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 3089 base pairs
                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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400..2280
TELEPHONE:
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US-08-461-145C-5
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1707 dagcricrgacadadagrgrgrgacccgcaagracacccggcadarrcrggagggcarcrar 1766
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APPLICANT: CADUS PHARMACEUTICAL CORPORATION

TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES

TITLE OF INVENTION: AND USES THEREFOR

TITLE OF INVENTION: AND USES THEREFOR

CURRENT APPLICATION NUMBER: US/09/423,890

PRIOR PLING DATE: 2000-03-06

PRIOR PLING DATE: 1998-03-16

PRIOR PLING DATE: 1998-09-04

NUMBER OF SEQ ID NOS: 38
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              Pred. No. 7.7e-12;
0; Mismatches 202;
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; Patent No. 6312934
              52.6%;
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          Best Local Similarity 52.6
Matches 234; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: (25)..(1902)
US-09-423-890-5
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SEQ ID NO 5
LENGTH: 1935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1745 ACCICCACTCACGAAGGAITCTGCATGGGGACGTCAAAGCTGACAACGTGCTCCTGTCCA 1804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1835 ACCIGCACAACAIGAIIGIGCAICGGACAICAAGGGAGCCAAIAICCICCGAGACI 1894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1805 GCGATGGGAGCCACGCAGCCCTCTGTGACTTTGGCCATGCTGTGTGTCTTCAACCTGATG 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1895 CAŚCTGGGA---ATGTGARGCTTGGGGATTTTGGGGGCCAGCAAACGCCTACAGACCATCT 1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGAGGTGGTGCTGGGCAGGAGCTGCGACGCCAAGGTGGATGTCTGGAGCAGCTGCTGTA 1984
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APPLICANT: CADUS PHARMACEUTICAL CORPORATION

TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES

TITLE OF INVENTION: AND USES THEREFOR

TITLE OF INVENTION: AND USES THEREFOR

CURRENT APPLICATION NUMBER: US/09/423,890

CURRENT APPLICATION NUMBER: US/09/423,890

CURRENT FILING DATE: 1998-03-06

PRIOR APPLICATION NUMBER: USSN 60/078,153

PRIOR FILING DATE: 1998-03-16

PRIOR FILING DATE: 1998-09-04

NUMBER OF SEQ ID NOS: 38

SOFTWARE: PATCHTIN VET. 2.0

SEC ID NO 11
                                                                                                                                                                                                                                                                                                                          Length 3089;
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                                                                                                                                                                                                                                                                                                           1.8%; Score 83.8; DB 3;
Similarity 52.6%; Pred. No. 7.4e-12;
14; Conservative 0; Mismatches 202;
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US-08-423-890-11
Sequence 11, Application US/09423890
; Patent No. 6312934
                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (400)..(2277)
US-08-628-829-9
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; NAME/KEY: CDS
; LOCATION: (332)..(2209)
US-09-423-890-11
                                LENGTH: 3089
TYPE: DNA
ORGANISM: Mus musculus
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Matches 234;
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Best Local
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1520 CAGCTGGGA---ATGTGAAGCTTGGGGATTTTGG-----GGCCAGCAAACACCTACAGA 1570
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                                                    1805 GCGATGGGAGCCACGCACCCTCTGTGACTTTGGCCATGCTGTGTCTTCAACCTGATG 1864
                                                                                                         1865 GCCTGGGAAAGTCCTTGCTCACAGGGGACTACATCCCTGGCACAGAGACCCACATGGCTC 1924
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Search completed: June 10, 2005, 20:46:52 Job time : 511.934 secs

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                                               June 10, 2005, 06:13:19; Search time 11495.3 Seconds (without alignments) 16321.674 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                               - nucleic search, using sw model
                                                                                                                 IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                               US-09-155-676B-6
4596
                                                                                Title:
Perfect score:
                                                                                                                 Scoring table:
                               OM nucleic
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                                                                                                                                           Searched:
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                                                Run on:
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RESULT 1

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/cgn2_6/ptodata/1/pna/US6056_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		equence 6,	, Api	Sequence 1529	975,	equence 975,	se 123	se 437	e 17,	equence 975	e 294	975	ce 14	equence 1	equence 887	12	equence 448	4 Sequence 32	equence 226,	Sequence 5384,	Sequence 5384,	S	Sequence 2732,	Sequence 5384,	equence 566,	equence 912,	e 566,	Sequence 912,	Sequence 3494,	Sequence 10109,	Sequence 227	Sequence 5385,	Sequence 5385,	Sequence 2733,	Sequence 2733,	Sequence 5385,	equence 567,	equence 913,	ednence	e 913,	Sequence 6881,	Sequence 6881,	Sequence 532	Sequence 4571,	Sequence 4571,	Section 1000s
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181 AGTGACCTGCTCTGTGTTTGGTCTCTCTCAGGATGAGCAAGACCTGGGAGATGGCAGTG 240 61 AGGATGTTTGGAGGATGAGTATGTGTGGCAGAGGCACACATAAACAGGCAGAGACCCTTT 120 121 GCCCCTGCCTTTCTCCCCCCAACCCAAGGCTGACCTGTGTTCTCCCAGGTCTGGGATTCTA 180 AGTGACCTGCTCTGTGTTTGGTCTCTCTCAGGATGAGCACAAGCCTGGGAGATGGCAGTG 240 121 eccertecerriterececeaacecaaeereaecrererrereceaeereresarrera 180 1 Accesesesacrerecesistaceaacereracrericaacereaacerererracarre 60 1 AGCGGGGGACTGTGCCGTGTGGAACGTGTAGCTGTTGAAGGTGGACTCTGTTACCATTG Gaps GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: MALININ, Nikolai
APPLICANT: BOLDIN, Mark
APPLICANT: BOLDIN, Mark
APPLICANT: MITT, 1gor.
TITLE OF INVENTION: PACTOR (TRAF), THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
DORRESPONDENCE ADDRESS:
DORRESPONDENCE ADDRESS:
STREET: 624 Ninth Street, N.W., Suite 300
CITY: Washington ó, DB 17; Length 4596; 0; Indels COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/155,676
FILING DATE: 04-JAN-1999
CLASSIFICATION: 530 100.0%; Score 4596; 100.0%; Pred. No. 0; iive 0; Mismatches CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IL97/00117
FILING DATE: 01-APPR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117800
FILING DATE: 02-APPR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 119133
FILING DATE: 26-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L. WALLACH=21 25,618 REFERENCE/DOCKET NUMBER: WA TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197 TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 4596 base pairs Query Match Best Local Similarity 100. Matches 4596; Conservative TYPE: nucleic acid STRANDEDNESS: single REGISTRATION NUMBER: ; TOPOLOGY: linear ; MOLECULE TYPE: CDNA US-09-155-676-6 STATE: D.C. COUNTRY: USA 20001 US-09-155-676-6 181 유 엄 ð a qq 8 ò ò

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ALIGNMENTS

	1561 TGTGCAGGATTGACCCCAGAATTGTCCCTTTGTATGAGGCTGTGAGAGGAGGCCT 1620 1621 TGGGTCAACATTCATGGAGGTGGCTGGTCCCTGGGCCAGCTGGTGAGGAG 1620 1621 TGGGTCAACATCTTCATGGAGGTGGCTGGTCCCTGGGCCAGCTGGTCAAGGAG 1680 1621 TGGGTCAACATCTTCATGGAGCTGCTGGAGGCTCCCTGGAGCTGGTCAAGGAG 1680 1631 CAGGGCTGTCTCCCAGAGGACCGGGCCCTGTACTACCTGGGCCCTGGAGGGTCTG 1740 1631 CAGGGTGTCTCCCAGAGGACCGGGCCCTGTACTACCTGGGCCCTGGAGGGTCTG 1740 1631 GAATACCTCCCAGAAGGATTCTGCATGGGGCCTCAAAGCTGGACAACGTGCTCCTG 1800 1741 GAATACCTCCACAGAAGGATTCTGCATGGGGACGTCCAAAGCTGACAACGTGCTCCTG 1800 1741 GAATACCTCCACAGAAGGATTCTGCATGGGGACGTCAAAGCTGACAACGTGCTCCTG 1800 1741 GAATACCTCCACAGAAGATTCTGCATGGGGACCTCAAAGCTGACAACGTGCTCCTG 1800 1741 GAATACCTCCACAGAAGATTCTGCATGGGGACGTCAAAGCTGACAACGTGCTCCTG 1800 1741 GAATACCTCCACAGAAGATTCTGCATGGGGACGTCCAAACGTGCTCCTG 1800 1741 GAATACCTCCACAGAAGATTCTGCATGGGGACGTCCAAACGTGCTCCTG 1800 1741 GAATACCTCCACAGAAGATTCTGCATGGGGACGTCCAAACGTGCTCCTG 1800 1741 GAATACCTCCACAGAAGATTCTGCATGGGGACGTCCAAACGTGCTCCTG 1800 1741 GAATACCTCCACACAAAGCTGCAAACGTGCTCCTG 1800 1741 GAATACCTCCACACAAAGCTGCAAACGTGCTCCTG 1800 1741 GAATACCTCCACACAAAGCTGCTCCTG 1800 1741 GAATACCTCCACACAAAGCTCCAACAGCTGCTCCTG 1800 1741 CACAGAACACTCACACAACACTCCAACACTCCTCTG 1800 1741 CACAGAACACTCACACAAACCTCCAACACCTCCTCTG 1800 1741 CACAGAACACTCACACAACACTCCAACACTCCAACACTCCTCTG 1800 1741 CACAGAACACTCCACACAACACTCCAACACTCCAACACTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC		1981 TGTATGATGCTGACGGCTGCCACCCCTGGACTCAGTTCTTCCGAGGCCG 2040 1981 TGTATGATGCTGCACCCCCTGGACTCAGTTCTTCCGAGGGCCG 2040 1981 TGTATGATGCTGCACGCTGCCACCCCCCCCCCCTGGACTCCATTCCGAGGGCC 2041 TGTATGATGACGACTGCCACCCCTGTGAGGAATCCCACCCTCCTGCGC 2041 CTCTGCCTCAAGATTGCCAGCGCCTCCGCCTGTGAGGAATCCCACCCTCCTGCGCC 2100 11 11 11 11 11 11	2161 GCAGGGAGCTGGAAGGTGAACCGGCACTACAGCAAGTGGGAGGTCTGAAGAGC 2220 2161 GCAGGGAGCTGGGAAGGTGAACCGGCACTACAGCAAGTGGGAGGTCTGAAGAGC 2220 2161 GCAGCGGAGCTGGGAAGAGAAGACGAGCACTACAGAGCACACTGAAGAGC 2220 2161 GCAGCGGAGGAATATAAAGAACCAGACATCCACCGCCAAATCAAGAGC 2220 2221 CCTTGGAGGGAGAATATAAAGAACCAAGACATCCACCGCCAAATCAAGCCAATTACCAC 2280 2281 CCTTGGAGGGAGAATATAAAGAACCAAGACATCCACCGCCAAATCAAGCCCAATTACCAC 2280 2281 CAGACCCTCCATGCCCAGCCGAGAGACTTTCGCCAAGGGCCCCAGGGCCCCGGCCAGCT 2340 2281 CAGACCCTCCATGCCCAGCGAGAGACTTTCGCCAAAGGGCCCCAGGGCCCCGGCCAGCT 2340 2341 GAGGAGACAACAGGCCCCTAAGCTCCAGGCCCCCAGAGGCCCCAGAGGCCCCAGAGGCCCCAGAGGCCCCAGAGGCCCCAGAGGCCCCAGAGGCCCCAGAGGCCCCAGAGGCCCCAGAGGCCCCAGAGGCCCCAGAGGCCCCAAACAAC
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241 ATGGAAATGGCCTGCCCTGGCTCAGCAGTGGGGCAGCAGAAGGAACTCCCC 300	GCTGGGTGTGAGAATAGCCAAGAGTTCAGCCCTTTTCAGAACGCATTTTCATCGCT GGGTCCAACAATAGCCAAGAGTTCAGCCCCATTTTCAGAACGCTTTTCATCGCT GGGTCCAACAACAGCCAGTCCGAGAGTCTTGATCAGATCCCCAACAATGTGGGCCCAT [12 CCCTCCCCAGGACCCCTGAGCAGCTCATGCAGGAGTGGCCTTGGCCAAA 720 721 CCCTCCCCAGGAGCAGCAGGAGGAGCCTTGGCCAAA 720 721 CCCTCCCCAGGACCCCTGAGCAGGAGGAGCATCAGTGCAGGAGGATCAGTT 780 721 CCCTCCCCAGGACCCCTGAGGAGGATCAGTT 780 721 CCCTCCCCGGACCCATGAGGAGCTCCCAGTGCAGGAGGATCAGTT 780 721 CCCTCCCGGACCCCTATGATAGAAACACCCCGCAGTTCACCAGGCCTCTGAAGGACCA 840 781 CCATCGGCGCCCCATATGATAGAAACACCCGGCAGTTCACCAAGCCTCTGAAGGAACCA 840 781 GGCTTGGGCGCCCCATATGATAGAAACACCCCGGAGTTCACCAAGGCCTCTGAAGGAACCA 940 781 GGCTTGGGCAACTCTGTTTAAAGAACACCCGGCGTTCACCAGGCCTACCCCCGA 941 78		1081 CTGGGCAAACTGGCCTGTGTAGACAGCCAGAAACCTTGCCTGACCCCACACCTGAGGAAA 1140

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                   Sequence 6, Application US/09155676A

GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: WALLININ, Mikolai
APPLICANT: ROUDIN, Mark
APPLICANT: ROVALENKO, Andrei
APPLICANT: METY, Igox
TITLE OF INVENTION: PACTOR (TRAF), THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C.
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                                                                                                                                                                                                                         ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,676A
FILING DATE: 04-JAN-1999
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17;
                                                                                                                                  STREET: 624 Ninth Street, N.W., Suite 300 STATE: D.C. STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 4596; D; Pred. No. 0; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IL97/00117

FILING DATE: 01-APR-1997

PRIOR APPLICATION NUMBER: IL 117800

FILING DATE: 02-APR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 119133

FILING DATE: 26-AUG-1996

ATTONNEY AGENT INFORMATION:

NAME: BROWDY, ROGER L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: 25,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEPHONE: 202-628-5197
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Best Local Similarity 100.0%;
Matches 4596; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4596 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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RESULT 2
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	2461 CCTCTGTCCTCCTGGAGCCAGCCTGCCAGAAACCCCAGCTCACCAGAGCGGAAAGCA 2520 2461 CCTCTGTCCTGGAGCCAGCCTGCCAGAAACCCCAGCTCACCAGAGCGGAAAGCA 2520	2521 ACCGTCCCGGAGCAGCAGCAGCAGCTGGAAATAGAATTATTCCTCAACAGCCTGTCC 2580 2521 ACCGTCCCCGGAGCAGGAACTGCAGCAGCAGGAATTATTCCTCAACAGCTGTCC 2580	2581 CAGCCATTTCTCTGGAGGAGCAGGAAATTCTCTCGTGCCTCAGCATCGACCACC 2640 2581 CAGCCATTTTCTCTGGAGGAGCAGGAACAATTCTCTCGTGCCTCAGCATCGACGCCTC 2640	TCCTGTCGGATGACAGTGAGAAGAACCATCAAAGGCCTCTCAAAGCTCGCGGGACACC 	2701 CTGAGCTCAGGCGTACACTCCTGGAGCAGCCAGGCCGAGGCTCGAAGCTCCAGCTCGAAC 2760 2701 CTGAGCTCAGGCGTACACTCCTGGAGCAGCCAGGCCGAGGCTCGAAGCTCCAGGCGAAGCTCCAGGCGAGCCAGGCCGAGGCTCGAAGCTCCTGGAGCAGCCAGGCCGAGGCTCGAAGCTCCAGGCGAAGCTCCAGGCTGGAAC 2760	2761 ATGGTGCTGGGGGGGGGCCCACCGACCTAATTTCAATGGTGTAAAGTC 2820 		2881 GGAGACNICGCCACTGGCATCAGCAGCCAGATCCCAGCTGCAGCTTCAGCTTTGGTCACC 2940 2881 GGAGACATCGCCACTGGCATCAGCAGCCAGATCCCAGCTGCAGCCTTCAGCTTGGTCACC 2940	2941 AAAGACGGCGCAGCCTGCTACGACATGGAGGTGCCAGACTCGGGCATCGACTTGCAG 3000 2941 AAAGACGGCCAGCCTGTTCGCTACGACATGGAGGTGCCAGACTCGGGCATCGACTTGAG 3000	3001 TGCACACTGGCCCCTGATGGCAGCTTCGCCTGGAGCTCGAGGGTCAAGCATGGCCAGCTG 3060 3001 TGCACACTGGCCCCTGATGGCAGCTTCGCCTGGAGCTGGAGGGTCAAGCATGGCCAGCTG 3060	GAGAACAGGCCCTAACCCTGCCCTCCACGGCTGCCACACTGCCGGAAAGCAGCCTTC	3121 CTGCTCGGTGCACGATGCTGCCCTGAAACACACGCTCTGCCGGTTCCCAGGGGTTTGCCA 3180	3181 GCCCCCGGCTCACAGTGGGAACCAGGGCCTCGCAGCAAGGTGGGGGGCAAGCAGAAAT 3240 3181 GCCCCCCGGCTCACAGGGGAACCAGGGCCTCGCAGCAAGGAGGGGGGGAAGCAAAT 3240	3241 GCCTCCCAGGATTTCACACCTGAGCCCTACCCTGCTGAAAAAACATCCGCCACGT 3300 3241 GCCTCCCAGGATTTCACACCTGAGCCCTGCCCACCCTGCTGAAAAAACATCCGCCACGT 3300	3301 GAAGAGACAGAAGGAGGAGGAGTTACCTGGGGAAACAAAACAGGATCTTTTCT 3360 	3361 GCCCTGCTCCAGTCGAGTTGGCCTGACCCGCTTGGATCAGTGACCATTTGTTGGAGAC 3420	3421 AGGGGAGCAGCTTCCAGCCTGGGTCAGAAGGGTGGGCGAGCCCTTCGGCCCTCACC 3480 3421 AGGGGAGAGCAGCTTCCAGCCTGGGTCAGAAGGGCTGGGCGAGCCCTTCGGCCCTCACC 3480 3421 AGGGGAGAGCTTCCAGCCTGGGTCAGATGTGTAAGGGCTGGGCCATCGGCCCTCACC 3480 3481 CTCCAGGCTGCTGTGAAGTGTCAAGTGTGTAAGGCCCAAACTCAGGTTCAGTGCAGAA 3540	
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                                               APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 2127-2049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR PLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR PLING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUBLOM
SEQ ID NO 15294
LENGTH: 4596
                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1117)...(1581)
; OTHER INFORMATION: 100% homologous to Homo sapiens sperm I; OTHER INFORMATION: number M82968, Smith-Waterman Score=809. PCT-US01-08631-15294
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larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                  Sequence 15294, Application PC/TUS0108631
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Matches 4590; Conserv
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LOCATION: (1117).
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QY 3904 GCAGGATATGCCTGACAGGAACAGTCTGTGGATGGACATGATCAGTGCTAAGGAAAGCAG 3963 Db 3905 GCAGGATATGCCTGACAGGAACAGTCTGTGGATCGACATGATCAGTGCTAAGGAAAGCAG 3964 QY 3364 CAGAGAGGACGTCCCGGCCCCCACTATCAGTGCTCCAGCTGCTGGTTCCCCAG 4023 Db 3965 CAGAGAGAGGACGTCCGGCCCCACTATCAGTGTCCAGCGTGCTGGTTCCCCAG 4024 QY 4024 AGCACAGGCTCAGCATCACACTCAACTCACCTGCCCTGC	4085 CGACGGCACTTTGCACTCTGATGACCTCAAAGCACTTTCATGGCTGCCCTCTGGCAGGGC 4144 AGGGCAGGCACTTTGCACTCTGATGACAAAGCACTTTCATGGCTGCCCTCTGGCAGGGC 4145 AGGGCAGGCAGTGACACTGTAGGAGCATAGCAAGGAGAATGGGGTGAAGGGACACA 4204 GTCTTGAGCTGTCACATGCAAGCACTCCTCAAACCTCTTCCAGATTTCTCTAAGAATA 4205 GTCTTGAGCTGTCCACATGCAATGTGACTCCTCAAACCTCTTCCAGATTTCTCTAAGAATA 4205 GTCTTGAGCTGTCCACATGCAATGTGACTCCTCAAACCTCTTCCAGATTTCTCTAAGAATA 4205 GTCTTGAGCTGTCCACATGCAATGTGACTCCTCAAACCTCTTCCAGATTTCTCTTAAGAATA	Qy 4264 GCACCCCTTCCCCATTGCCCCAGGGGAGCTACTCAGGAGCTACTCAGGACTCTCAGGACTCTCAGGACTCCTAGGACTCCTAGGACTACTCAGACTCAGACTCAGGACTACTCAGGACTACTCAGGACTACTCAGGACTACTCAGGACTACTCAGGACTACTCAGGACTACTCAGAGACTCATTCCCAAGACAGCCTTTACTAGAGACTCATTCCCAAGACAGCCTTTACTAGAGACTCATTCCCAAGACAGAC	Oy 4444 TGTCCAGCTGTCCAATTGAGTCCCCGGGGGGGGGGGGGG	RESULT 4 PCT-US02-18947-975 ; Sequence 975, Application PC/TUS0218947 ; GENERAL INFORMATION: ; APPLICANT: Rosetta Inpharmatics ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients ; TITLE REFERENCE: 9301-175-228 ; CURRENT PPLICATION NUMBER: PCT/US02/18947 ; CURRENT FILING DATE: 2002-06-14 ; PRIOR PLICATION NUMBER: 60/380,770 ; RIGR FILING DATE: 2002-05-14 ; NUMBER OF SEQ ID NOS: 2699 ; SEQ ID NO 975 ; LENGTH: 4596	TYPE: DNA ORCANISM: Homo sapiens DATABASE ACCESSION NUMBER: NM 003954 DATABASE ENTRY DATE: 2001-06-18 PCT-US02-18947-975 Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 4590; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
2824 ATACAGTCTCTTAATGGTGAACACTGCACATCCGGGAGTTCCACCGGGTCAAAGTGGGA 2883 2825 ATACAGTCTCTTAATGGTGAACACTGCACATCCGGGAGTTCCACCGGGTCAAAGTGGGA 2884 2884 GACATCGCCACTGGCATCAGCAGCCAGATCCCAGCTTCAGCTTGGTCACCAA 2943 2885 GACATCGCCACTGGCATCAGCAGCCAGATCCCAGCTGCAGCTTGGTCACCAA 2944 2944 GACGGCAGCTGGCATCAGCAGCAGATCCCAGCTGCAGCTTCAGCTTGGTCACCAA 2944 2945 GACGGCAGCTGTTCGCTACGACATGGAGGTGCCAGCTCGGGCATCGACCTGCAGTGC 3003 [3004 ACACTGGCCCCTGATGGCTTCGCCTGGAGGTCAAGCATGGCCGGGGGGGG	GAATGCC GAATGCC GAATGCC ACGTGAA ACGTGAA ACGTGAA TTCTGCC	CCTGCTCCAGTTGGCTGACCTGGTTGATCAGTGACATTGTTGGCAGACAGG CCTGCTCCAGTTGGCAGTTGGCTGGTTGATCAGTGACATTGTTGGCAGACAGG CCTGCTCCAGTTGGCTGACCCTTGGTTGTTGGCAGACAGG CCTGCTCCAGTTCGAGTTGGCTTGGC	36 37 37	3725 GGTTCAGCCAAAGAACGTGTAAGTGAAGGTGGTTCTCAGTCCCAGACATGT 3784 3784 GCCCCTTTGCTGCTACCACTCTTCCCCAGAGCCCCCGAGCCCCTTCAGGC 3843

GGGGGGACTCTGGCCGTGTGGAACGTGTAGCTGTTGA-AGGTGGACTCTGTTACCATTGAGG GGGGGGGACTCTGGCGTGTGGAACGTGTAGCTGTTGAGAGGTGCTGTTACCATTGAGG GGGGGGGACTCTGTGTGCGAACGTGTTGAGAGGTGCTGTTACCATTGAGG ATGTTTGGAGGATGAGTATGTGGCAGAGGCACACATAACAGGCAGAGACCCTTTGCC ATGTTTGGAGGATGAGTATGTGGCAGAGGCACACATAACAGGCAGAGACCCTTTGCC ATGTTTGGAGGATGAGTATGTGGCAGAGGCACACATAACAGGCAGAGACCCTTTGCC ATGTTTGGAGGATGAGTATGTGGCAGAGGCACACATAACAGGCAGAGACCCTTTGAGT CCTGCCTTTCTCCCCCAACCCCAACGCAGAGACCCTTGAGAGACCCTTTAACT CCTGCCTTTCTCCCCCAACCCCAACACCCAACACCCAACACCCAACACCCAACAC	0.00000000000000000000000000000000000
724 CTCCCAGGACCCCTGAGCAGGAGGCTGCCAGTGCAGGAGGATGAGTCTCCA 783 725 CTCCCCAGGACCCCTGAGCAGGAGGATGCACCCCA 784 784 CTCGCGGACCCCTGAGGAGGAGCTGCACCTCCCAGGAGGATGAGTCTCCA 784 785 CTCGCGCCCCATATGTTAGAAACACCCCCGCAGTTCACCAAGCCTCTGAAGGATCACCG 843 785 CTCGGCGCCCCATATGTTAGAAACACCCCCGCAGTTCACCAAGCCTCTGAAGGAACCAGGC 844 844 CTTGGGCAACTCTGTTTTAGACAGCTTGGCGGGCCTCTGCCTCGATCA 903 845 CTTGGGCAACTCTGTTTTAAGCAGCTTGGCGGGCCTCTGCCTGATCA 904 846 CTTGGGCAACTCTGTTTTTAAGCAGCTTGGCGGGGCCTAGCCTGCTCGATCA 904 847 CTTGGGCAACTCTGTTTTTAAGCAGCTTGGCGGGCCTCTGCTGCTCGATCA 904 848 CTTGGGCAACTCTGTTTTTAAGCAGCTTGGCGGGGCCTCTGCTGGCTCGATCA 904 849 CTTGGGCAACTCTGTTTTTAAGCAGCTTGCCAGGCCTGCTGGAAACTGCCTCCAACCTGATCAGAACTGCACCAC 963 849 CTTGGGCAACTCTGTTTTTAAGCAGCCCTTGCAAGCTGGCTCTGAACTGCCTCTGAACTGCCTCTGAACTGCACCACCACCACGCACCCCTTCCCCTATAGCAGAACTGCCCTCTGAGAACTGCCTTCCTGTTAGCAGACTGCCTTCCTGTTAGCAGACTGCCTTCCTGTTAGCAGACTGCCTTCCTGTTAGCAGACTGCCTTCCTGTTAGCAGACTGCCTTCCCTTTCCTTGTTAGCAGACTTCCTTTCTTT	

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QY 1504 CAGTGCGCTGTCAAAAGGTGCGCCTGGAAGTATTTCGGGCAGAGGAGCTGATGGCATGT 1563 Db 1505 CAGTGCGCTGTCAAAAAGGTGCGGCTGGAAGTATTTCGGGCAGAGGAGCTGATGGCCATGT 1564	QY 1564 GCAGGATTGACCTCACCAGAATTGTCCCTTTGTATGGAGCTGTGAGAAGACGCCTTGG 162. Db 1565 GCAGGATTGACCTCACCAGAATTGTCCCTTTGTATGGAGCTGTGAGAGAGA	QY 1624 GTCAACATCTTCATGGAGCTGCTGGAAGGTGGCTCCTGGGCCAGCTGGTCAAGGAGCAG 168	Oy 1684 GGCTGTCTCCCAGAGGCCCCGTACTACCTGGGCCAGGCCCTGGAGGCTCTGGAA 1743	OY 1744 TACCTCCACTCACGAAGGATTCTGCATGGGGACGTCAAAGCTGACAACGTGCTCCTGTCC 1803 Db 1745 TACCTCCACTCACGAAGGATTCTGCATGGGGACGTCAAAGCTGACAACGTGCTCCTGTCC 1804	OY 1804 AGCGAFGGGAGCCACGCACCCTCTGFGACTTTGGCCATGCTGTGTGTCTTCAACCTGAT 1863 1805 AGCGAFGGGAGCCACGCAGCCCTCTGFGACTTTGGCCATGCTGTGTCTTCAACCTGAT 1864	Qy 1864 GGCCTGGGAAAGTCCTTGCTCACAGGGACTACATCCCTGGCACAGAGACCCCACATGGCT 1923 Db 1865 GGCCTGGGAAAGTCCTTGCTCACAGGGGACTACATCCCTGGCACAGAGACCCACATGGCT 1924	OY 1924 CCGGAGGTGGTGCTGGGCAGGCGCGAGGTGGTGTCTGGAGCAGCTGCTGT 1983	OY 1984 ATGATGCTGCACATGCTCAACGCTGCCACCCCTGGACTCAGTTCTTCCGAGGGCCGCTC 2043	OY 2044 TGCCTCAAGATTGCCAGCGAGCCTCCGCCTGTGAGGGAGATCCCACCTCCTGCGCCCCT 2103	Oy 2104 CTCACAGCCCAGGCCATCCAAGAGGGCTGAGGAAAGAGCCCATCCACCGCGTGTCTGCA 2163 Db 2105 CTCACAGGCCATCCAAGAGGGGCTGAGGAAAGAGCCCATCCACCGGGTGTCTGCA 2164	Qy 2164 GCGGAGCTGGGAGGGAAGGTGAACCGGCACTACAGCAAGTGGGAGGTCTGAAGAGCCT 2223	Qy 2224 TGGAGGGGAGAATATAAAGAACCAAGACATCCACCGCCAAATCAAGCCAATTACCACCG 2283	Qy 2284 ACCTCCATGCCGAGAGAGCTTTCGCCAAGGGCCCCAGGGCCCGGCCAGCTGAG 2343	Qy 2344 GAGACAGCAGAGCCCCTAAGCTCCAGCCTCCTCTCCCCCCAGAGCCCCCAGAGCCA 2403	Qy 2404 AACAAGTCTCCTTGACTTTGAGGAGGAGGAGTCTGGGATGTGGGAACCCTTACCT 2463	CTGTCCTCCCTGGAGCCAGCCCTGCCAGAAACCCCAGCTCACCAGAGCAAAGCAACC	Qy 2524 GTCCCGGAGCAGGAACTGCAGCAGCAGAATATTCCTCAACAGCCTGTCCCAG 2583
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17.1	RESULT 8 US-09-981-397A-17 ; Sequence 17, Application US/09981397A ; GENERAL INFORMATION: ; APPLICANT: Axxima Pharmaceuticals AG ; APPLICANT: Schubart, Daniel ; APPLICANT: Habenberger, Peter ; APPLICANT: Stein-Gerlach, Matthias ; APPLICANT: Bevec, Dorian
284 CONTITIONAGAGAGAGAGAAATACTATACTAGAGCATCAGAGACCTCTC 2644 284 CTGTCGGATGAACAACAACAAAAAACACCAAACAAACAACCATCAAAACACCTCTCC 2644 284 CTGTCGGATGAACACTCAAAAAACACCAAACAAACACCAAACAACAACCTCCCGGAACACCCTC 2704 2704 AACTCAGAGCATCAACTCCTGGAACAACAACCCCTCAAAACACTCCCGGGAACACCCTC 2704 2705 AGCTCAGAGCATCAACTCCTGGAACAACAACCCCTCAAAACACCCCCGGAACACCCTCGAACACCTCCAAACACCACCAACACAACACCAAACACCAAACACCAAAA	3544 GGTCAGCAGGTATGCCCGCCCGTAAGGGGGCCCTCTTAAACCCCTTGCCTGGCCTC 3603

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APPLICANT: Dai, Hongyue
APPLICANT: Linaley, Peter
APPLICANT: Linaley, Peter
APPLICANT: Moberts, Chris
APPLICANT: Won 't Veer, Laura
APPLICANT: Van 't Veer, Laura
APPLICANT: Van 'd Very, Marc
APPLICANT: Bernards, Rene
ITILE OF INVENTION: Diagnosis and Prognosis of
FILE REPERENCE: 3010-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 975
LENGTH: 4556
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Matches 4590; Conservative
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PUBLICATION INFORMATION
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	RESULT 10 US-10-283-975A-294 i Sequence 294, Application US/10283975A j GENERAL INFORMATION: APPLICANT: Ortho-Clinical Diagnostics, Inc. TITLE OF INVENTION: Methods For Assessing and Treating Leukemia FITLE OF INVENTION: Whethods For Assessing and Treating Leukemia FITLE REPRENCE: CDS 293 PCT. CURRENT APPLICATION NUMBER: US/10/283,975A CURRENT FILING DATE: 2002-10-30 PRIOR PELIGATION NUMBER: 60/340,938 PRIOR PPLICATION NUMBER: 60/340,081 PRIOR PILING DATE: 2001-10-30 PRIOR PELIGATION NUMBER: 60/340,081 PRIOR PELIGATION NUMBER: 60/341,012 PRIOR PELIGATION NUMBER: 60/341,012 PRIOR FILING DATE: 2001-10-30 NUMBER OF SEQ ID NOS: 900 SOFTWARE: ParentIn version 3.1 SEQ ID NO 294 LENGTH: 4596 TYPE: DNA CREANIEM: HUMAN CREANIEM: HUMAN	ZMO ZMO C R K R K R K R K R K R K R K R K R K R
3364 CCTGCTCCAGTCGAGTTGGCCTGCATCCGCTTGGATCAGTGACCATTTGTTGGCAGACAGG		3904 GCAGGATATGCCTGACAGGAACATCTTGTGATGACATGATCAGTGCTAAGGAAAGCGG 3963 3905 GCAGGATATGCCTGACAGAACATCATTGAGACATGATCAGTGCTAAGGAAAGCGG 3964 3906 GCAGGATATGCCTGCAGGACCACATGATGACATGATCATAGGAAAGCGG 3964 3965 CAGAAGAACATCCTGCGCCCCCACTATCAGTGTCCAGCTTCCCCCG 4023 3965 CAGAAGAACATCACTGACCTCACCTCACTCTCCCTGCCCTGCTCTCCCCGG 4024 4026 CAGAAGACACTCACCTCACTCACTCACCTGCCCTGCCCT

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CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-06-14
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2404 AACAAGTCTCCTTGACTTTGAGCAAGGAGTCTGGGATGTGGGAACCCTTACCT 2463 	2464 CTGTCCTCCTGGAGCCAGCCTGCCAGAAACCCCAGCTCACCAGAGCGGAAAGCAACC 2523	2524 GTCCCGGAGCAGGAACTGCAGCAGCTGGAAATAGAATTATTCCTCAACAGCCTGTCCCAG 258:	2584 CCATTTCTCTGGAGGAGCAGGAAATTCTCTCGTGCCTCAGCATCGACAGCCTCTC 2643	2644 CTGTCGGATGACAGTGAGAAGAACCCATCAAAGGCCTCTCAAAGCTGGGGGACACCCTG 2703 2645 CTGTCGGATGACAGAGAACACATCAAAGGCCTCTCAAAGCTCGCGGGACACCCTG 2704	2704 AGCTCAGGCGTACACTCCTGGAGCCAGGCCGAGGCTCGAAGCTCCAGCTGGAACATG 2763 2705 AGCTCAGGCGTACACTCCTGGAGCAGCCAGGCCGAGGCTCGAAGCTCCAGCTGGAACATG 2764	2764 GTGCTGGCCGGGGGCCCCACCGACACCCCAAGCTATTCAATGGTGTGAAAGTCCAA 282: 2765 GTGCTGGCCCGGGGGCGCCCCCCCCAACCCCAAGCTATTTCAATGGTGTGAAAGTCCAA 282:	2824 ATACAGTCTTTAATGGTGAACACCTGCACATCCGGGAGTTCCACCGGGTCAAAGTGGGA 288:	2884 GACATCGCCACTGGCATCAGCAGATCCCAGCTGCAGCCTTCAGCTTGGTCACCAAA 2943	2944 GACGGGCAGCCTGTTCGCTACGACATGGAGGTGCCAGACTCGGGCATCGACTGCAGTGC 3003	3004	3064 AACAGGCCTAACCCTGCCCTCCACGGCTCCACACTGCGGGAAAGCAGCCTTCCTG 3123 1065 AACAGGCCCTAACCCTGCCCTCCACCGCTCCACACACGGAAAGCAGCCTTCCTG 3124	3124 CTCGGTGCACGATGCTGCCCTGAAAACACACGCTCAGCCGTTCCCAGGGGATTGCCAGCC 3183	3184 C	3244 TCCCAGGATTTCACCTGAGCCCTGCCCCCCTGCTGAAAAAACATCCGCCACGTGAA 3303 3245 TCCCAGGATTTCACACCTGACCCTGCCCACCTGCTGAAAAAACATCCGCCACGTGAA 3304	3304 GAGACAGAAGGAGGATGGCAGGAGTTACCTGGGGAACAAACA	3364 CCTGCTCCAGTCGAGTTGGCCTGACCCGCTTGGATCAGTGACCATTTGTTGGCAGACAGG 3423	3424 GGAGAGCAGCTTCCAGCCTGGGTCAGAAGGGGTGGGCGAGCCCTTCGGCCCCTCACCTC 3483 1425 GGAGAGCAGCTTCCAGCTGGGTCAGAAGGGGTGGGCGAGCCTTCGGCCCTCACCCTC 3484 1484 CAGGTGTGTGAGATGTGAAGTGTGTAAGGCCCAAACTCAGGTTCAGTGCAGAACCA 3543	
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                                                                 Sequence 1291, Application US/09949003C
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GEN
TITLE OF INVENTION: DISORDERS, METHODS OF DET
FILE REPRERECE: CLOO0791
CURRENT APPLICATION NUMBER: US/09/949,003C
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION UNMBER: 60/231,446
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 74065
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Pred. No. 0;
0; Mismatches
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AGADAACGGAAGAAGAAGCTCAAAGTCCCTGGCTCATGCAGGAGTGGCCTTGGCCAAAC CCCTCCCCAGGACCCCTGGAGAGAGCTGCACCATCCCAGGAGGATGAGCTCTC CCTCCCCAGGACCCCTGAGAGAGAGCTGCACCATCCCAGTGCAGGAGGATGAGTCTC CCCTCCCCAGGACCCCTGAGAGAGAGCTGCACCATCCCAGTGCAGGAGAATGATCTC CACTCGGCGCCCCATATGTTAGAAACACCCCGCAGTTCACCAAGCCTCTGAAGGAACCAG [843 GCCTTGGGCAACTCTGTTTTAAGCAGCTTGGCAAGGCCTACGGCCGCTCTGGTT 902	TGGGCAAACTGGCCTGTGTAGACAGAGAACCCTTGCCTGACCCACCTGGCCAACTGGCCAAACTGGCCAAACTGGCCAAACTGGCCAAACTGGCCAAACTGGCCAAACTGGCCAAACTGGCCAAACCCTGGCCAACCTGAGCAAACTGGCCTGAGCCAACCTGAGCCAACTGAGCCAAACTGGCCTGGCCTGAGCCAACTGAAACCCTGAGCCCAACCTGGAGCCCAACTGGAGCCCTGTGTAAAACCCTGAAACCTGCTGGCCCACCTGGAGCCCAACTGTGAAAACCCTGCTGCCTGGCCCAACTGGAGCCCAAGAGCCTGTGCCTGTGCAAAGCCCTGGCCTGGCCCAACTGGAAACCCTGGCAACTGAAACCCTGGCAAGAGCCAACTGGAAAGCCCAAGAGAAAACCCTGGCAACAACTGAAAACCCTGGCAAAACCCTGGCAACACTGAAACCCTGAAAACCCTGGCAACACTGAAACCCTGAAAACCCTGGCAAACCCTAGAAAACCCTAGAAAACCCTAGCAAACTTTTCTGTGGAAAAACCCAAGCCAACTGAAACCCTAGAAAACTTTTCTGTGGAAAAACCCAACTAGAAACCCAACTGAAACCCTAGAAACCCTAGAAAACCCTAGAAAAACCCTAGAAAACCCAACTAGAAAACCCTAGAAAACCCTAGAAAAACCCTAGAAAACCCTAGAAAAACCTAAAAAAAA	1262 GCGTGAGCTCAAGCCCACAGGAAGTTTTCTGTGGAAGGAA	TCCGCCGGGCGGGGGGCGCCTCGGGGGGGGGGGGGGGG	1563 GYGCAGGATTGACCTCACCCAGAATTGTCCCTTTGTATGGAGCTGTGAGAGAGA

1142 TGGCCTGTGTAGACAGTCCAAAGCCCTGGCCGCCACCTGGAGCCCAGCTGCCTGT 1201	2 GCTCCAGATCCCGGAGCCCAGCCCCAAACTGAGGACAACGGGGGGTGTCCTGCTGATGGGGGGTGTCCTGCTGATGGGGGAGACCCGGGGGGGG	12 TCCGCCTGGGCAGAGGCTCCTTCGGAGAGGTGCACAGGATGGAGGACAAGCAGACTGGCT 1	1562 GTGCAGGATTGACCTCACCCAGAATTGTCCCTTTGTATGGAGCTGTGAGGAGGAGGGCCTT 1621	1682 AGGGCTGTCTCCCGAGGACCGGGCCCTGTACTACCTGGGCCGGGCCCTGGAGGTCTGG 1741	1802 CCAGCGATGGGAGCCAGCAGCCCTGTGACTTTGGCCATGCTGTGTCTTCAACCTG 1861	1922 CTCCGGAGGTGGTGCTGGGAGCTGCGAGGTGGATGTCTGGAGCAGCTGCT 1981	2042 TCTGCCTCAAGATTGCCAGCGAGCCTCCGCCTGTGAGGAGATCCCACCTCCTGCGCCC 2101 2093 TCTGCCTCAAGATTGCCAGCGAGCCTCCGCCTGTGAGGAGATCCCACCCTCCTGCGCCC 2152 2102 CTCTCACAGCCACGCCATCCAAGAGGCCTGAGGAAAAGAGCCCATCCACCGCGTGTCTG 2161 2153 CTCTCACAGCCCAGGCCATCCAAGAGGGCTGAAAGAGCCCATCCACCGCGTGTTG 2212 2162 CAGCGGAGCTGCAGGCACTCAAGAGGGCACATCCACCGCGTGTTG 2212 2162 CAGCGGAGCTGCAGGCAACAGAGAGAAAGAGCCCATCCACCGCGTGTTG 2212 2163 CAGCGGAGCTGGAGGGAAGGTGAACCGGCACTACAGCAGTGGGAGGTCTGAAGAGCC 2221 21513 CAGCGGAGCTGGGGAAGGTGAACCGGGCACTACAGCAAGTGGGAAGGTCTGAAGAGCC 2272 2113 CAGCGGAAGCTGGAAAGGTGAACCGGGCACTACAGCAAGTGGGAAGGTCTGAAGAGCC 2272
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53 CCGGGGACTGTGCCGTGTGCAACGTGTAGCTGTTGAGAGGTGGACTCTGTTACCATTGA 112 62 GGATGTTTGGAGGATGAGTATGTGTGGCAGAGGCACATAAACAGGCAGAGACCCTTTG 121 113 GGATGTTTGGAGGATGAGTATGTGTGGCAGAGGCACATAAACAGGCAGAGACCCTTTG 172 122 CCCCTGCCTTTGTAGAGATGTGGCCAAGGCAGACATAAACAGGCAGAGACCCTTTG 172 123 CCCCTGCCTTTCTCCCCCAAGGCTGACCTGTGTTCTCCCAGGTTCTAA 181 113 CCCCTGCCTTTCTCCCCCAAGGCTGACCTGTGTTCTCCCAGGTTCTAA 232 114 CCCTGCCTTTCTCCCCCAAGGCTGACCTGTGTTTCTCCCAGGTTCTAA 232 115 CTGACCTGCTTTTGGTCTCTCTCTAGGAGTGCTGGGAGATTCTAA 232 116 GTGACCTGCTTTTGGTCTCTCTCAGGATGAGCTGGGAGATGCTAG 241 116 HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	233 GYGACCYGCTCTGTGTTTTGGTCTCTCAGGATGAGCACAAGCCTGGGAGATGCCAGTGA 292 242 TGGAAATGGCCTGCCCGGGTGCCCCTGGCTGGGGAGGAGATGCCAGTGA 291 293 TGGAAATGGCCTGCCCGGGTGCCCCTGGCTGGGGGCAGCAGGAGGAACTCCCCA 301 293 TGGAAATGGCCTGCCCGGGTGCCCCTGGCTCAGCGGGCAGCAGGAACTCCCCA 352 302 AGCCAAAGGAAAAAGGGCCGCCCTGGGGAAAAAAAAAGGGAGCTCGCTACAAGCTTGAGG 361 22 AGCCAAAGGAAAAAAAGAGAAAAAAAAAAAAAAAAAA	CCGTGGAGAAGAGCCTGTGTTCTGCGAAAGTGGGGAGATCCTGAATGACGTGATCCTGAATGACGTGATCCTGAATGACGTGATCCTGAATGACGTGATCCTGAATGACGTGATCCTGAATGACGTGATCCTGAATGACGTGATCCTGAATGACGTGATATCTGTGAATGATCCTGAATGATCCTGAATGACGTGCAAGGAAGG	482 CTGAGTGTGAGAATAGCCAAGAGTTCAGCCCCACCTTTTCAGAACGCATTTTCATCGCTG 541	CTACAGAGGGCAAAATGGCCCGTGTGTGGAAGGGAAAGGGTCGCAGCAAAGCCCGGA 6 CTACAGAGGGCAAAATGGCCCGTGTGTTGGAAGGGAAAGGGTCGCAGCAAAGCCCGGA 6 CTACAGAGGGCAAAATGGCCCGTGTTTGGAAGGGAAAGGGTCGCAGAAAGCCCGGA 7 AGAAACGGAAGAAGAAGACCTCAAAGTCCCTGGCTCATGCCAGAGTGGCCTTGGCCAAAC 7 AGAAACGGAAGAAGAAGAATGAAAGAAAGAAAGAAAAGA	CCTCCCCAGACCCCTGAGCAGAGAGCTGCACCATCCCAGTGCAGAGCAGAGAGATGAGCTTC	833 CACTCGGCGCCCCATAIGTTAGAAACACCCCGCAGTTCACCAAGCCTCTGAAGGAACCAG 892	ACCCCCAGGACGGACCCCTGCCCTGCCCTTCCCTTTAGGACTGC 102

Db 593 Oy 602 Oy 662 Oy 713 Oy 782 Oy 782 Oy 842 Oy 843 Oy 902 Ob 953 Oy 962 Ob 1013	10.000 1
Db 4425 TGGGGCAGGCAGCACCGAGACTCCGGGGAGAGCTCCATTTCCCACATTTCCCAAGACAC 4484	Query Match 96.64; Score 4440; DB 49; Length 4684; Best Local Similarity 99.14; Pred. No. 0; 0;<

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Sequence 6, Application US/09155676B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-09-155-676B-6
                                                                                                                                                               June 10, 2005, 09:44:05; Search time 1758.13 Seconds (without alignments) 11471.453 Million cell updates/sec
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Sequence 6, Appli Sequence 15294, A Sequence 566, App Sequence 3, Appli Sequence 12129, A Sequence 12129, A Sequence 1229, A Sequence 560, App Sequence 32424, A Sequence 32424, A Sequence 15296, A Sequence 10785, A Sequence 10785, A Sequence 10785, A Sequence 11056, A Sequence 7882, Ap Description US-60-680-544-10785 US-60-680-544-11056 US-60-680-473-110785 US-60-680-473-11056 US-60-659-397-7882 US-60-659-397-7883 US-11-060-756-560 US-11-060-756-4832 US-60-680-544-32424 US-60-680-473-32424 US-10-450-763-15296 US-09-155-676B-3 US-60-659-397-12129 US-10-450-763-15295 4596 4684 4458 2631 65967 2760 1400 3658 3658 722 761 761 761 761 201 1474.4 1345.6 1345.6 676.2 676.2 627.6 440.6 440.6 200.6 200.6 4243.2 440.4

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Sequence 7885, Ap	Sequence 7886, Ap	Seguence 7887, Ap	Sequence 7888, Ap	7889,	7891,	7892,		Sequence 32722, A		Sequence 32758, A	Sequence 7884, Ap		Sequence 32757, A		Sequence 813, App	Sequence 32755, A	Sequence 37753, A	Seguence 37753, A	Seguence 32710, A	Seguence 5071, Ap	Sequence 32726, A	Sequence 9, Appli		Sequence 7876, Ap	Sequence 7875, Ap	15297,
S US-60-659-397-7885	S US-60-659-397-7886	3 US-60-659-397-7887	S US-60-659-397-7888	S US-60-659-397-7889	S US-60-659-397-7891	S US-60-659-397-7892	S US-60-659-397-7893	S US-60-659-397-32722	S US-60-659-397-32724	S US-60-659-397-32758	S US-60-659-397-7884	S US-60-659-397-7890	S US-60-659-397-32757	S US-60-659-397-32751	PCT-US05-00517-813	. US-60-659-397-32755	S US-60-680-544-37753	3 US-60-680-473-37753	. US-60-659-397-32710	US-10-940-774A-5071	: US-60-659-397-32726	US-09-608-890A-9	. US-60-659-397-32752	US-10-972-079-7876	US-10-972-079-7875	US-10-450-763-15297
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4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	3.3	3.3	3.3	3.3	3.0	2.8	5.6	5.6	2.1	1.9	1.9	1.8	1.7	1.7	1.6	1.5
200.6	200.6	200.6	200.6	200.6	200.6	200.6	200.6	200.6	200.6	200.6	153.2	153.2	153.2	150	136.8	128.6	119.2	119.2	98	88.8	88	83.8	78	78	75.2	70
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ALIGNMENTS

APPLICANT: MALININ, Nikolai
APPLICANT: BOLDIN, Mark
APPLICANT: KOVALENKO, Andrei
APPLICANT: METT, Igor
TITLE OF INVENTION: MODULATORS OF THE RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR AGGATGTTTGGAGGATGAGTATGTGTGGCAGAGGCACATAAACAGGCAGAGACCCTTT 120 61 AGGATGTTTGGAGGATGAGTATGTGTGGCAGAGGCCACATAAACAGGCAGAGACCCTTT 120 121 GCCCCTGCCTTTCTCCCCCAACCCAAGGCTGACCTGTGTTCTCCCAGGTCTGGGATTCTA 180 8 1 AGCGGGGGGACTGTGCGTGTGGAACGTGTAGCTGTTGAAGGTGGACTCTGTTACCATTG 60 1 AGCGGGGGGACTGTGCCGTGTGGAACGTGTAGCTGTTGAAGGTGGACTCTGTTACCATTG Gaps ö Length 4596; Indela DB 6; i; Score 4596; Ii; Pred. No. 0;0; Mismatches TILE REFERENCE: WALLACH-21
CURRENT APPLICATION NUMBER: US/09/155,676B
CURRENT FILING DATE: 1999-01-04
FRIOR APPLICATION NUMBER: PCT/IL97/00117
PRIOR FILING DATE: 1997-04-01
PRIOR FILING DATE: 1996-04-02
PRIOR APPLICATION NUMBER: IL 119133
PRIOR FILING DATE: 1996-04-02
FRIOR PILING DATE: 1996-08-26
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.3
SEQ ID NO 6 100.0%; llarity 100.0%; Conservative 0 ORGANISM: Homo sapiens Query Match Best Local Similarity Matches 4596; Conserv LENGTH: 4596 US-09-155-676B-6 61

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CAGCCATTTTCTCTGGAGGAGCAGAGCAAATTCTCTGGGCCTCAGCATCGACCGCCCCCCCC	장 <u>염</u>	3661 GCTCCCTGGTAGAATACACCACACTTTCAGGTTGTTGCAACACAGGTCCTGAGTTGACC 3720
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GARGACATCCCCACTGGCATCAGCCCCACTGCCCGCGCACTTCCCCCCCC	상 염	3961 CAGCAGAGAGACGTCCGGCGCCCCAGCCCCACTATCAGTGTCCAGCGTGCTGGTTCCC 4020
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GAGAACAGGCCCTACCCTGCCCTCCACCGGCTCCACCTGCAGGTCAGGCAGG	상 염	4141 GGCAGGGCAGGCAGTGACACTGTAGGAGCATAGCAAGACAGGGAGATGGGGTGAAGGGAC 4200
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	SCCADADATGGCCCGTGTGTGGTGGAGGGAAAGCGTCGCAGCAAAGCCCGGAAAGCGTCGCAGCAAAATGGCCCCGGAAAATGGCCCGGAAAATGGCCCGGAAAATGGCCCGGGAAAGCGTCGCAGCAAAATGGCCCGGGAAAGCGTCGCAGCCTTGGCCCAAACCAGAAAAAAGCGTCGAGAGCGTCGGAGCCTTGGCCCAAACCAGAGAGAG		4 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	05 CGTGGTGCCCATGAGAAGTTTTCTGTGGAGAATACCTAGTGCATGCTCTGCAAGGCAGC 12 64 GTGAGCTCAAGGCCCACAGGCCTGACGCTGGCCAAGACCTGGCAGCAGCAGC 12 65 GTGAGCTCAAGCCAGGCCCACAGCCTGACCTGGCCAAGACCTGGGCAGCAGGGC 13 65 GTGAGCTCAAGCCAGGCCCACAGCCTGACCAGGCCAAGACCTGGGCAGCAGGGGG 13 24 TCCACATCCCGGGAGCCCAAAACTGAGGACAACGAGGGTGTCCTGCTCACTGAG 13 25 TCCAGATCCCGGGAGCCCCAAAACTGAGGACAACGAGGGTGTCCTGCTCACTGAG 13 26 TCCAGATCCCGGGAGCCCCAAAACTGAGGACAAACGAGGGTGTCCTGCTCACTGAG 13 27 TCCAGATCCCGGGAGCCCCAAAACTGAGGACAAACGAGGGTGTCCTGCTCACTGAG 13	1384 AMACTCAAGCCAGTGGATTATTAGGTACCGAGAGCAGCAGCACCAGCCCCAGCTCGAGTCATGGGCCAGCCCCAGCTCGAGTCATGGGCCAGCCCAGCTCGAGTCATGGGCCAGCCCAGCTCGAGTCATGGGCCAGCCCAGCTCGAGTGGAGAGAAGAAGTCCACTGGGCCAGCCCAGCTCCTCGGGAGAGAGA
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	RESULT 2 US-10-450-763-15294 Sequence 15294, Application US/10450763 Sequence 15294, Application US/10450763 Sequence 15294, Application US/10450763 GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES FILE REFERENCE: 790CIP3/US CURRENT APPLICATION NUMBER: US/10/450,763 CURRENT FILING DATE: 2003-06-11 PRIOR FILING DATE: 2001-03-31 PRIOR FILING DATE: 2001-03-31 PRIOR PILING DATE: 2000-03-31 PRIOR PILING DATE: 2000-03-31 PRIOR FILING DATE: 2000-03-31 PRIOR FILING DATE: 2000-03-31 PRIOR FILING DATE: 2000-03-31 PRIOR FILING DATE: 2000-03-31 NUMBER OF SEQ ID NOS: 60736	; SOFTWARE: CUSTOM ; SEQ ID NO 15294 ; LENGTH: 4596 ; TYPE: DNA ; GRANISM: Homo sapiens ; FEATURE: ; NAME/KEX: SIMILAR ; OTHER INFORMATION: 100% homologous to Homo sapiens sperm protein 10, accession ; OTHER INFORMATION: number M82968, Smith-Waterman Score=809. US-10-450-763-15294 ; Query Match 99.6%; Score 4578.4; DB 8; Length 4596;	Matches 4590; Conservative 0; Mismatches 1; Indels 1; Gaps 5 GGGGGACTGTGCCGTGTGCACGTGTAGCTGTTGA-AGGTGGACTCTGTTACCATTGAGG 63	Qy 124 CCTGCCTTTCTCCCCCAAGGCTGACCTGTGTTCTCCCAGGTTCTGGGATTCTAAGT 183 Db 125 CCTGCCTTTCTCCCCAAGGCTGACCTGTGTTCTCCCAGGTTCTAAGT 184 Qy 184 GACCTGCTTTTGTCTCTCTCAGGATGACACAGGCAGATGAGTTGTAGT 184 Db 185 GACCTGCTCTGTTTTTGTTCTCTCTCAGGATGACACAAGCCTGGAGATGAGTGTTGTTTTTTTT	AGGCC AGGCC CCAAG CCAAG CCAAG AGGCT AGGCT CTGGG

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                                                                                               Length 4684;
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                                                                                           Score 4437.6;
Pred. No. 0;
6; Mismatches
                                                                                             96.6%;
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LENGTH: 4684
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                             Query Match
Best Local Similarity
    ; LENGTH: 4684
; TYPE: DNA
; ORGANISM: HOMO
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GENERAL INFORMATION:
APPLICAMT: CARGILL, Michele
APPLICAMT: CARGILL, Michele
APPLICAMT: CHANG, Sheng-Yung
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
TITLE OF INVENTION: THEREOF
FILE REFREENCE: CLOUA 470
CURRENT APPLICATION NUMBER: US/60/659,397
CURRENT FILING DATE: 2005-03-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FastSEQ for Windows Version 4.0
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	2282 AGACCTCCATGCCCAGCGAAGAGCTTTCGCCAAGGCCCCAGGGCCCCGGCCAGCTG 2341	2402 CAAACAAGTCTCCTCCCTTGACTTTGAGGAGGAGTCTGGGATGTGGGAACCCTTAC 2461	2522 CCGTCCCGGAGCAGGAACTGCAGCTGGAAATAGAATTATTCCTCAACAGCTGTCCC 2581	2642 CCCTGTCGGATGACAGTGAGAACCCATCAAAGGCCTCTCAAAGCTCGCGGACACCC 2701 2693 CCCTGTCGGATGACAGTGAGAACCCATCAAAGGCCTCTCAAAGCTCGCGGGACACCC 2752 2702 TGAGCTCAGGGTTACACTCCAGGCAGCCGGGGGGCTCCAGAGCTCCAGGCGGAACA 2761 2703 TGAGCTCAGGCGTACACTCCTGGAGCAGCCAGGCCGAGGCTCGAAGCTCCAGCTGGAACA 2761 2753 TGAGCTCAGGCGTACACTCCTGGAGCAGCCAGGCCGAGGCTCCAAGCTCCAGCTGGAACA 2812	TGGTGCTGGCCGGGGGCCCACCGACACCCCCAAGCTATTTCAATGGTGTGAAAGTCC	GAGACATCGCCACTGGCATCAGCAGCTGCCAGCTGCCAGCTTCCACCGGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCACCAGCTGCAGCTGCAGCTGCAGCTGCACCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTTGATTAGATCAGATCGCAGCTGCAGCTTCAGCTTGGTSACCAAAAGACGGCAGCTGCAGCTTGGAGTGCCAGGCTGCAGCTTGATTGA	2993 AAGACGGGCAGCCTGTTCGCTACGACATGGAGGTGCCAGCATCGGGCATCGACCTGCAGT 3052 3002 GCACACTGGCCCTGATGGCAGCTTCGCCTGGAGCTGGAGGTCAAGCATGGCCAGCTGG 3061	3062 AGAACAGGCCCTAACCTGCCCCCCCCCCCCCCCCCCCCC
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QY 4260 AATAGCACCCCCTTCCCCATTGCCCCAGGCTTAGCCTCTTCCCCAGGGAGCTACTCAGG 4319 Db 4305 AATAGCACCCCCTTCCCCATTGCCCCAGCTTAGCCTCTTCTCCCCAGGGGAGCTACTCAGG 4364 QY 4320 ACTCACGTAGATTAAATCAGCTGTAGACTCTCCCCAGGGGAGCTACCTCCAGGGGAGCTACTCCCAGGGGGGGTACTCACTC	1850LT 4 1856LT 4 1856C59-397-567 1856C69-397-667 1856C69-397-667 1856C69-397-667 1856C69-397-667 1856C69-397-667 1856C69-397-667 1856C69-397-667 1871LE 0F INVENTION: RESPONSE TO INVESTERON TREATMENT IN HERATITIS C TITLE OF INVENTION: RESPONSE TO INVESTERON TREATMENT IN HERATITIS C TITLE OF INVENTION: THEREOF SUBJECTS, METHODS OF DETECTION AND USES TITLE OF INVENTION: THEREOF SUBJECTS, METHODS OF DETECTION AND USES TITLE OF INVENTION: THEREOF SUBJECTS, METHODS OF DETECTION AND USES TITLE OF INVENTION: THEREOF SUBJECTS, METHODS OF DETECTION AND USES TITLE OF INVENTION: THEREOF SUBJECTS, METHODS OF DETECTION AND USES TITLE OF INVENTION: THEREOF SUBJECTS, METHODS OF DETECTION AND USES TITLE OF INVENTION: THEREOF SUBJECTS, METHODS OF DETECTION AND USES TITLE OF INVENTION: THEREOF SUBJECTS SUBJECTS AND THE SUBJECTS SUBJECTS SUBJECTS AND THE SUBJECTS SUBJECTS SUBJECTS AND THE SUBJECTS S
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1634 TCATGGAGCTGCTGGACCCTGGGCCAGCTGGTCAAGGAGCAGGGCTGTCTCC 1693 1509 TCATGGAGCTGTTCTCCTGGGCCAGCTGGTCTGTCTTCC 1509 TCATGGAGCTGCTGTATCTCCTGGGCCCAGGCTGTGTTCTCC 1568 1694 CAGAGGACTGTGTACTACTGGGCCCTGGAGGGTCTGGAATACCTCCACT 1753 111	1814 GCCACGCAGCCTCTGTGACTTTGGCCATGCTGTGTGTCTTCAACCTGATGGCCTGGGAA 1689 GCCACGCAGCCTCTGTGACTTTGGCCATGCTGTGTCTTCAACCTGATGGCCTGGGAA 1874 AGTCCTTGCTCACAGGGACTACATCCCTGGCACAGAGACCCACATGGCTCGGAGAGTG 1749 AGTCCTTGCTCACAGGGACTACATCCCTGGCACAGAGACCCACATGGCTCCGGAGGTGG 1749 AGTCCTTGCTCACAGGGACTACATCCCTGGCACAGAGACCCACATGGCTCCGGAGGTGG 1934 TGCTGGGCAGGAGCTGCACAGGTGGATGTCTGGAGCAGCTGCTGTATGATGCTGC 1909 TGCTGGGCAGGAGCTGCAAGGTGGATGTCTGGAGCAGCTGCTGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1994 ACATGCTCAACGGCTGCCACCCCTGAATCTTCCGAGGGGCCGCTCTAGA 2053 1869 ACATGCTCAACGGCTCCTGGATTCTTCCGAGGGGCCGCTCTAGA 2053 1869 ACATGCTCAACGGCTCCCCCCTCGGATTCTTCCGAGGGCCGCTCTAGA 1928 2054 TTGCCAGCGGCTCTCCCCCTCTCGCTCCTCTCTCCCCTCTCACACCC 2113 21929 TTGCCAGCGAGCTCTGCACCCTCTCACACCCC 2114 AGGCCATCCAAGAGGAGAACAGCCCATCCACCCCTCTCACACCCC 2115 2114 AGGCCATCCAAGAGGGAAAGAGCCCATCCACCGCGTGTCTGCAGCGGAGCTGG 2173 2114 AGGCCATCCAAGAGGGGAAAGAGCCCATCCACCGCGTGTCTGCAGCGGAGCTGG 2173 2174 GAGGGAAGGTGAAAGAGCCCATCCACCGCGTGTCTGGAGGGGAGCTGG 2048 2174 GAGGGAAGGTGAACCGGGCACTACAGCAAGTGGGAGGGTCTGAAGAGGCCCTTGGAGGGGGGG 2133 2114 GAGGGAAGGTGAACCGGGCACTACAGCAAGTGGGAGGGTCTGAAGAGGCCCTTGGAGGGGGGG 2133 2114 GAGGGAAGGTGAACCGGGCACTACAGCAAGTGGGAGGGTCTGAAGAGCCCTTGGAGGGGGG 2133 2114 GAGGGAAGGTGAACCGGGCACTACAGCAAGTGGGAGGGTCTGAAGAGCCCTTGGAGGGGGG 2108 2116 1111	2234 AATATAAAGAACCAAGACCAAATCAAGCCAATTACCACCAGACCCCCCATG 2293 [2474 TGGGGCGCCCTGCCAGAACCCCAGGCGGAAAGCAACGCCCGGGGGCGAAAGCAACGCCCCGGGGGCCCCGGGGGCCCCGGGGCCCCGGGGCCCC
169 ATAGCCAGCCCCCCCCTTTTCAGAACGCATTTCATCGGGGTCCAACGGT 428	CCCCTGAGCAGGAGGCTGCACCACCCAGGAGGATGAGCTCCCCCCCC	AACTGATCAGCCCTTGCAATGTCTGAACCGCGTGGGAAACTGCACCCCCGGGACG	1154 ACAGTCCAAAGCCTTGCCTGAACCTGTGTGTGTGTGTGTG	CAAGC 1268 GGGCA 1453 GGGCA 1328 GGCTG 1513 GGCTG 1513 GGCTG 1388 ATTGA 1448 ATTGA 1448 CATCT 1633 CATCT 1633

	RESULT 5 US-09-155-676B-3 US-09-155-676B-3 i Sequence 3. Application US/09155676B j GENERAL INFORMATION: APPLICANT: WALLACH, David APPLICANT: WALLACH, Wark APPLICANT: MAIN, Mark APPLICANT: MAIN MARK APPLICANT: MOUDLATORS OF THE RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR TITLE OF INVENTION: WALLACH=2. FILE REFERENCE: WALLACH=2. FURRENT APPLICATION NUMBER: US/09/155,676B CURRENT FILING DATE: 1999-01-04 PRIOR FILING DATE: 1997-04-01 PRIOR PLICATION NUMBER: PCT/1L97/00117 PRIOR PPLICATION NUMBER: 11 117800
2114 TACATCCTGGAGCAGCCCGGGCTCGAACTCCAGCTGGAGCACTCGGCTGGAGCTGGCCC 2773 2569 TACATCCTGGAGCACCAGGCCCGGGCTCGAACTCGGAGCACTCGGACCTGGACCTGGCCC 2648 2774 GGGGGCGCCCCACCCAGCCCCAGCTCCAGCTGGACCTGGACCTGGCCTGGACCTGGCCC 2648 2814 TACATCCTGGACCACCCCCAGCTTTTTCATCGTGTGAACTCCGAACACTCGCC 2648 2814 TACATGGTGAACACTGCACACTCCAGGCTTCAACTCGCGAGCACACTGCCC 2768 2815 TACATGGTGAACACTGCAACTCCAGGCTTCAACTCGCGAGCACACTGCCC 2768 2816 TTATGGTGAACACTGCAACTCCAGGCTTCAACTCCACCTGCAGCACACTGCCC 2768 2817 TACATGGTGAACACTGCAACTCCAGGCTTCAACTCCACCTGCAGTCACACTGCCC 2768 2817 TACATGGTGAACACTGCAACTCCAGGCTTCAACTCCACCTGCAGTCACACTGCCC 2768 2818 TTATGGTGAACACTGCAACTCCAGGCTTCAACTCCACCTGCAGTCACACTGCCC 2768 2819 TTATGGTGAACACTGCAACTCCAGGCTTCAACTCCACCTGCAGTCACACTGCCC 2768 2810 TTATGGTGAACTCCACACTCCAGGCTTCAACTCCACCTGCAGTCACACTGCCC 2768 2810 TTATGGTGAACTCCACACTCCAGGCTCAACTCCACCTGCAGTCACACTGCCC 2768 2811 TACATGGTGAACTCCACACTCCAGCTTCAACTCCACCTGCAGTCACACTGCCC 2768 2811 TACATGGTGAACTCCACACTCCAGGCTCAACTCAACTCCACCTGCAGTCACACTGCCC 2768 2812 TCACCTCCCTCCACACTCCACACTTCAACTCCACCTCCACTCAACTCGCCC 2768 3813 TACATGGTGAACTCCACACTCCACACTCCACCTCCACTCCACTCACT	

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NAME/KEY: misc feature
LOCATION: (1310) ..(1310)
JTHER INFORMATION: n is a, c, g, or t
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PRIOR FILING DATE: 1996-04-02
PRIOR APPLICATION NUMBER: IL 119133
PRIOR FILING DATE: 1996-08-26
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.3
SEQ ID NO 3
LENGTH: 2631
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LOCATION: (1125)...(1125)
OTHER INFORMATION: n is a, c,
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LOCATION: (1146)...(1146)
DTHER INFORMATION: n is a, c,
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NAME/KEY: misc_feature
LOCATION: (1208)..(1208)
OTHER INFORMATION: n is a, c,
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MAME/KEY: misc feature
LOCATION: (1297)

JTHER INFORMATION: n is a, c,
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LOCATION: (1120)..(1120)
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OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
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OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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LOCATION: (1170)..(1170)
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OTHER INFORMATION: n is a,
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LOCATION: (1239) ..(1239)
OTHER INFORMATION: n is a,
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LOCATION: (1248)..(1249)
OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (1278)..(1278)
OTHER INFORMATION: n is a,
                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1534)..(1534)
OTHER INFORMATION: n is a, c, g, or t
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NAMES/KEY: misc feature
LOCATION: (1540).(1540)
OTHER INFORMATION: n is a, c, g, or
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OTHER INFORMATION: n is a, c, g, or
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LOCATION: (1423)..(1423)
OTHER INFORMATION: n is a, c, g,
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OTHER INFORMATION: n is a, c, g,
NAME/KEY: misc feature
LOCATION: (1322)..(1322)
OTHER INFORMATION: n is a, c, g,
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NAME/KEY: misc_feature
LOCATION: (1520)..(1520)
OTHER INFORMATION: n is a, c,
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LOCATION: (1409)..(1409)
OTHER INFORMATION: n is a,
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LOCATION: (1445)..(1445)
OTHER INFORMATION: n is a,
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DTHER INFORMATION: n is a,
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LOCATION: (1345)..(1345)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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LOCATION: (1546)..(1546)
OTHER INFORMATION: n is a,
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LOCATION: (1713)..(1713)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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LOCATION: (1507)..(1508)
OTHER INFORMATION: n is
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OCATION: (1478)..(147
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LOCATION: (1895)..(189)
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OTHER INFORMATION: n is a, c,
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OTHER INFORMATION: n is a, c
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NAME/KEY: misc_feature
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LOCATION: (1988)...(1988)
OTHER INFORMATION: n is a, c
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NAME/KEY: misc feature
LOCATION: (1994)...(1994)
OTHER INFORMATION: n is a, c
 EY: misc_feature
ON: (1934)..(1934)
INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (1974)..(1974)
OTHER INFORMATION: n is a,
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                            GCTACCACTTCCCCCAGAGCAGCCCCCGAGCCCCTTCAGGCCCAGCCCCCAG
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                   CTTTTGGGTGTAGGGGAAAAGAATGCCTGACCCTGGGAAGGCT-CCCTGGTAGAATACAC
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RESULT 6 US-60-659-397-12129

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INFERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/60/659,397
CURRENT FILING DATE: 2005-03-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 12129
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Pred. No. 0;
5; Mismatches
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Best Local Similarity 97.7%;
Matches 1645; Conservative
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; ORGANISM: Homo E
US-60-659-397-12129
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                                                                                                                                                                                                                                                      LOCATION: (1282)..(1566)
OTHER INFORMATION: 73% homologous to Mus musculus Pro-Pol-dUTPase
OTHER INFORMATION: polyprotein, accession number Y12713, Smith-Waterman
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73.4%; Pred. No. v,
... 0; Mismatches
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILIMG DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PGT/USO1/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
SOFTWARE: CLUSTOM
SEQ ID NO 15295
LENGTH: 2760
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Matches 2370; Conservative
                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
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NAME/KEY: SIMILAR
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                                                                                                        CTTCCCCAGAGCAGCCCCCGAGCCCCTTCAGGCCCCAGCACTGCCCCAGACTCGCTGG
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US-10-450-763-15295/c
; Sequence 15295, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
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1648 GAAGGTGGCTCCCTGGGCCAGCTGGTCAAGGAGCAGGGCTGTCTCCCCAGAGGACCGGGCC 1 	1708 CTGTACTACCTGGGCCAGGCCTGGAGGGTCTGGAATACCTCCACTCACGAAGGATTCTG 1	1768 CATGGGGACGTCAAAGCTGACAACGTGCTCCTGTCCAGCGATGGGAGCCACGCAGCCTC 1	1828 TGTGACTTTGGCCATGCTGTGTCTTCAACCTGATGGCCTGGGAAAGTCCTTGCTCACA 1 		1948 TGCGACGCCAAGGTGGATGTCTGGAGCAGCTGCTGTATGATGCTGCACATGCTCAACGGC 2	2008 IGCCACCCTGGACTCAGITCTTCCGAGGCCGGCTTGCCTCAAGATIGCCAGGAGCCT 2	2068 CCGCCTGTGAGGGAGATCCCACCTCCTGCGCCCCTCTCACAGGCCATCCAAGAG 2	2128 GGGCTGAGGAAAGAGCCCATCCACCGCGTGTCTGCAGCGGAGCTGGGAGGAAGGTGAAC 2 	2188 CGGCACTACAGCAAGTGGGAGGTCTGAAGAGCCCTTGGAGGGGGAGAATATAAAGAACCA 2 702 CGGGCACTACAGCA	2248 AGACATCCACCGCCAAATCAAGCCAATTACCACCAGACCCTCCATGCCCAGCCGAGAGAG 2	2308 CTTTCGCCAAGGGCCCCCGGCCAGCTGAGGAGACAACAGGCAGAGCCCCTAAG 2688	2368 CTCCAGCCTCCTCCCACAGAGCCCAAAGAACAAGTCTCCTCCCTTGACTTTG 2	2428 AGCAAGGAGGAGTCTGGGAACCCTTACCTCTGTCCTCCCTGGAGCCAGCC	2488 GCCAGAAACCCCAGCTCACCAGAGCGAAAGCAACCGTCCCGGAGCAGGAACTGCAGCAG 2	2548 CIGGAAAIAGAAITATICCTCAACAGCCIGTCCCAGCCAITTTCTCTGGAGGAGCAGGAG 2 	2608 CAARTTCTCTCGTGCCTCACATCGACAGCCTCTCCCTGTCGGATGACAGTGAGAAGAAC 2 	2668 CCATCAAAGGCCTCTCAAAGCTCGCGGGACACCCTGAGCTCAGGGGTACACTCCTGGAGC 2	2728 AGCCAGGCCGAGGCTCGAAGCTCCAGCTGGAACATGGTGCTGGCCCGGGGGGGG
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Sequence 33424.

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Sequence 32424.

APPLICANT: Cooper, Matthew

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APPLICANT: Subramaniam, S. Sai

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APPLICANT: Li, Huo

APPLICANT: Li, Huo

APPLICANT: Li, Huo

TITLE OF INVENTION: Pragments of, Cynomolgus Monkey Genes and the Use Thereof

TITLE OF INVENTION: Pragments of, Cynomolgus Monkey Genes and the Use Thereof

TITLE OF INVENTION: VUMBER: US/60/680,544

CURRENT FILING DATE: 2005-05-13

NUMBER OF SEQ ID NOS: 48714

SOFTWARE: Patent Sequence Analysis Tool Version 1.0

SEQ ID NO 33424

LENGTH: 3658
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| NAME/KBY: misc feature
| LOCATION: (1)._.(3658)
| OTHER INFORMATION: n = A,T,C
| US-60-680-544-32424
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98.6%; Pred. No. 5.3e-293;
ive 5; Mismatches 9;
Sequence 4832, Application US/11060756
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wouts,
TITLE OF INVENTION: Nucleic Acid Arrays for Mon
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
FILE REPERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4832
LENGTH: 1400
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.3
Best Local Similarity 98.6
Matches 1384; Conservative
                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
US-11-060-756-4832
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14.7%; Score 676.2; DB 15; Length 3658; Similarity 22.6%; Pred. No. 4.5e-142; 32; Conservative 0; Mismatches 2824; Indels 30; Gaps 10;	ACTCCACAAACTGATCAGCCCTTGCAATGTCTGAACCACGTGTGGAAACTGCACCC 965		NNINNINNINNINNINNINNINNINNINNINNINNINNI	TCCTTCCCATTCCACCCTCTCCAGCCCTGGAAACCTCACCCTCTGGAGTCCTTCCT	CAAACTGGCCTGTGTA-GACAGCCAGAAACCCTTGCCTGACCCACACCTGAGCAAACTGG 1144		CCTGTGTAGACAGTCCAAAGCCCCTGCCTGGCCCACACCTGGAGCCCAGCTGCCTGTCTC 1204	NININININININININININININININININININI	GTGGTGCCCATGAGAAGTTTTCTGTGGAGGAATACCTAGTGCATGCTCTGCAAGGCAGCG 1264	NNININININININININININININININININININ	TGAGCTCAAGCCAGGCCCACAGCCTGACCAGGCCAAGACCTGGGCAGCACGAGGCT 1324	NNININININININININININININININININININ	CCAGATCCCGGGAGCCCAGCCCCAAAACTGAGGACAACGAGGGTGTCCTGCTCACTGAGA 1384	NININININININININININININININININININI	AACTCAAGCCAGTGGATTATGAGTACCGAGAAGAAGTCCACTGGGGCCACGCACCAGGTCC 1444	ИКИЛИКИКИМИКИКИМИКИКИМИКИКИМИКИКИМИКИКИМИКИКИМИК	GCCTGGGCAGAGGCTCCTTCGGAGAGGTGCACGAGGAGGAGAAGCAGACTGGCTTCC 1504	NYMININININININININININININININININININI	AGTGCGCTGTCAAAAAGGTGCGCCTGGAAGTATTTCGGGCAGAGGAGGAGCTGATGGCATGTG 1564	NNININININININININININININININININININ	CAGGATTGACCTCACCCAGAATTGTCCCTTTGTATGGAGCTGTGAGAGAGA	NNININININININININININININININININININ	TCAACATCTTCATGGAGCTGCTGGAAGGTGGCTCCCTGGGCCAGCTGGTCAAGGAGCAGG 1684	NININININININININININININININININININI	GCTGTCTCCCAGAGGACCGGGCCCTGTACTACCTGGGCCCAGGCCCTGGAGGGTCTGGAAT 1744	NININININININININININININININININININI	ACCTCCACTCACGAAGGATTCTGCATGGGGACGTCAAAGCTGACAACGTGCTCCTGTCCA 1804	NINDAMANININININININININININININININININININ	GCGATGGGAGCCACGCAGCCCTCTGTGACTTTGGCCATGCTGTGTGTCTTCAACCTGATG 1864	0.50 בא האורים היים היים היים היים היים היים היים ה	
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1925 CGGAGGTGCTGCCCAGGAGCTGCGACGCCAAGGTGGATGTCTGGAGCAGCTGCTGTA 1984 2285 CCCTCCATGCCCAGCCGAGAGAGCTTTCGCCAAGGGCCCCAGGGCCCCGGCCAGCTGAGG 2344 1985 TGATGCTGCACATGCTCAACGGCTGCCACCCCTGGACTCAGTTCTTCCGAGGGCCGCTCT 2044 2045 GCCTCAAGATTGCCAGCGAGCCTCCGCCTGTGAGGGAGATCCCACCCTCCTGCGCCCCTC 2104 2105 TCACAGCCCAGGCCATCCAAGAGGGGCTGAGGAAAGAGCCCCATCCACCGCGTGTCTGCAG 2164 2165 CGGAGCTGGGAAGGAAGGTGAACCGGGCACTACAGCAAGTGGGAGGTCTGAAGAGCCCTT 2224 2225 GGAGGGGAGAATATAAAGAACCAAGACATCCACCGCCAAATCAAGCCAATTACCACCAGA 2284 2345 AGACAACAGGCAGAGGCCCCTAAGCTCCAGCCTCCTCCCCACCAGAGCCCCCAGAGCCAA 2404 2405 ACAAGICICCICCTIGACTITIGAGCAAGGAGTCTGGGGATGTGGGGAACCCTTACCTC 2464 1560 retriccerdeaeccaeccerdecagaaaccecaecreaecagagagaaaccaaaccr 1619 TCCCGGAGCAGGAACTGCAGCAGCTGGAAATAGAATTATTCCTCAACAGCCTGTCCCAGC 2584 2585 CATTITCTCTGGAGGAGCAGGAGCAAATTCTCTCGTGCCTCAGCATCGACAGCCTCTCCC 2644 2705 GCTCAGGCGTACACTCCTGGAGCAGCCAGGCCGAGGCTCGAAGCTCCAGCTGGAACATGG 2764 TACAGTCTCTTAATGGTGAACACCTGCACATCCGGGAGTTCCACCGGGTCAAAGTGGGAG 2884 2945 ACGGGCAGCCTGTTCGCTACGACATGGAGGTGCCAGACTCGGGCATCGACCTGCAGTGCA 3004 TGTCCTCCTGGAGCCAGCCCCTGCCAGAAACCCCAGAGCCAGAGCGAAAGCAACCG 2524 2645 IGTCGGATGACAGTGAGAAGCACCATCAAAGGCCTCTCAAAGCTCGCGGGACACCCCTGA 2704 2765 TGCTGGCCCGGGCGCCCACCGACACCCCAAGCTATTTCAATGGTGTGAAAGTCCAAA 2824 2885 ACATCGCCACTGGCATCAGCAGCCAGATCCCAGCTGCAGCCTTCAGCTTGGTCACCAAAG 2944 3005 CACTGGCCCCTGATGGCAGCTTCGCCTGGAGCTGGAGGGTCAAGCATGGCCAGCTGGAGA 3064 1500 NNNNNNNNNNNNNNNNNNNNNNSAGCAAGCAGCAGTCTGGGATGTGGGAACCCTTACGTC 2525 2825 2465

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APPLICANT: Kinch, Deborah
APPLICANT: Kinch, Deborah
APPLICANT: Rosenberg, Michael
APPLICANT: Subramaniam, S. Sai
APPLICANT: Subramaniam, S. Sai
APPLICANT: Subramaniam, S. Sai
APPLICANT: Li, Huo
APPLICANT: Li, Huo
APPLICANT: Bandaru, Raj
APPLICANT: Bandaru, Raj
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APPLICANT: Derbel, Mahner
ITILE OF INVENTION: Pragments of, Cynomolgus Monkey Genes and the Use Thereof
ITILE OF INVENTION: Pragments of, Cynomolgus Monkey Genes and the Use Thereof
ITILE OF INVENTION: WINMER: 2055-05-13
NUMBER OF SEQ ID NOS: 48714
SOFTWARE: Parent Sequence Analysis Tool Version 1.0
SEQ ID NO 32424
LENGTH: 3658
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GACAGCACTTTGCACTCTGATGACCTCAAAGCACTTTCATGGCTGCCCTCT----GGCA 3220
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OTHER INFORMATION: n = A,T,C or
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APPLICANT: Kinch, Deborah
PEPLICANT: Rosenberg, Michael
APPLICANT: Subramaniam, S. Sai
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NAME/KEY: misc_feature
LOCATION: (1)...(3658)
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Sequence 11056, Application US/60680544

j GENERAL INFORMATION:
APPLICANT: Cooper, Matthew
APPLICANT: Cooper, Matchew
APPLICANT: Subramaniam, S. Sai
APPLICANT: Subramaniam, S. Sai
APPLICANT: Stak, Suzanne
APPLICANT: Bandaru, Raj
APPLICANT: Bandaru, Raj
APPLICANT: Bandaru, Raj
APPLICANT: Derbel, Maher

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ITILE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
ITILE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
CURRENT APPLICATION NUMBER: US/60/680,544
CURRENT APPLICATION NUMBER: US/60/680,544

CURRENT FILING DATE: 2005-05-13
NUMBER OF SEQ ID NOS: 48714
SOFTWARE: Patent Sequence Analysis Tool Version 1.0
SEQ ID NO 11056
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ORGANISM: Macaca Fascicularis
FRATURE:
INDEFER: misc_feature
LOCATION: (1)...(761)
OTHER INFORMATION: n = A,T,C or
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APPLICANT: Kinch, Deborah

APPLICANT: Rosenberg, Michael

APPLICANT: Subramaniam, S. Sai

APPLICANT: Sark, Suzanne

APPLICANT: Sark, Suzanne

APPLICANT: Li, Huo

APPLICANT: Li, Huo

APPLICANT: Derbel, Maher

TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary t

TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary t

TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary t

TITLE OF INVENTION: NUMBER: US, $60,600,544

CURRENT FILING DATE: 2005-05-13

NUMBER OF SEQ ID NOS: 48714

SOFTWARE: Patent Sequence Analysis Tool Version 1.0

SEQ ID NO 10785

LIBRICANT: Totle
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9.6%; Score 440.6; DB 15; Length
Best Local Similarity 72.6%; Pred. No. 3.6e-89;
Matches 566; Conservative 0; Mismatches 192; Indels
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2.60-680-544-10785/c
; Sequence 10785, Application US/60680544
; GENERAL INFORMATION:
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CATION: (1)...(761)
OTHER INFORMATION: n = A.T.C or
US-60-680-544-10785
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                                                                                                                                                                                                                                    Length 761;
                                                                                                                                                                                                                               Query Match 9.6%; Score 440.6; DB 15; Length Best Local Similarity 72.6%; Pred. No. 3.6e-89; Matches 566; Conservative 0; Mismatches 192; Indels
                                                              Version 1.0
FILE REFERENCE: 21590290000
CURRENT APPLICATION NUMBER: US/60/680,473
CURRENT FILING DATE: 2005-05-13
NUMBER OF SEQ ID NOS: 48714
SOFTWARE: Patent Sequence Analysis Tool V6
SEQ ID NO 10785
LENGTH: 761
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                                                                                                      TYPE: DNA
ORGANISM: Macaca Fascicularis
FEATURE:
                                                                                                                                                               OTHER INFORMATION: n = A,T,C
US-60-680-473-10785
                                                                                                                                                       NAME/KEY: misc feature LOCATION: (1)...(761)
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; GENERAL INFORMATION:
; APPLICANT: Cooper, Matthew
; APPLICANT: Rosenberg, Michael
; APPLICANT: Subramaniam, S. Sai
; APPLICANT: Sabramaniam, S. Sai
; APPLICANT: Sabrame
; APPLICANT: Bandaru, Raj
; APPLICANT: Derbel, Maher
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
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                              Length 761;
                            9.6%; Score 440.6; DB 15; Length 72.6%; Pred. No. 3.6e-89; tive 0; Mismatches 192; Indels
                                           Best Local Similarity 72.6
Matches 566; Conservative
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Compugen Ltd.
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1 MAVMEMACPGAPGSAVGQQK......PDGSFAWSWRVKHGQLENRP 947 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692

2105692 seqs, 386760381 residues

Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*geneseqp2001s:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aaw42402 Amino aci	Aau80371 Human cel	Adf45075 Human kin	Ads88253 Human pro	Aay31665 NF-kB ind	Aaw82497 Human NIK	Aaw81564 Human NF-		Aay31667 NIK kinas	Abm85491 Human pro	Aay31668 NIK kinas	Adp29813 Human sec		Add67717 Novel hum	Abr61616 Human NIK	Abr61608 Human NIK	Aay31666 NF-kB ind	Aag02579 Human sec	Abr61615 Human NIK	Abr61607 Human NIK			Adil7346 Polypepti		Adil7340 Polypepti
ID	AAW42402	AAU80371	ADF45075	ADS88253	AAY31665	AAW82497	AAW81564	AAW81561	AAY31667	ABM85491	AAY31668	ADP29813	ABM85490	ADQ67717	ABR61616	ABR61608	AAY31666	AAG02579.	ABR61615	ABR61607	ABB78798	ADI17263	ADI17346	ADI17320	ADI17340
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% Query Match	100.0	100.0	100.0	100.0	6.66	99.8	8.66	99.8	99.8	99.8	99.6	68.1	49.1	45.5	33.7	33.7	21.8	9.5	8.8	8.8	7.3	7.3	7.3	7.3	7.3
Score	5052	5052	5052	5052	5045	5044	5044	5044	5040	5040	5032	3439.5	2481.5	2301	1703	1703	1101	479	446	446	367	367	367	367	367
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The present sequence represents a NF-kappa inducing kinase (NIK). The full length DNA sequence was obtained by PCR using clone 10 (AAV03124). What was found to induce NF-kappaB even more effectively than TRAF2. Proteins capable of binding to TRAF2 and NIK were identified. The NIK or TRAF-2 binding proteins can be used for modulation or mediation in cells of NF-kappaB activity or any other intracellular signalling activity modulated or mediated by TRAF2. TRAF-binding proteins are especially used for prevention or treatment of pathological conditions associated with NF-kappaB induction, e.g. acute hepatitis, autoimmune-induced cell death,

Disclosure, Fig 6, 127pp, English.

Aae10314 Rat Tp12 Ade10313 Human Tp1 Adj94980 Novel NOV Adj94790 Novel NOV Adj94790 Novel NOV Adj94799 Novel NOV Adj94798 Novel NOV Adj94798 Novel NOV Adj94798 Novel NOV Adj94792 Novel NOV Adj94792 Novel NOV Adj94792 Novel NOV Adj94792 Novel NOV Adj94792 Novel NOV Adj94792 Novel NOV Adj94792 Novel NOV Adj94793 Movee Ful	Human Human Human Novel Human
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ALIGNMENTS

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DNA encoding tumour necrosis factor receptor-associated factor binding molecule - used for modulation or mediation in cells of the activity of
                                                                      Human tumour necrosis factor receptor-associated factor 2; TRAF2; TRAF-2 binding protein; NF-kappaB activity; NF-kappaB induction; intracellular signalling activity; acute hepatitis; autoimmune-induced cell death.
                                                                                                                                                                                                                                                 Mett I;
                                                       Amino acid sequence of NF-kappaB inducing kinase.
                                                                                                                                                                                                                                                 Kovalenko A,
AAW42402 standard; protein; 947 AA
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96IL-00119133.
                                     (first entry)
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N-PSDB; AAV03325.
                                    15-APR-1998
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                  AAW42402;
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e.g. death of the beta Langerhans cells or the pancreas that results in diabetes, the death of cells in graft rejection, the death of colls of graft rejection, the death of colls death of cells in multiple sclerosis, and AIDS-inhibited T cell suicide which causes proliferation of the AIDS virus and hence the AIDS disease. The proteins are also useful for screening of ligands capable of binding to a protein, which are useful for modulating cellular activity modulated/mediated by TRARS
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The present invention relates to a new method for identifying compounds for treating and/or preventing cytomegalovirus (CMV) infection and/or related diseases. The method of the invention comprises contacting a test compound with at least one of the callular kinases RICK, RIP, Nck-Interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase activity. The method of the invention can be used to treat and/or prevent CMV infections and related diseases. Oligonucleotides that can detect the specified kinases can also be used for diagnosis of infection. The present amino acid sequence represents the human callular kinase NIK (Nck-Interacting kinase) protein of the invention, as described above
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                                                                                                                                                                                                                                                                                 The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase. The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.
                                                                                             kinase (T) comprises contacting the conformation of target protein contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New protein complex comprising at least one first and second protein of the Tumor Necrosis Factor-alpha(TMR-alpha) signaling pathway, useful for diagnosing or treating inflammation, neurological diseases, infectious diseases or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein complex; tumour necrosis factor-alpha signalling pathway; INF-alpha; chronic inflammatory disease; rheumatoid arthritis, inflammatory bowel disease; inflammatory bowel disease; septic shock; bacterial infection; neurological disease; stroke-induced inflammation; neurodegenerative disease; cancer; antiinflammatory; antiarthritic; antirheumatic; cytostatic; antibacterial; gene therapy; human.
                 SWNMVLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS
LKSPWRGEYKEPRHPPPNQANYHQTLHAQPRELSPRAPGPRPAEETTGRAPKLQPPLPPE
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cancer. Accordingly, these complexes can be used for the development of pharmaceutical compositions that exhibit antiinflammatory, antiarthritic, antirthematic, cytoscatic and antibacterial activities and can be used for gene therapy purposes. In particular, the invention further provides siRNA-oligonucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that specification to form novel complexes of the TNF-alpha signalling pathway of the invention.
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The present sequence represents human wild-type NIK, a NF-kB inducing kinase having serine/threenine kinase activity. The invention relates to: (a) an N-terminus deletion mutant NIK protein (see AAY31666), and (b) a kinase deficient NIK mutant protein (see AAY31667 and AAY31668) that inhibits auto-phosphorylation or transphosphorylation. The invention provides the molecular basis for cytokine induction of N-kB-dependent immune and inflammatory responses, emphasising a role for both NIK-NIK and NIK-IKK (IkB-specific kinase) interactions. A novel and highly specific method for modulating NF-kB-dependent immune, inflammatory and anti-apoptotic responses is based on interruption of the critical protein interaction of NIK and IKK. The mutant NIK proteins are used in claimed methods for inhibiting NF-kB-dependent gene expression. The kinase-deficient NIK mutant proteins hinbit activation of IKK. The N-terminal deletion NIK mutant proteins bind to IKK, thus inhibiting NIK/IKK
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SWIMVLARGRPTDTPSYFNGVKVQIQSLINGEHLHIREFHRVKVGDIATGISSQIPAAAFS
                  SWNWVLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS
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                                                             LVTKDGQPVRYDMEVPDSGIDLQCTLAPDGSPAWSWRVKHGQLENRP 947
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NIK; Nuclear factor-kappa B; NF-kB; signal transduction; TNF; human; tumour necrosis factor; NF-kB-inducing kinase; screening; interaction; modulator; immune response; inflammatory response; viral gene;
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                                            VAHATEGKMARVCWKGKRRSKARKKRKKSSKSLAHAGVALAKPLPRTPEQESCTIPVQE
                                                               VAHATEGKMARVCWKGKRRSKARKKRKKKSSKSLAHAGVALAKPLPRTPEQESCTIPVQE
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VKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVC
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                                                                                         LOPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF
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                                                                                                                                                                                                                                                                                                                                                                          LVTKDGQPVRYDMEVPDSGIDLQCTLAPDGSFAWSWRVKHGQLENRP
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                                                                                                                                                                                                                        Screening agents for modulating interaction of nuclear factor kappas inducing kinase - with kinase-binding target, useful for controlling levels of the kinase, for treatment and diagnosis of conditions associated with e.g. inhibition of signal transduction by tumour necrosis
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                                                                                                                                                                                                                                                                                                                   This sequence represents a novel human nuclear factor-kappaB (NFkB)-
inducing kinase (NIK) which is used in a method for screening for agents
that modulate the interaction of NIK with a NIK-binding target. This
protein can be used as a modulator of cellular functions at the NIK
level, or for development of such compounds. NFkB is involved in
expression of many immune and inflammatory responses and of some
important viral genes. The protein may be used diagnostically and
therappeutically, in conditions associated with abnormal utilisation of
pathways that involve NFkB, e.g. inhibition of signal transduction by
tumour necrosis factor (TNF)
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N-PSDB; AAV73917.
diagnostic; therapy
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947 947 Probe, vector or recombinant nucleic acid encoding a polypeptide, especially human nuclear factor kappa-B-inducing kinase protein - useful for producing recombinant protein.

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This represents a nuclear factor kappa B (NF-kB)-inducing kinase (NIK) polypeptide or its fragment has one or more activities selected from kinase activity and inhibitory activity; IkB kinase-alpha and beta binding activity and inhibitory activity; IkB kinase-alpha and beta binding activity and binding inhibitory activity; activity; IkB binding activity and binding inhibitory activity, NF-kB activating and inhibitory activity and binding inhibitory activity and binding inhibitory activity. NF-kB activating and inhibitory activity and cortor containing the NK nucleic acid can be used to transform host cells for the recombinant production of the protein. The NIK nucleic acid and the polypeptide may be used in diagnosis (e.g. genetic hybridisation screen for NIK transcripts), therapy (e.g. NIK kinase inhibitors to inhibit TNF signal transduction), and in the biopharmaceutical industry
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781 SLSOPFSLEEGEOILSCLSIDSLSLSDDSEKNPSKASOSSRDTLSSGVHSWSSQAEARSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAVMEMACPGAPGSAVGQQKELPKPKEKTPPLGKKQSSVYKLEAVEKSPVFCGKWEILND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated peptide comprising a specified 947 amino acid sequence e.g. kinase activity, kinase inhibitory activity, IkB kinase-alpha binding activity, and IkB kinase-alpha binding inhibitory activity.
                                                                                                                                                                                                                                                                                                                                                  tumour necrosis factor; binding; genetic hybridisation; screening; signal transduction; biopharmaceutical; immunogen; pharmacological;
                                                                                                                                                                                                                                                                                                                                     NIK; IkB; NF-kB; TNF; kinase; nuclear factor kappa B; inhibition;
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llarity 99.9%; Pred. No. 0;
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/note= "wild-type Thr is substituted by Ala"

Location/Qualifiers 559

Misc-difference

WO9943704-A1 02-SEP-1999.

anti-apoptotic; human; mutant

sapiens

Synthetic

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The present sequence represents a kinase-deficient mutant of human NF-kB conducing kinase (NIK), in which the threonine residue at position 559 of the midic-type protein (see AAY11655) is replaced by alanine. The invention relates to: (a) an N-terminus deletion mutant NIK protein (see AAY1666); and (b) a kinase deficient NIK mutant protein, especially the present sequence of the sequence given in AAY31688, that inhibits autopresent sequence of the sequence given in AAY31688, that inhibits autopresent sequence of the sequence given in AAY31688, that inhibits autocompletely and an information of NF-kB-dependent immune and information of NF-kB-dependent immune and information of the specific kinase) interactions. A novel and highly specific method conformation of the critical protein interaction of the critical protein interaction of the critical protein interaction of inhibiting NF-kB-dependent immune, inflammatory and anti-apoptotic confinibiting NF-kB-dependent immune, inflammatory and anti-apoptotic confinibiting NF-kB-dependent gene expression. The kinase-deficient NIK mutant proteins inhibit the activation and phosphorylation of endogenous confined from the wild-type NIK sequence given in figure 10
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                                                                                                                     KLHHPQDGGPLPLPTHPFPYSRLPHPFPFHPLQPWKPHPLESFLGKLACVDSQKPLPDPH
                                                  VAHATEGKMARVCWKGKRSKARKKKKKKSSKSLAHAGVALAKPLPRTPEQESCTIPVQE
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New NF-kB inducing kinase proteins, used for inhibiting a kB-dependent immune response, e.g. an inflammatory response or an anti-apoptotic

Claim 8; Page; 48pp; English.

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98US-0076299P

27-FEB-1998; 25-FEB-1999;

(REGC) UNIV CALIFORNIA

WPI; 1999-518837/43.

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61 VITKGTAKEGSEAGPAAISIIAQAECENSQEFSPTFSERIFIAGSKQYSQSESLDQIPNN 120
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Sequence 947 AA;

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DISCOVERY

SAGRES

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                                                                                        are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vii) for inhibiting the activity of CAP; (iv) for treating carcinoma; (vii) for inhibiting the activity of CAP; (ix) as a biochip; (x) for diagnosing carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CAP. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
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Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                               present invention relates to novel DNA and protein sequences which
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                SWNWYLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS
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interactions. A novel and highly specific method for modulating NF-kB-dependent immune, inflammatory and anti-apoptoric responses is based on interruption of the critical protein interaction of NK and IKK. The mutant NIK proteins are used in claimed methods for inhibiting NF-kB-dependent gene expression. The kinase-deficient NIK mutant proteins inhibit the activation and phosphorylation of endogenous IKK. Note: The present sequence is not shown in the specification but is derived from the wild-type NIK sequence given in figure 10
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAHATEGRMARVCWKGKRRSKARKKRKKKSSKSLAHAGVALAKPLPRTPEQESCTIPVQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAVMEMACPGAPGSAVGQQKELPKAKEKTPPLGKKQSSVYKLEAVEKSPVFCGKWEILND
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Haishan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 68.1%; Score 3439.5; DB 8; Best Local Similarity 72.7%; Pred. No. 5.8e-246; Matches 688; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                    Lee E, Hest...
MM, Kothakota S, Halbura.
TAP, Wu G, Zhang H;
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                                                                                                                                                                                                                                                                                                    (FIVE-) FIVE PRIME THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                         Halenbeck RF, Huang MM, Kotna
Pierce K, Wang Y, Wong JGP,
              2003US-0463732P.
2003US-0467199P.
2003US-0467201P.
2003US-0467230P.
2003US-0471306P.
2003US-0472420P.
2003US-0472420P.
2003US-0472420P.
2003US-0472430P.
2003US-047669P.
2003US-0485218P.
2003US-0485218P.
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2003US-0486891P.
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                                      02-MAY-2003; 2
02-MAY-2003; 2
19-MAY-2003; 2
19-MAY-2003; 2
22-MAY-2003; 2
22-MAY-2003; 2
09-JUN-2003; 2
                                                                                                                                                                   08-JUL-2003;
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Immunosuppressive; Antibacterial; Virucide; human secreted protein.
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                                                   Human secreted protein SEQ ID #580.
                                                                                                                     ADP29813 standard; protein; 697 AA
                                                                                                                                                                                                                Cytostatic; Antiinflammatory; cancer; inflammatory; immune;
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2002US-0406579P.
2002US-0406585P.
2002US-0406588P.
2002US-0406608P.
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2002US-0406612P.
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18-APR-2003;
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) PA, Benram. L, Linnemann T;

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             LSKLACVDSPKPLPGPHLEPSCLSRGAHEKFSVEEYLVHALQGSVSSSQAHSLTSLAKTW
                                                                                                   -----YGAVREGPWVNIFMELLEGGSLGQL
                                                                                                                           VKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVC
                                                                                                                                           VKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVC
                                                                                                                                                                  LOPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF
                                                                                                                                                                               PPEPNKSPPLTLSKEESGMWEPLPLSSLEPAPARNPSSPERKATVPEQELQQLE1---LN
                                                                                                                                                                                                                                                                                                                                                                                  SWNMVLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS
                                                                                                                                                                                                                                                                                                                                                                                              ----LARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS
                                        AARGSRSREPSPKTEDNEGVLLTEKLKPVDYEYREEVHWATHQLRLGRGSFGEVHRMEDK
                                                                                 QTGFQCAVKKVRLEVFRAEELMACAGLTSPRIVPLYGAVREGPWVNIFMELLEGGSLGOL
                                                                                                                                                                                                                                                       LKSPWRGEYKEPRHPPPNQANYHQTLHAQPRELSPRAPGPRPAEETTGRAPKLQPPLPPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; carcinoma; lymphoma; cancer; murine.
                                                                                                        QTGFQCAVKK-----
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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates, (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP), (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for adagnosing the effect of a candidate carcinoma fung; (v) for diagnosing carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CAP. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                                     526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHMLNGCHPWTQFFRGPLCLKIASEPPPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAE 646
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           Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                            467 IFMELLEGGSLGQLVKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSD
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                                                                                                                                                                                                                                                                                                                                                                            407 GRGSFGEVHRMEDKQTGFQCAVKKVRLEVFRAEELMACAGLTSPRIVPLYGAVREGPWVN
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                                                                                                                                                                                                                                                                                                                   49.1%; Score 2481.5; DB 786.1%; Pred. No. 4.9e-175; ive 32; Mismatches 36;
                                                    SEQ ID NO 885; Opp; English.
                                                                                                                                                                                                                                                                                                                                               Matches 466; Conservative
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                           Sequence 548 AA;
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ADQ67717 standard; protein; 477 AA.

RESULT 14 ADQ67717 ADQ67717

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HIREFHRVKVGDIATGISSQIPAAAFSLVTKDGQPVRYDMEVPDSGIDLQCTLAPDGSFA
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                                                                                                                                                                 ABR61616 standard; protein; 324
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08-OCT-2002; 2002IL-00152183.
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                                                                           or atherosclerosis.
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                                                         WSWRVKHGOLENRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% to 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a protein sequence of the invention.
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                                                        osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic, gene therapy, diagnostic marker, morbid state, osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103
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                                                                                                                                                                                                                                                                                                                                                                                                                           neurological diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Alzheimer's diseases, Parkinson's diseases, dementia and various cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPRAPGPRPAEETTGRAPKLQPPLPPEPPREPNKSPPLTLSKEESGMWEPLPLSSLEPAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             514 GDVKADNVLLSSDGSHAALCDFGHAVCLQPDGLGKSLLTGDYIPGTETHMAPEVVLGRSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAKVDVWSSCCMMLHMLNGCHPWTQFFRGPLCLKIASEPPVREIPPSCAPLTAQAIQEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPRAPGPRPAEETTGRAPKLOPPLPPEPPRKSPPLTLSKEESGMWEPLPLSSLEPAPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKASQSSRDTLSSGVHSWSSQAEARSSSWNMVLARGRPTDTPSYFNGVKVQIQSLNGEHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRKEPIHRVSAAELGGKVNRALQQVGGLKSPWRGEYKEPRHPPPNQANYHQTLHAQPREL
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                                                                                                                                                                                                                                                                                                                                  Sato H,
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                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA, useful for treating osteoporosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2301; DB 8; Dred. No. 9.8e-162;
                                                                                                                                                                                                                                                                                                                                  Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 4878; 2449pp; English.
                                                                                                                                                                                                                                                                                                                                               Irie R;
                            Novel human protein sequence #2383
                                                                                                                                                                                                                                                                                                                                 Sugiyama T, Otsuki T,
Isono Y, Nagai K, I
                                                                                                                                                                                                                                                                                                   (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.5%;
99.3%;
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09-MAY-2003; 2003JP-00131392.
                                                                                                                                                                                                                         21-JAN-2004; 2004EP-00001196.
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                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-535376/
N-PSDB; ADQ67410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 477 AA;
                                                                                                                                   Homo sapiens
                                                                                                                                                               EP1440981-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nuclear factor inducing kinase or its mutein, variant, fusion protein, functional derivative, circularly permutated derivative or fragment, useful for treating an autoimmune disease, infarct, Alzheimer's
                                                                     463
933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIK; IL-2; interleukin 2; common gamma chain; cgammac; antiinflammatory; gastrointestinal; antiarthritic; antirheumatic; osteopathic; cardiant; antiasthmatic; notroopic; neuroprotective; antiarteriosclerotic; NIKK; immunosuppressive; antithyroid; nuclear factor kB inducing kinase; gene therapy; antianemic; NIK kinase; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                            624 PLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGGLKSPWRGEYKEPRHPPPNQANYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.7%; Score 1703; DB 7; I 100.0%; Pred. No. 1.3e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NIK C-terminal fragment (residues 624-947).
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        Qy
        684 QTLHAQPRELSPRAPGPRAEETTGRAPKLQPPLPPEPPERKSPPLTLSKEESGAWEPL 743

        Db
        61 QTLHAQPRELSPRAPGPRPAEETTGRAPKLQPPLPPEPPERKSPPLTLSKEESGAWEPL 120

        Cy
        744 PLSSLEPARANDSSPERKATVPEQELQQLEIELFLNSLSQPFSLEEGEGLISCLSIDSL 803

        Db
        121 PLSSLEPARANDSSPERKATVPEQELQQLEIELFLNSLSQPFSLEEGEQILSCLSIDSL 180

        Qy
        804 SLSDDSEKNPSKASQSSRDTLSSQHSWSSQAEARSSSWNWYLARGRPTDTPSYFNGVKV 240

        Qy
        864 QIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFSLVTKDGQPVRYDMEVPDSGIDLQ 923

        Db
        241 QIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFSLVTKDGQPVRYDMEVPDSGIDLQ 300

        Qy
        924 CTLAPDGSFAWSWRVKHGQLENRP 947

        Cy
        924 CTLAPDGSFAWSWRVKHGQLENRP 324

        Db
        301 CTLAPDGSFAWSWRVKHGQLENRP 324

        Search completed: June 7, 2005, 11:57:28
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

June 7, 2005, 11:40:40; Search time 138.585 Seconds (without alignments) 3499.208 Million cell updates/sec

US-09-155-676B-7 5052 1 MAVWEMACFGAPGSAVGQQK......PDGSFAWSWRVKHGQLENRP 947 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q99558 homo sapien	Q8iyn1 homo sapien	mus m	Q6zmz1 homo sapien	homo	homod	рошо	พนธ ก	Q63562 rattus norv	Q9wtr2 mus musculu	P53349 mus musculu	Q61083 mus musculu	Q62925 rattus norv	yarro	рошо	homo	homo	рошо	lycop	•	Q7z8j5 yarrowia li	-	Q6rfy4 nicotiana b	Q8h334 oryza sativ	Q7xurl oryza sativ	Q6zi89 oryza sativ	_			Q75pk3 homo sapien	
SUMMAKIES	•	ID	M3KE HUMAN	QBIYNI	M3KE MOUSE	Q62M <u>Z</u> 1	Q68D39	M3K8 HUMAN	Q6FG <u>2</u> 5	M3K8 MOUSE	M3K8_RAT	Q9WTR2	M3K1 MOUSE	M3K2 MOUSE	M3K1 RAT	Q6C2G1	Q9NYK3	Q8NC32	M3K1_HUMAN	M3K2 HUMAN	Q6RFY3	Q6C1T1	Q728J5	65uvc9	Q6RFY4	Q8H334	Q7XUR1	06ZI89	Q7XV58	M3K3 ARATH	M3K2_ARATH	Q75PK3	BCK1_YEAST
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æ	Query	Match	100.0	8.66	83.1	45.5	41.8	7.1	7.1	7.1	7.1	7.0	7.0	7.0	7.0		6.9			٠	٠	٠	6.8	6.7		٠	٠	٠	6.5	6.5	6.4	6.4	6.4
		Score	5052	5040	4196.5	2301	2110	360	360	357.5	356.5	356	•	353	353	in	350.5	346	346	4	343.5	341.5	341.5	341	338.5	335.5	332.5	332	32	326.5	325	325	325
	Result	No.	7	8	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

HSSP; P71584; 1MRU.

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Q95yh6 drosophila O8msd4 drosophila	095yh7 drosophila	Q96b75 homo sapien	Q6eshl oryza sativ	Q9ule2 homo sapien	Q8tc32 homo sapien	Q9nrp7 homo sapien	Q6h602 oryza sativ	Q95zn5 caenorhabdi	_	
Q95YH6 OBMSO4	Q95YH7 Q9VR37	Q96B75	Q6ESH1	Q9ULE2	Q8TC32	Q9NRP7	Фенео2	095ZNS	QBNJX3	082667
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1497	1571	797	894	1311	1315	1315	674	650	839	591
6.4	4.4	4.4	6 0	6.4	6.4	6.4	6.4	6.3	6.3	6.3
324.5	324.5	323	322.5	322	322	322	321.5	320.5	320	319.5
32	4 4 4 4	300	38	39	40	41	42	43	44	45

ALIGNMENTS

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REDUENCE FROM N.A.

REDUINE_2198257; PubMed=12477912; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Jodin T.B., Toshiyuki S.I., Wang J., Haieh F.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S.W. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S.W. Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hilalon D.K., Muzny D.M., Schergren E.D., Dickson M.C.,

RA Hakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Jones S.J., Marra M.A.,

RY Green E.D., Myers R.M., Butterfield Y.S.,

RY Juniting M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RY Generation and initial analysis of more than 15,000 full-length human mouse C.D.
        781 SLSQPPSLEEQEQILSCLSIDSLSLSDDSEKNPSKASQSSRDTLSSGVHSWSSQAEARSS
                                                                                                                                                                                                                              841 SWNWYLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS
                                                                                        SLSQPFSLEEQEQILSCLSIDSLSDDSEKNPSKASQSSRDTLSSGVHSWSSQAEARSS
                                                                                                                                                                                                  SWNMVLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS
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Eukaryota; Metazona; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Homo sapiens (Human)
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429 ATP (By similarity).
515 Proton acceptor (By similarity).
430 KK->AA: Loss of autophosphorylation.
104097 MW; D307F76993BC9661 CRC64;
                                         MIN, 604655; ...
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR00821; Ser thr_pkin_AS.
Pfam; PF00069; Pkinase; I.
ProDon; PD000001; Prot Kinase, I.PROSITE; PS00107; PROTEIN KINASE ATP; I.PROSITE; PS50011; PROTEIN KINASE DOM; I.PROSITE; PS00108; PROTEIN KINASE ST; I.PROSITE; PS00109; PROTEIN KINASE ST; I.PROSITE; PS00109; Phosphorylation; Sefine/threonine-protein kinase;
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Best Local Similarity 100.0%;
Matches 947; Conservative 0
IntAct; Q99558; -.
Genew; HGNC:6853; MAP3K14.
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                                                                                                                                                                           DESPLGAPYVRNTPQFTKPLKEPGLGQLCFKQLGEGLRPALPRSELHKLISPLQCLNHVW
                                                                                                                                                                                                               KLHHPQDGGPLPLPTHPFPYSRLPHPFPFHPLQPWKPHPLESFLGKLACVDSQKPLPDPH
                                                                                                                                                                                                                                                                                                                                                                         VKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVC
                                                                                                                                                                                                                                                                                                                                                                                                             LQPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGPLCLKIASEPPVREI PPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGG
                                              1 MAVMEMACPGAPGSAVGQQKELPKPKEKTPPLGKKQSSVYKLEAVEKSPVFCGKWEILND
                                                          VAHATEGKMARVCWKGKRRSKARKKRKKKSSKSLAHAGVALAKPLPRTPEQESCTIPVQE
                                                                                                                                                               DESPLGAPYVRNTPOFTKPLKEPGLGOLCFKQLGEGLRPALPRSELHKLISPLQCLNHVW
                                                                                                                                                                                                                                           LSKLACVDSPKPLPGPHLEPSCLSRGAHEKFSVEEYLVHALQGSVSSSQAHSLTSLAKTW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWNWVLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFHRVKVGDIATGISSQIPAAAFS
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                            Gaps
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                           Indels
          Length
        Score 5040; DB 2;
Pred. No. 2.5e-240;
); Mismatches 2;
                           0; Mismatches
        99.8%;
                           Matches 945; Conservative
                  Similarity
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         Query Match
Best Local S
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PRT;

STANDARD;

M3KE_MOUSE ID _M3KE_MOUSE

RESULT 3

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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--- STBURIT: Binds to TRAFE, TRAFE, TRAFE, IKKA and NF-kappa-B 2/P100. Interacts with PELI3 (By similarity).

--- SUBCELDULAR LOCATION: Cytoplasmic.

--- SUBCELDULAR LOCATION: Cytoplasmic.

--- FTM: Autophosphorylated.

--- DISEASE Defects in Map3/14 are the cause of alymphoplasis (ALY) which is characterized by systemic absence of lymph nodes and peyer's patches and disorganized splenic and thymic structures with immunodeficiency.

--- SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP kinase kinase kinase subfamily.
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FUNCTION.
MEDLINE=21138222; PubMed=11239468; DOI=10.1016/S1097-2765(01)00187-3;
Xiao G., Harhaj E.W., Sun S.-C.;
"NF-kappaB-inducing kinase regulates the processing of NF-kappaB2
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                                                                                                                                                                                                                                                                                         Euteleostomi;
Murinae; Mus.
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UTL-2004 (Rel. 44, Last annocation update)
Mitogen-activated protein kinase kinase kinase 14 (EC 2.7.1.37) (1)
Mitogen-activated protein kinase kinase kinase 14 (EC 2.7.1.37) (1)
Mitogen-activated protein kinase) (Serine/threonine-protein kinase NIK)
Mame=Map3k14; Synonyms=Nik;
Mus musculus (Mouse).

      Serine/threonine-protein kinase; Transferase.

      ND MAIN
      402
      657
      Protein kinase.

      NP BIND
      408
      416
      ATP (By similarity).

      BINDING
      431
      431
      ATP (By similarity).

      ACT SITE
      517
      Proton acceptor (By similarity).

      VARTANT
      855
      G -> R (in ALY, no binding to IKKA)

      SEQUENCE
      942 AA; 103079 MW; 3BE4E4BA2D25C200 CRC64;

                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND VARIANT ALY ARG-855.
STRAIN=C57BL/6; TISSUB=Spleen;
MEDLINE=99251583; PubMed=10319865; DOI=10.1038/8780;
Shinhura R., Kitada K., Mateuda F., Tashiro K., Ikuta K., Suzuk
Kogishi K., Serikawa T., Honjo T.;
"Alymphoplasia is caused by a point mutation in the mouse gene
encoding Nf-kappa b.inducting kinase.";
Nat. Genet. 22:74-77(1999).
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84.0%; Pred. No. 9.3e-199;
ive 53; Mismatches 90; Indels 9;
                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleosto
Sciurognathi; Muridae; Murinae;
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS000101; PROTEIN KINASE DOM; 1.
PROSITE; PS000108; PROTEIN KINASE ST; 1.
ATP-binding; Disease mutaTion; Phosphorylation;
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InterPro; IPR008271; Ser thr pkin AS
Pfam; PF00069; Pkinase; ī.
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InterPro; IPR011009; Kinase_like.
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Mammalia; Eutheria; Rodentia;
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Best Local Similarity 84.01
Matches 797; Conservative
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TISSUE-Esophageal;

A Tanai H., Watanabe S., Ishida Y., Fujimori K., Hiraoka S.,

A Tanai H., Watanabe S., Ishida S., Ono Y., Horuta T., Watanabe M.,

A Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishi S.,

RA Yamamoro J., Isono Y., Kawai H., Y., Sato K., Nishikawa T.,

RA Yamamoro J., Isono Y., Kawai H., Y., Satio M., Kikuchi H., Kanda K.,

RA Magatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,

RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

BRO GO:0006524; F:ATP binding; IEA.

GO; GO:0006468; P:Protein Minase activity; IEA.

DR GO; GO:0006468; P:Protein maino acid phosphorylation; IEA.

InterPro; IPROU1009; Kinase like.

DR ProDom; PD000001; Prot Kinase.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                   Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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068D39;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686J04131 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
45.5%; Score 2301; DB 2;
Best Local Similarity 99.3%; Pred. No. 1.1e-105;
Matches 431; Conservative 1; Mismatches 2;
protein FLJ16568
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                                                                                 SEQUENCE FROM N.A.
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                   KLHHPQDGGPLPLPTHPFPYSRLPHPFPFHPLQPWKPHPLES-FLGKLACVDSQKPLP-D
    MAVMEMACPGAPGSAVGQQKELPKPKEKTPPLGKKQSSVYKLEAVEKSPVFCGKWEILND
                                                         VITKGTAKEGSEAGPAAISIIAQAECENSQEFSPIFSERIFIAGSKQYSQSESLDQIPNN
                                                                                                                                 DESPLGAPYVRNTPQFTKPLKEPGLGQLCFKQLGEGLRPALPRSELHKLISPLQCLNHVW
                                                                                                                                                                                           PHLSKLACVDSPKPLPGPHLEPSCLSRGAHEKFSVEEYLVHALQGSVSSSQAHSLTSLAK
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Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR4745592; CAH189911.1; -.
InterPro; IPR010109; Kinase like.
InterPro; IPR00219; Prot Kinase.
InterPro; IPR00220; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
PF00069; Pkinase: I.
                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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86.5%; Pred. No. 2.5e-96;
iive 3; Mismatches 15;
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SMART; SM00220; S TKc; 1.
SMART; SM00219; TyTKc; 1.
PROSITE; PS500107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
                                                                                                                                                                   The German cDNA Consortium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
Name=DKFZp686J04131;
Homo sapiens (Human)
                                                                                                                        SEQUENCE FROM N.A. TISSUE=Uterus;
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                                                                                 NCBI_TaxID=9606;
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M3K8_HUMAN STANDARD; PRT; 467 AA. P41279; Q14275; Q9HC81; 01-FEB-1995 (Rel. 31, Created) 25-OCT-2004 (Rel. 45, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update)

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MEDLINE=92019818; PubMed=1833717;
A Aoki M., Akiyama T., Miyoshi J., Toyoshima K.;
Aoki M., Akiyama T., Miyoshi J., Toyoshima K.;
"Identification and characterization of protein products of the cot
"Identification and characterization of protein products of the cot
"Identification and characterization of protein products of the cot
"Identification and characterization of protein produces of the cot oncogene 6:1515-1519(1991)
"In Characterization of the cot oncoprotein and the cot oncoprotein call though it is much weaker than the activated cot oncoprotein.
"In Characterization of the cot oncoprotein.
"In SUBUNIT: Interacts with NFKB1/plo5.
"In SUBCELLULAR LOCATION: Cytoplasmic.
"In SUBCELLULAR LOCATION: Cytoplasmic.
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-!- TISSUE SPECIFICITY: Expressed in several normal tissues and human tumor-derived call lines.
-!- DEVELOPMENTAL STAGE: The 58 kDa form is activated specifically during the 5 and G2/M phases of the cell cycle.
-!- PTM: Autophosphorylared. The longer form undergoes phosphorylation on Ser residues mainly, and the shorter form on both Ser and Thr
                                                           (C-COT) (Cancer Osaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=94043034; PubMed=8226782; Aoki M. Sugimoto T., Toyoshima K Aoki M., Sugimoto T., Sumida S., Hamada F., Akiyama T., Toyoshima K The human cot proto-oncogene encodes two protein serine/threonine kinases with different transforming activities by alternative initiation of translation.";
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miyoshi J., Higashi T., Mukai H., Ohuchi T., Kakunaga T.; Structure and transforming potential of the human cot oncogene encoding a putative protein kinase."; Mol. Cell. Biol. 11:4088-4096[1991].
2.7.1.37)
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"SeattleSNPs. NHLBI HL66682 program for genomic applications,
FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=23241735; Pubmed=8479752;
MEDLINE=32341735; Pubmed=8479752;
Aaronson S.A.; Miki T.,
Aaronson S.A.;
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Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
     Mitogen-activated protein kinase kinase 8 (EC
                                   proto-oncogene serine/threonine-protein kinase) thyroid oncogene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 268:22723-22732(1993).
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                                                                                                                                                                             Name=MAP3K8; Synonyms=COT;
Homo sapiens (Human).
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CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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614 PVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGGLKSPWRGEYKEPR 673
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                                                                                                             674 HPPPNOANYHOTLHAOPRELSPRAPGPRPAEETTGRAPKLOPPLPPEPPEPNKSPPLTLS
                                                                                                                                                         385 -----HEALN-PPREDQPRC---QSLDSALLERKRLLSRKELELPENIADSSCTGS
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22 M. Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
32 M. Neubert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,
32 Neubert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,
33 Korn B., Zuo D., Hu Y., LaBaer J.;
34 Korn B., Zuo D., Hu Y., LaBaer J.;
35 EmBL; CR542254; CA47079.1;
36 EMBL; CR542254; CA47079.1;
37 EMBL; CR542254; CA47079.1;
38 EMBL; CR542254; CA47079.1;
39 GO: 00004674; F: Protein serine/threonine kinase activity; IEA.
30 GO: 00004713; F: Protein serine/threonine kinase activity; IEA.
37 GO: 00016740; F: transferase activity; IEA.
38 GO: 00006468; P: Protein amino acid phosphorylation; IEA.
38 GO: 00006468; P: Protein amino acid phosphorylation; IEA.
39 GO: 00006468; P: Protein amino acid phosphorylation; IEA.
30 GO: 00006468; P: Protein amino acid phosphorylation; IEA.
38 InterPro; IPR00229; Ser thr pkinase.
39 InterPro; IPR00229; Ser thr pkinase.
30 FEAM; PR00169; Prot. kinase; 1.
30 FroDom; PD000001; Prot. kinase; 1.
31 FroDom; PD000001; Prot. kinase; 1.
32 FROSITE; PS0011; PROTEIN KINASE DOM; 1.
33 PROSITE; PS0011; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
NON_TER 467 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazona; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%; Score 360; DB 2; Length 467; 27.2%; Pred. No. 4.6e-10; tive 69; Mismatches 155; Indels
                                                    467 AA; 52914 MW; 7728969EA3E4EA3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAP3K8 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                    734 KEESGM 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=MAP3K8;
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                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  MIN; 191195; -.

R Genew; HGNG: 6860; MAP3K8.

R MIN; 191195; -.

R GO; GO:0005629; C:cytcosol; TAS.

R GO; GO:0004648; P:protein amino acid phosphorylation; TAS.

GO; GO:0006468; P:protein amino acid phosphorylation; TAS.

R InterPro; IPR01009; Kinase like.

R InterPro; IPR000271; Ser_thr_pkin_AS.

R InterPro; IPR000171; Prot kinase.

R InterPro; IPR000171; Prot kinase.

R Probom; Pr00009; Primase; I.

R PROSITE; PS00110; PROTEIN KINASE DOM; I.

R PROSITE; PS00110; PROTEIN KINASE DOM; I.

R PROSITE; PS00110; PROTEIN KINASE ST; I.

M Alternative initiation; ATP-binding; Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase; Iransferase.

T CHAIN I 467
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COSLDSALLERKRLLSRK -> GHQVIHEGSSTNDPNNSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitogen-activated protein kinase kinase kinase 8, isoform 58 kDa. Mitogen-activated protein kinase kinase kinase 8, isoform 52 kDa. For isoform 52 kDa.
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Ser/Thr protein kinase family. MAP
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7.1%; Score 360; DB 1; Length 46
Best Local Similarity 27.2%; Pred. No. 4.6e-10;
Matches 116; Conservative 69; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VAR 006199.

Q -> T (in Ref. 1 and 2).

7728969EA3E4E8EC CRC64;
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ATP (By similarity).
ATP (By similarity).
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Missing (i
                  kinase kinase kinase subfamily.
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52924 MW;
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HSSP; Q13153; 1F3M.
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 ----- VYFPKDLR 288
                                                                                        PVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGGLKSPWRGEYKEPR 673
                                                                                                                                                    733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression.";
Jpn. J. Cancer Res. 84:518-525(1993).
-!- Cancer Res. 84:518-525(1993).
-!- Cancer Res. 84:518-525(1993).
-!- CATALYTIC Able to activate NF-kappa-B 1 by stimulating proteasomemediated proteolysis of NF-kappa-B 1/pl05. Plays a role in the cell cycle (By similarity).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBUNIT: Interacts with NFKB1/pl05.
-!- SUBCELLUAR LOCATION: Cytoplasmic.
-!- SUBCELLUAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: High in adult submandibular gland, thymus, spleen and newborn digestive tract.
-!- PTM: Autophosphorylated (By similarity).
-!- PTM: Autophosphorylated (By similarity).
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP kinase kinase kinase subfamily.
                                             ||| :||||| | | | | | | | ::|
GTEIYMSPEVILCRGHSTKADIYSLGATLIHMQTGTPPWVKRYPRSAYPSYLYIIHKQAP
                              GTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF---RGPLCLKIA-SEPP
                                                                                                                                                   674 HPPPNQANYHQTLHAQPRELSPRAPGPRPAEETTGRAPKLQPPLPPEPPEPNKSPPLTLS
                                                                                                                                                                             -----HEALN-PPREDQPRC---QSLDSALLERKRLLSRKELELPENIADSSCTGS
                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
mitogen-activated protein kinase kinase kinase 8 (EC 2.7.1.37) (COT proto-oncogene serine/threonine-protein kinase) (C-COT) (Cancer Osaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CS7BL/6 X CBA, TISSUE=Thymus;
MEDLINE=9330016; PubMed=8320169;
Ohara R., Miyoshi J., Aoki M., Toyoshima K.;
"The murine cot proto-oncogene: genome structure and tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
GLDFLHSKKVIHHDIKPSNIVFMS--TKAVLVDFGLSVQMTED---
                                                                                                                   PLEDIADDCSPGMRELIEASLERNPNHRPRAADL-----
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InterPro; IPR00719; Prot Kinase.
InterPro; IPR00871; Ser thr pkin AS.
Pfam; PF00069; Pkinase; I.
ProDom; PF000001; Prot kinase; I.
PROSITE; PS00101; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00111; PROTEIN KINASE DOM; I.
PROSITE; PS00109; PROTEIN KINASE DOM; I.
                                                                                                                                                                                                                                                                                                                     467 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Map3k8; Synonyms=Cot;
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                               734 KEESGM 739
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Q07174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Able to activate NF-kappa-B 1 by stimulating proteasome-mediated proteolysis of NF-kappa-B 1/p105. Plays a role in the cell cycle.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBGNIT: Interacts with NFKB1/p105.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489 EDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVCLQPDGLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602 GPLCLKIA-SEPPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGG
                                                                                                                                                                                                                                                                                                                                                                                           GVLLTEKLKPVDYEYREE-----VHWATHQLRLG-----RGSFGEVHRMEDKQTGFQCAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429 KKVRLEVFRAEELMACAGLTSPRIVPLYGAVREGPWVNIFMELLEGGSLGQLVKEQGCLP
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MEDLINE=3311339; PubMed=7681591;
Patriotis C., Makris A., Bear S.E., Tsichlis P.N.;
Tumor progression locus 2 (Tpl-2) encodes a protein kinase involved in the progression of rodent T-cell lymphomas and in T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION, AND MAP3X8-NFKB1/P105 BINDING.
MEDLINE=99133929; PubMed=9950430; DOI=10.1038/16946;
Belich M.P., Salmeron A., Johnston L.H., Ley S.C.;
"TPL-2 kinase regulates the proteolysis of the NF-kappaB-inhibitory protein NF-kappaB p105.";
Nature 397:363-368(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 BFEIIWVTKHILKGLDFLHSKKVIHHDIKPSNIVFMS--TKAVLVDFGLSVKMTED-
                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                         similarity)
                                                                                                                                                                                                                                                         7.1%; Score 357.5; DB 1; Length 29.2%; Pred. No. 6.2e-10; ative 60; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine/threonine-protein kinase; Transferase.

DOMAIN 138 388 Protein kinase.

NP BIND 144 152 ATP (By similarity).

BINDING 167 167 ATP (By similarity).

ACT SITE 253 253 Proton acceptor (By similarity).

SEQÜENCE 467 AA; 52941 MW; 60C2A34E530866BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              661 LKSPWRGEYKEPRHPPPNQANYHQTLHAQPRELSPR 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LK------BALN-PPREDOPR 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-UGL-activated protein kinase kinase kinase
progression locus 2) (TPL-2).
Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467 AA.
Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Map3k8; Synonyms=Tpl2;
                                                                                                                                                                                                                                                                                                                              98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                           Similarity
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SEQUENCE FROM N.A.
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PPYSRLPHPFPFHPLQPWKPHPLESFLGKLACVDSQKPLPDPHLSKLACVDSPKPLPGPH 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416 RMEDKQTGFQCAVKKV----RLEVFRAEELMACAGLTSPRIVPLYGAVREGPWVNIFME 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHAALCDFGHAVCLQPDGLGKSLLTG-----DYIPGTETHMAPEVV--LGRSCDAKVDVW 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               471 LLEGGSLGQLVKE-QGCLPEDRAL--YYLGQALEGLEYLHSRRILHGDVKADNVLLSSDG 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSCCMMLHMLNGCHPWTQFFRGPLCLKIASEPPVREI-----PPSCAPLTAQA---IQ 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLGCTVIEMATGRPPFHE-----LGSPQAAMFQVGMYKVHPPVPGSLSAEAQAFIL 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 KSSKSLAHAGVALAKPLPRTPEQESCTIPVQ---EDESPLGAPYVRNTPQFTKPLKEPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDSEELRLIGMKLACLLAR----KGCVEKMQYYWDVGFYLGAQILANDP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 GOLCFKOLGEGLRPALPRSELHKLISPLOCLANTWWK----LHH----PODGGPLPLPTHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLLKISDFGTS-----KRLAGITPCTETFTGTLQYMAPEIJDOGPRGYGKAADIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEPSCLSRGAHEKFSVEEYLVHALQGSVSSSQ-----AHSLTSLAKTWAARGSRSR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  684 QTLHAQ--PRELISPRAPGPRPAEE--TTGRAPKLQPPLPP---EPPEPNKSPPLTLSKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SATQSQTFPRPQAPSQHPPSPPKRCLSYGDTSQLRVPEEPAABEPASPEESSGLSLLHQE
                                                                                                                                         RESP: Q16539; IXVI.

RESP: Q16539; IXVI.

RG); MG1:1855691; Map3&6.

G); G0:0004674; F:ATP binding; IEA.

G); G0:0004674; F:Protein serine/threonine kinase activity; IEA.

G); G0:0016740; F:transferase activity; IEA.

G); G0:0016740; F:protein amino acid phosphorylation; IEA.

RG); G0:0016648; P:protein amino acid phosphorylation; IEA.

RG); G0:0016740; F:transferase activity; IEA.

RG); G0:0016740; F:transferase activity; IEA.

RG); G0:0016740; F:transferase activity; IEA.

RG); G0:0010079; PROTEIN kinase.

RITEPPO; IPR001209; S:r thr_pkinase.

RR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

RROSITE; PS00107; PROTEIN KINASE ATP; 1.

RROSITE; PS00109; PROTEIN KINASE ST; 1.

RROSITE; PS00109; PROTEIN KINASE ST; 1.

RATP-binding; Kinase; Serime/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 207; Conservative 127; Mismatches 350; Indels 240;
                                                SEQUENCE FROM N.A.
Saitoh M., Ichijo H.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase fa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.0%; Score 356; DB 2; 22.4%; Pred. No. 2.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
            NCBI_TaxID=10090;
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                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 EFEIIWVIKHVLKGLDFLHSKKVIHHDIKPSNIVFMS--TKAVLVDFGLSVQMTED---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 YPSYLYIIHKQAPPLEDIAGDCSPGMRELIEAALERNPNHRPKAADL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLLTGDYIP----GTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF---R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPLCLKIA-SEPPPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
SPECIFICITY: Expressed in spleen, thymus, liver and lung.
                     PTM: Autophosphorylated.
SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP
kinase kinase kinase subfamily.
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Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467;
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PIR; A47388; A47388.
RGD; 620969; Map388.
InterPro; IPR000719; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR00821; Set thr pkin AS.
ProDom; PD00069; Pkinase; I.
ProDom; PE0017; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00108; PROTEIN KINASE ST; I.
PROSITE; PS00108; PROTEIN KINASE ST; I.
ATP-binding; Phosphorylation; Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
kinase 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.1%; Score 356.5; DB 1; Best Local Similarity 29.2%; Pred. No. 6.9e-10; Matches 98; Conservative 60; Mismatches 115;
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ATP (By similarity)
ATP (By similarity)
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Eukaryota, Metazoa; Chordata; Cr Mammalia; Eutheria; Rodentia; Sc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253
52807 M
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467 AA;
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VAL-1401; LEU-1402; ARG-1403 AND GLY-1404
            PubMed=14500727;
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MOD RES
MOD RES
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 1054 AQELRTLQAQLRAQSLGPALLKGPLFAFPDAVKQILRRRQIRPHWMFVLDSLLSRAVRAA 1113
                                                                                                                             1114 LAVLDAESEKKAVLPRSEESSKE-----ESQQKPQESQALQSQLPPEQGPPS----- 1160
                                                                                                                                                                            161 -LMVELGLLRAETDRLRDLLAEKERECQALVQQALHRVHAETRKYAPASETPÄT----LP 1215
                                                                                                        --SLSDDSEKNP--SKASQSSRDTLSSGVHSWSSQAEARSSSWNMVLARGRPTDTPSYFN 859
                                                                                                                                                     860 GVKVQIQSLNGEHLHIRE------FHRVKVGDIATGISSQIPAAFSLVT 903
            SGMWEPLP--LSSLEPAPARNPSSPERKATVPEQELQQLEIELFLNSLSQPFSLEEQEQI 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION, INTERACTIONS WITH IKBKB AND MAP2K4, ENZYME REGULATION, AND MUTAGENESIS OF THR-1381; THR-1393; ISO-1394; PHE-1396; MET-1397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99455010; PubMed=10523642; Ito M., Yoshioka K., Akechi M., Yamashita S., Takamatsu N., Sugiyama K., Hibi M., Nakabeppu Y., Shiba T., Yamamoto K.-I.; "USAPl, a novel jun N-terminal protein kinase (JNK)-binding protein that functions as a scaffold factor in the JNK signaling pathway."; Mol. Cell. Biol. 19:7539-7548(1999).
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEK
                                                                                                                                                                                                                                                                                            P53349; Q60831; Q9R0U3; Q9R256; 01-0CT-1996 (Rel. 34, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 25-0CT-2004 (Rel. 45, Last annotation update) Mitogen-activated protein kinase kinase kinase 1 (EC 2.7.1.37) Name-Map3k1; Synonyms-Mekk, MEKK1; MEKK 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A divergence in the MAP kinase regulatory network defined by kinase and Raf.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lange-Carter C.A., Pleiman C.M., Gardner A.M., Blumer K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME REGULATION, AND MUTAGENESIS OF THR-1381 AND THR-1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9078260;
Deak J.C., Templeton D.J.;
Regulation of the activity of MEK kinase 1 (MEKK1) by autophosphorylation within the Kinase activation domain.";
Biochem. J. 322:185-192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BALB/c; TISSUE=Heart; Whitmarsh A.J., Shore P., Sharrocks A.D., Davis R.J.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Lange C.A., Blumer K.J., Sather S.L., Johnson G.L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                      PRT; 1493 AA
                                                                                                                                                                                                                        1216 KDONLVRWLOELSVDPATIOTLLS 1239
                                                                                                                                                                                                    904 KDGQPVRYDMEVPDSGIDLQCTLA 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BALB/c; TISSUE-Brain;
MEDLINE-93227040; PubMed-8385802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 660-1493 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 796-1493 FROM N.A.
                                                          195 LSCLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-659 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 260:315-319(1993).
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson G.L.;
                                                                                                                                                                                                                                                                                     M3K1 MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Binds both upstream activators and downstream substrates in multimolecular complexes through its N-terminus.
-!- TISSUE SPECTIFICITY: Highly expressed in the heart and spleen while a lower level expression is seen in the liver.
-!- PTM: Autophosphorylated.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP kinase kinase kinase subfamily.
-!- SIMILARITY: Contains 1 SWIM-type zinc finger.
-!- SIMILARITY: Contains 1 SWIM-type zinc finger.
R GO; GO: 0001747; P: eye morphogenesis (sensu Mammalia); IMP.
R GO; GO: 0001747; P: eye morphogenesis (sensu Mammalia); IMP.
R GO; GO: 0003034; P: regulation of actin filament polym. . .;
R GO; GO: 0007179; P: tregulation of cell migration; IMP.
R GO; GO: 00042060; P: wound healing; IMP.
R InterPro; IPR00109; Kinase like.
R InterPro; IPR00109; Kinase like.
R InterPro; IPR00219; Ser thr pkin AS.
R InterPro; IPR002290; Ser thr pkin AS.
InterPro; IPR001841; Znf fring.
R InterPro; IPR00431; Ser thr pkin Be.
R InterPro; IPR00431; Ser thr pkin Be.
R Pfam; PF00069; Pkinase; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding, Magnesium, Metal-binding, Phosphorylation,
Serine/threonine-protein kinase, Transferase, Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphothreonine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphothreonine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probom; Froyl, Strip, 1.

SMART; SM00184; RING; I.

SMART; SM00184; RING; I.

SMART; SM00120; STRC; I.

PROSITE; PS00107; PROTEIN KINASE ATP; I.

PROSITE; PS00108; PROTEIN KINASE ST; I.

PROSITE; PS00518; ZF RING[]; FALSE_NEG.

PROSITE; PS0089; ZF RING[2; I.

PROSITE; PS50086; ZF RING[2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poly-Gly.
Pro-rich.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L13103; AAA97500.1; ALT INIT.
EMBL; U23470; AAA85038.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF117340; AAD25049.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB014614; BAA85878.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; Q16539; 1KV1.
MGD; MGI:1346872; Map3k1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1238
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	348	1130 FKSEVAVLSPEKAENDDTYKDDVN	373	1190 QVENGEDIIIIQQDT	y 425 OCAVKKVRIEUFRAEELMACAGLTSPRIVPLYCAVREGFWVNIFMELLE 473	474 GGSLGQLVKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALC	1309 GGSVAHLLSKYGAFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQRLRIA	534 DEGARACLQPUGLGKSLTGDYIPGTETHMAPEVUGRSCDAKVDVWSSCCMMLHWINGC 593 1369 DFGAAARLASKGTGAGEFQGQLL-GTIAFMAPEVIRGQQYGRSCDVWSVGCAIIENACAK 1427	594 HPWTOFFRGPLCLKIASEPPPVREIPPSCAPLIAQAIQEGLRKEP	1428	/ 639 IHRVS 643 : : D 1488 VFRIT 1492		2 2	Q61083; 01-NOV-1997 (Rel. 35, Created)	r 01-NOV-1997 (Rel. 35, Last sequence update) r 25-OCT-2004 (Rel. 45, Last annotation update)	Mitogen-activated protein MAPK/ERK kinase kinase 2)	Name=Map3k2; Synonyms=Mekk2; Mus musculus (Mouse).	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCRT 7-x10-10000.									activation of the ERK5 pathway."; J. Biol. Chem. 278:36989-36992(2003)!- FUNCTION: Component of a protein kinase signal transduction	cascade. Regulates the JNK and ERKS pathways by phosphorylating and activating MAPZKS and MAPZK7. -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
•	ŝ	셤	õ	셤	& A	δ	යි (r R	ò	đ	S A	Î	M33	AC	TO TO	DE C	S O	888	R R R	S X	RT RT	RL	R R P R	RA RT RT	R R R	RA RT	동물망	8888
												-						•					****					
T->S: Reduced kinase activity and	T-SE Loss of kinase activity and	autophosphorylation. T-A: Fails to activate MAP2K1, MAP2K4,	T->5 Reduced kinase activity and	autophosphorylation. T->E: Loss of kinase activity and	autophosphorylation. T->A: Loss of kinase activity and autophosphorylation. Fails to activate	rwarzal, warzas, watzak, CHOK and IKBKB. I->A: Loss of NP-kappa-B transcription factor activity and reduced ability to	activate MAPZKI, MAPZKA, MAPZKY. No effect on APP activity or activation of CHTM and APPN 1 activity or activity or activity or activity and APPN 1 activity or activity and APPN 1 activity and APPN 1 activity and APPN 1 activity activity.	D C	ability to activate MAP2K1, MAP2K4, MAP2K7, CHUK and IKBKB. M->1. Fince of 10-1 and NP-Lanna D	transcription factor activity. Reduced ability to activate MAP2K1, MAP2K4,	MAPZKV, CHUK and IKBKB. V->A: Loss of AP-1 and NF-kappa-B transcription factor activity. Reduced ability to activate MAPZKI. MAPZK4.	MAP2K7, CHUK and IKBKB.	activity and reduced ability to activate CHUK and IKBKB. No effect on NF-kappa-B	activity or activation of MAP2K1, MAP2K4, MAP2K7. Loss of binding to MAP2K4.	R->A: Loss of AP-1 transcription factor activity, no effect on NF-kappa-B	activity. G-A: Loss of AP-1 and NF-kappa-B	GGGLGCTLPCTOI ACCOL ACCIVILY. GGGLGCGCT -> ALQGG (in Ref. 2).	(in Ref. (in Ref. (in Ref.	S -> C (in Ref. 2). V -> A (in Ref. 2).	V -> L (in Ref. 3). V -> L (in Ref. 3).	SCOR	°, °, 81	77 AISIIAQAECENSQEFSPTFSERIFIAGSKQYSQESSLDQIPNNVAHATEGKMARVCWKG 136 	KRRSKARKKRKKKSSKSLAHAGVALAKPLPRTPEQESCTIPVQEDESPLGAPYVRNT 193 : ::	LNHVWKLHHPQDGGPL	DSDOL	PLPTHPFPXSKLPHPFPFHPLQPWKPHPLESFLGKLACVDSQKPLPDPHLSKLA 305 	306CVDSPKPLPGPHLEPSC-LSRGAHEKFSVEEXLVHALQGSVSS 347
1381	1381	1381	1393	1393	1393	1394		1396	1397		1401	1402			1403	1404	39	257	413 559	883 1467 AA: 16128		vat	ECENSQE! : SCLENSSI	ARKKRKKI : 3RPHSQCI	BPGLGQLC 	IPSI	YSRLPHPI SRPPPSS	GGGNSGNA
1381	1381	1381	1393	1393	1393	1394		1396	1397		1401	1402		,	1403	1404	30	257	413 559			1	ISIIAQA : : LQAVAPT	RRSK : :: KPAVQTK	QFTKPLK	PQAFVPCKIPS	PLPTHPFP) : SPVFT(CVDS SRCDDSFGC
MUTAGEN	MUTAGEN	MUTAGEN	MUTAGEN	MUTAGEN	MUTAGEN	MUTAGEN		MUTAGEN	MUTAGEN		MUTAGEN	MUTAGEN			MUTAGEN	MUTAGEN	CONFLICT	CONFLICT	CONFLICT	CONFLICT	uery Match	les 19	4 77 : 8 979	137 K			252 F	306 - 1070 S

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F-5A: No effect on autophosphorylation.
Fails to induce activation of the AP-1
ranscription factor, MapK7 or MAPK8.
I-5A: Loss of autophosphorylation. Fails
to induce activation of the AP-1
transcription factor, MAPK7 or MAPK8.
T-5A: Loss of autophosphorylation and
fails to induce activation of the AP-1
transcription factor, MAPK7 or MAPK8 when
associated with Ala-575 and Ala-576.
Q-5A: Loss of autophosphorylation and
fails to induce activation of the AP-1
transcription factor, MAPK7 or MAPK8 when
associated with Ala-574 and Ala-576.
P-5A: Loss of autophosphorylation and
fails to induce activation of the AP-1
transcription factor, MAPK7 or MAPK8 when
associated with Ala-574 and Ala-576.
P-5A: Loss of autophosphorylation and
fails to induce activation of the AP-1
transcription factor, MAPK7 or MAPK8 when
associated with Ala-575 and Ala-576.
P-5A: Loss of autophosphorylation and
fails to induce activation of the AP-1
transcription factor, MAPK7 or MAPK8 when
                  similarity)
SUBUNIT: Binds both upstream activators and downstream substrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autophosphorylation when associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and AP-1 transcription factor, MAPK7 or MAPK8 activity. Fails to induce activation and loss of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P->A: Loss of autophosphorylation.
L->A: No effect on autophosphorylation and AP-1 transcription factor, MAPK7 or MAPK8 activity. Falls to induce activation and loss of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P->A: No effect on autophosphorylation
ENZYME REGULATION: Activated by phosphorylation on Thr-524 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V->A: No effect on AP-1 transcription
                                                                          PTM: Autophosphorylated.
SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP
kinase kinase kinase subfamily.
                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1346817; mappixc.

R InterPro; IPR011009; Kinase like.

InterPro; IPR001209; Kinase like.

R InterPro; IPR0020719; ProE kinase.

R InterPro; IPR002291; Ser_thr_pkinase.

R InterPro; IPR002291; Ser_thr_pkinase.

R InterPro; IPR00019; ProE kinase; 1.

ProDom; Pro0069; Prinase; 1.

R SMART; SM00266; PB1; 1.

R SMART; SM00201; PROTEIN KINASE ATP; 1.

R SMART; SM00201; PROTEIN KINASE ATP; 1.

R PROSITE; PS001107; PROTEIN KINASE ATP; 1.

R PROSITE; PS001108; PROTEIN KINASE ST; FALSE NEG.

M ATP-binding; Magnesium; Metal-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase.

T DOMAIN 356 616 PROTEIN KINASE; ATP (By similarity).

T NP BINDING 385 385 ATP (By similarity).

T ACT_SITE 483 483 Proton acceptor (By similarity).

T MOD RES 524 524 Proton acceptor (By similarity).

T WOD RES 524 524 Proton acceptor (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor activity.
799A35218DDE7C41 CRC64;
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                                                      in multimolecular complexes.
                                                                                                                                                                                                                                                                                                              EMBL; U43186; AAB03536.1; -.
                                                                                                                                                                                                                                                                                                                                HSSP; Q13153; 1F3M.
MGD; MGI:1346873; Map3k2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     580
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619 AA; 69835 MW;

SEQUENCE

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                                                                            177 PVQED--ESPLGAP----YVRNTPQFTKPLKEPG-----LGQLC----FKQL-GEGLRP 219
                                                                                                                  PSPEDLNNTPLGAERKKRLSVVGPPNRDRSSPPPGYIPDILHQIARNGSFTSINSEG--E 191
                                                                                                                                                                                                                                                                                                                333 VEEY-----LVHALQGS----VSSSQA-HSLTSLAKTWAARGSRSREPSPKTED-- 376
                                                                                                                                                                                                                                                                                                                                                                                                                                 384
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                                                                                                                                                         220 ALPRSELHKLISPLQCLNHVWKLHHPQDGG-----PLPLPTHPFPYSRLPHPFPFHPL
                                                                                                                                                                                                                                     273 QPWKPHPLESFLGKLACVDSQKPLPDPHLSKLACVDSPKPLPGPHLEPSCLSRGAHEKFS
                                                                                                                                                                                                                                                                            ------AQSYPDNHQE---FTDYDNPIFEKFGKGGTYPRRYHVSYH
                                                                                                                                                                                                                                                                                                                                        326 IRRRGSDIDNPTLTVTDISPPSRSPRAPTNWRLGKL-LGQGAFGRVYLCYDVDTGRELAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----HAVCLQPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 FIPES-MDQMLDPL----SLSSPENSGSGSCPSLDSPLDGESYPKSRMPR----
                                                                                                                                                                                                                                                                                                                                                                                             -----NEGVLLTEKLKPVDYEYREEVHWATHQLRLGRGSFGEVHRMEDKQTGFQCAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429 KKVRL------EVFRAE-ELMACAGLTSPRIVPLYGAVR--EGPWVNIFMELLEGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGQLVKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCHPWTQFFRGPLCLKIASEPPPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAEL 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND MUTAGENESIS OF ASP-1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 353; DB 1; Length 619;
; Pred. No. 1.4e-09;
64; Mismatches 201; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
MEDINE-86224276; PubMed-8643568; DOI=10.1073/pnas.93.11.5291;
Xu S., Robins D.J., Christerson L.B., English J.M., Vanderbilt C.A.,
Cobb M.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegious (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- COFACTOR: Magnesium (By similarity).
-!- ENZYME REGULATION: Activated by phosphorylation on Thr-1381 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning of rat MEK kinase 1 cDNA reveals an endogenous membrane-associated 195-kDa protein with a large regulatory domain.";
Proc. Natl. Acad. Sci. U.S.A. 93:5291-5295(1996).
-!- FUNCTION: Component of a protein kinase signal transduction cascade. Activates the ERK and JNK kinase pathways by phosphorylation of MAP2K1 and MAP2K4. Activates CHUK and IKBKB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Mitogen-activated protein kinase kinase lice 2.7.1.37)
(MABK/ERK kinase kinase 1) (MEK kinase 1) (MEKK 1).
Name=Map3k1; Synonyms=Mekk, Mekk1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the central protein kinases of the NF-kappa-B pathway (By
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  Query Match
Best Local Similarity 27.4%;
Matches 147; Conservative 64
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990 FVPCKIPSASPOTORKFSLOPORTCSENRDSEKLSPVFTOSRPPPSSNIHRAKASRPVPG 1049
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----KTGKGLKATRLSASSEDISDRLAGVSVGLPSSATTEQPKPTVQTK-----GRPHS 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 GDVKADNVLLSSDGSHAALCDFGHAVCLQPDGLGKSLLTGDYIPGTETHMAPEVVLGRSC 573
                                                                  --VRNTPQFTKPLKEPGLGQLCFKQLGEGLRPALPRSELHKLISPLQCLNHVWKLHHPQD
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                                                                                                                                                       ---FPYSRLPHPFPFHPLOPWKPHP-
                                                                                                                                                                                                                                             280 LESFLGKLA------CVDS-----QKPLPDPHLSKLACVDSPKPLPGPHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
Yarrowia lipolytica chromosome F of strain CLIB99 of Yarrowia lipolytica (Fragment).
ORFNames=YALIOF08165g;
Yarrowia lipolytica CLIB99.
Eukaryota; Fungi; Ascar
                                                                                                            947 OCLNSSPLSPPQLMFPAISAPC----SSAPSVPAGSVTDA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
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                  and downstream substrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  791 FALQSIDNSHSMVGK---LSRRIYLSSARMVTTVPPLFSKLVTMLSASGSSHFARMRRL
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                                                                  SIMILARILY).
SUBCELLULAR LOCATION: Membrane-associated.
TISSUE SPECIFICITY: Most highly expressed in spleen, kidney and
                                                                                                                                                                          MAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 YKLEAVEKSPVFCGKWEILNDVITKGTAKEGSEAGPAAISIIAQAECENSQEFS--
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; Pred. No. 3.8e-09;
94; Mismatches 302; Indels 184;
                                                                                                                                          -!- FTM: Autophosphorylated.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-kinase kinase subfamily.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
-!- SIMILARITY: Contains 1 SWIM-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proton acceptor (By similarity). Phosphothreonine (By similarity) Phosphothreonine (By similarity)
                                       in multimolecular complexes through its N-terminus (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine/threonine-protein kinase; Transferase; Zinc-finger.
ZN_FING 328 356 SWIM-type.
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8C5F29F866898524 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity). (By similarity).
                SUBUNIT: Binds both upstream activators
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SMART; SM00184; RING; 1.
SMART; SM00220; STRC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS00189; ZF RING 2; 1.
PROSITE; PS0089; ZF RING 2; 1.
PROSITE; PS50086; ZF RING 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              send an email to license@isb-sib.ch).
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Poly-Glu.
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InterPro; IPRO00719; Prot kinase.
InterPro; IPRO08271; Ser thr pkin AS.
InterPro; IPRO02290; Ser thr pkin As.
InterPro; IPRO01841; Znf ring.
InterPro; IPRO07527; Znf SWIM.
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Matches 165; Conservative
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Pfam; PF04434; SWIM; 1.
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RGD; 620966; Map3k1.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 TKREITPPGSSTSSK-----PIPSITSALNKASRGSVSNK------LPSISKATRL 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPSSPERKATVPEQELQQLEIELFLNSLSQPF-SLEEQEQILSCLSIDSLSLSD-----D 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 FNQAVEETPRIPHRIQDDIYASIRKFSRQKQNEIISSGHIESWDDEFVGELNPRSPHIII 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEKNPSKASQSSRDTLSSGVHSWSSQAEARSSSWNMVLARGRPTD-----TPSYFNGVKV 863
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.L.; "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKEPIHRVSAAELGGKVNRALQQVGGLKSPWRGEYK---EPRH--PPPNQ-----AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----PRPAEETTGRAPKLQPPLPPEPPEPNKSPPLTLSKEESGMWEPLPLSSLEPAPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                          Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382132; CAG77958.1; -.
GO; GO:0006524; F:ATP binding; IEA.
GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.9%; Score 351; DB 2; Length 1158; 22.6%; Pred. No. 3.6e-09; tive 84; Mismatches 203; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1158 AA; 129085 MW; 0DCD5DA6745408C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
ATP-binding; Kinase; Transferase.
1 1 1 SEQUENCE 1158 AA; 129085 MW; ODCD5DA6745408
                                                                                                                                                                                                                                                                   InterPro; IPR008938; ARM.
InterPro; IPR011009; Kinase like.
InterPro; IPR001109; Kinase like.
InterPro; IPR00229; Ser thr pkinase.
InterPro; IPR00229; Ser thr pkinase.
InterPro; IPR00245; Tyr_pkinase.
Pfam, PP00009; Pkinase; I.
ProDom; PD000001; Prot, kinase; I.
SMART; SM00220; S_TKC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 22.6
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             864 QIQSLNGEH 872
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                             STRAIN-CLIB99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------AQSYPDNHQE---FSDYDNPIFEKFGKGGTYPRRYHVSYHH 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 LPRSELHKLISPLQCLNHVWKLHHPQDGG-----PLPLPTHPFPYSRLPHPFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 EEY-----LVHALQGSVSSSQA-----HSLTSLAKTWAARGSRSREPSPKTED---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NEGVLLTEKLKPVDYEYREEVHWATHQLRLGRGSFGEVHRMEDKQTGFQCAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 KVRLEVFRAE------ELMACAGLTSPRIVPLYGAVR--EGPWVNIFMELLEGGSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HAVCLQPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 IPES-MEQMLDPL-----SLSSPENSGSGSCPSLDSPLDGESYPKSRMPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQLVKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nang C., Lo H.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
HSRP, Q13153; IF3M.
GO: GO: 00005524; F:ATP binding; IEA.
GO; GO: 0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO: 0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR001009; Kinase like.
InterPro; IPR00219; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.9%; Score 350.5; DB 2; Length 619; 26.5%; Pred. No. 1.9e-09; Ative 64; Mismatches 180; Indels 105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                619 AA; 69766 MW; 242B0F562D797873 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                   619 AA
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Pfam; PF00069; Pkinase; 1.
SMORT; SM0066; PB1; 1.
SMART; SM00666; PB1; 1.
PR051TE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                     Q9NYK3;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2004 (TrEMBLrel. 26,
Protein kinase MEKK2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 26.59
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
| : |
541 SFSSSDKSH 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=9606;
```

558 KPPWAEFEAMAAIFKIATQPTNPK-LPPHVSDYTRDFLKR-IFVEAKLRPSADEL 610

g

Search completed: June 7, 2005, 12:02:21 Job time: 143.585 secs

us-09-155-676b-7.rpr

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

June 7, 2005, 11:43:10 ; Search time 32.7215 Seconds (without alignments) 2784.626 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-155-676B-7 5052 1 MAVMEMACPGAPGSAVGQQK......PDGSFAWSWRVKHGQLENRP 947

Scoring table:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	serine/threonine-s	proto-oncogene pro	serine/threonine p	MEK kinase - mouse	MAP kinase kinase	mitogen-activated	kinase-related tra	NPK1-related prote	protein kinase BCK	hypothetical prote	hypothetical prote	protein kinase (EC	protein kinase, p2	probable serine/th	probable MEK kinas	serine/threonine-p	STE11 protein kina	probable serine/th	hypothetical prote	probable serine/th	MAP kinase kinase	MAP kinase kinase	serine/threonine-s	protein kinase (EC	MAP kinase kinase	p21-activated prot	serine/threonine p	hypothetical prote	beta-p21-activated
SUMMARIES	OI	4871	149609	A47388	A46212	T10757	JE0363	A41253	A96591	S20117	T34356	A96662	S55694	S58682	T36746	G96575	T38073	A48084	528394	T16511	B96716	T30565	T39225	S40482	JC4070	T50298	G01773	T36502	T15467	A57597
	DB		7	7	~	~	~	7	7	~	~	7	~	~	7	~	7	~	7	7	~	N	7	~	н	~	~	~	~	7
	Query Match Length		467	467	687	1493	1288	415	651	1478	653	883	969	525	550	609	1116	206	939	1387	836	1338	1401	544	543	756	545	556	622	544
٠	Query Match		7.1		7.0	7.0	6.7	9.9	6.4		6.3	6.2		0.9	•	•	0.9	6.0	•	5.9	•	5.8		5.8			5.8			
	Score	ı ۳	357.5	356.5	355.5	353	336	331	325	325	319	313.5	307	305.5	305	304	303.5	301	301	298	295	294	294	292	291.5	2	291	291	288.5	288
	Result No.		7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20		22		24	25	26	27	28	29

microtubule-associ mitogen-activated	protein kinase hom	serine/threonine p	P21 activated kina	protein kinase STE	probable serine/th	serine/threonine p	hypothetical prote	p70 S6 kinase (EC	mitogen-activated	MAP3K alpha protei	probable serine/th	Ste20-like protein	protein kinase SSK
A54602 T52621	S47946 S46367	742100	149376	S51380	T18256	T18259	T19188	JE0377	T51735	T51625	B70754	S71886	S59801
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1734 372	490	556	544	738	1230	1230	1370	481	363	582	626	426	1579
5.7		. v	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.4	5.4
287 284	282	281	280	280	279	279	279	277.5	276.5	276.5	276.5	275	275

ALIGNMENTS

 RESULT 1 A48713 serine/threonine-specific protein kinase cot, 58K form - human serine/threonine-specific protein kinase cot, 58K form N;Alternate names: cot prote-oncogene, 58K form N;Contains: serine/threonine-specific protein kinase cot, 52K form C;Species: Homo sapiens (man) C;Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004 C;Accession: A48713; B31639 R;AOKi, M; Hamada, F; Sugimoto, T; Sumida, S; Akiyama, T; Toyoshima, K.
 D. BIOL. Chem. 289, 24/12, 1993. A; Title: The human cot proto-oncogene encodes two protein serine/threonine kinases with A;Title: The human cot proto-oncogene encodes two protein serine/threonine kinases with A;Reference number: A48713 MUID:94043034; PMID:8226782 A;Accession: A48713 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-467 <aok> A;Cross-references: UNIPROT:P41279 A;Experimental source: TCO-4 cells</aok>
A, Note: sequence inconsistent with nucleotide translation A, Note: sequence extracted from NCBI backbone (NCBIN:138970, NCBIP:138971) A, Accession: B48713 A, Status: preliminary A, Molecule type: mRNA A, Residues: 30.467 < AQ2> A, Experimental source: TCO-4 cells A, Note: sequence inconsistent with nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:138970, NCBIP:138972) R; Chan, A.W.; Chedid, M.; Aaronson, S.A.; Miki, T.; McGovern, E.S. submitted to the EMBL Data Library, July 1992 A; Description: A transforming gene isolated by expression cloning from Ewing's sarcoma c A; Reference number: S31639 A; Accession: S31639 A; Status: preliminary A; Molecule type: MRNA
A; Keardudes: 1-40, <cha> A; Creatudes: 1-40, <cha> A; Creatudes: 1-40, <cha> A; Creatudes: EMBL: Z14138; NID: 931244; PIDN: CAA78512.1; PID: 931245 A; Creatudes: EmBL: Z14138; Dictoroncogene F; 136-388/Domain: protein kinase homology <kin> Query Match Total Girl A; Score 360; DB 2; Length 467;</kin></cha></cha></cha>
 Heat Local Similarity 2/.2%; Fred. No. 1.38-09; Matches 116; Conservative 69; Mismatches 155; Indels 86; Gaps 14; Qy 332 SVEEYLVHALQGSVSSQAHSLTSLAKTWAARGSRSREPSPKTEDNEGVLLTEKLKPVDY 391
QY 392 EYREEVHWATHQLRLGRGSFGEVHRWEDKQTGFQCAVKKVRLEVFRAEEL 441

442 MACAGLISPRIVPLYGAVREGPWVNIFMELLEGGSLGQLVKEQGCLPEDRALYYLGQALE 501

à

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C.Species: Rattus norvegicus (Norway rat)
C.Joate: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C.Joate: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C.Joate: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C.Joate: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R.Patriotis, C.; Makris, A.; Bear, S.E.; Tsichlis, P.N.
Proc. Natl. Acad. Sci. U.S.A. 90, 2251-2255, 1993
A.Aititle: Tumor progression locus 2 (Tpl-2) encodes a protein kinase involved in the proc. A.Accession: A47388
A.Accession: A47388
A.Accession: A47388
A.Accession: A47388
A.Accession: A47388
A.Accession: A77 cpg.
A.Accession: A77 cpg.
A.Accession: A77 cpg.
A.Accession: A77 cpg.
A.Accession: A77 cpg.
A.Accession: A7842185.1; PID:g207083
A.Experimental source: liver
A.Note: sequence extracted from NCBI backbone (NCBIN:128133, NCBIP:128134)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M46212

WER Kinase - mouse

G.Species: Mus musculus (house mouse)

C.Species: Mus musculus (house mouse)

C.Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-May-1999

C.Accession: A46212

R.Isange-Carter, C.A.; Pleiman, C.M.; Gardner, A.M.; Blumer, K.J.; Johnson, G.L.

Science 260, 315-319, 1993

A;Title: A divergence in the MAP kinase regulatory network defined by MEK kinase and Rat

A;Title: A divergence number: A46212; MUID:93227040; PMID:8385802

A;Reference number: not compared with conceptual translation

A;Residues: nucleic acid

A;Residues: l-687 cLMN>

A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: sequence extracted from NCBI backbone (NCBIP:129292)
C;Superfamily; unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc C;Keywords: ATP
F;416-683/Domain: protein kinase homology <KIN>
F;416-683/Domain: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                 7.1%; Score 356.5; DB 2; Length 467; 29.2%; Pred. No. 2.1e-09; Ive 60; Mismatches 115; Indels 63.
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                                     serine/threonine protein kinase - rat
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613
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C;Species: Mus musculus (house mouse)
C;Date: 02-011-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149609
R;Ohara, R.; Miyoshi, J.; Aoki, M.; Toyoshima, K.
A;Ohara, R.; Miyoshi, J.; Aoki, M.; Toyoshima, K.
A;Title: The murine cot proto-oncogene : genome structure and tissue-specific A;Reference number: 149609; MUID:93308016; PMID:8320169
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-467 <RES>
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                                                              GLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVCLQPDGLGKSLLTGDYIP----
                                                                                                                                                   GTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF---RGPLCLKIA-SEPP
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GTBIYMSPEVILCRGHSTKADIYSLGATLIHMQTGTPPWVKRYPRSAYPSYLYIIHKQAP
                                                                                                                                                                                                                                     PVREI PPSCAPLTAQAIQEGLRKEPIHRVSAAELGGKVNRALQQVGGLKSPWRGEYKEPR
                                                                                                                                                                                                                                                             proto-oncogene protein - mouse
C.Species: Mus musculus (house mouse)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                       HPPPNQANYHQTLHAQPRELSPRAPGPRPAEETTGRAPKLQPPLPPEPPREPNKSPPLTLS
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77 AISIIAQAECENSQEFSPTFSERIFIAGSKQYSQSESLDQIPNNVAHATEGKMARVCWKG 136

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RESULT 3

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990 FVPCKIPSASPQTQRKFSLQFQRTCSENRDSEKLSPVFTQSRPPPSSNIHRAKASRPVPG 1049
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FALQSIDNSHSMVGK---LSRRIYLSSARMVTTVPPLFSKLVTMLSASGSSHFARMRRL 847
                                                                                        PTFSERIFIA----GSK-----GSK------QYSQSESLDQIPNNVAHATEGKMARV 132
                                                                                                                                                                                                                                                                                                                                                                               : ::| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                     MAIADEVEIAEVIQLGSEDTLDGQDDSSQALAPPRYPESSSLE----HTAHVE-----
                                                                                                                                                                                                                                                    RMLGATCEKSNYNLFIEWMAGASVAHLLSKYGAFKESVVINYTEQLLRGLSYLHENQIIH
                                                                                                                                                                                                                 CWKGKRRSKARKKKKKKSSKSLAH - - AGVALAKPLPRTPEQESCTIPVQEDESPLGAPY -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 PLYGAVREGPWVNI FMELLEGGSLGQLVKEQGCLPEDRALYYLGQALEGLEYLHSRRILH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1050 STSKLGDASKNSMTLDINSASQCDDSFGSGSNSGSAVIPSEETAFTPAEDKCRLDVNPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1468 RCLELOPODRPPSRELLKHPVFRTT 1492
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A;Molecule type: mRNA
A;Residues: 1-1288 <WAN>
A;Coss-references: GB:AF100318
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPLPLPTHP-----
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MAP kinase kinase (BC 2.7.1.-) 1 - rat
MAP kinase kinase (BC 2.7.1.-) 1 - rat
MAP kinase kinase (BC 2.7.1.-) 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2004
C;Accession: T10757
R;Xu, S.; Robbins, D.J.; Christerson, L.B.; English, J.M.; Vanderbilt, C.A.; Cobb, M.H.
R;Xu, S.; Robbins, D.J.; Christerson, L.B.; English, J.M.; Vanderbilt, C.A.; Cobb, M.H.
R;Xu, S.; Robbins, D.J.; Christerson, L.B.; English, J.M.; Vanderbilt, C.A.; Cobb, M.H.
R;Xu, S.; Robbins, D.J.; Christerson L.B.; PIDB, 8643568
A;Reference number: Z17123; MUID:96224276; PMID:8643568
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: L1493 - xMGs
A;Residues: L1493 - xMGs
A;Residues: L1493 - xMGs
A;Cross_references: UNIPROT:Q62925; EMBL:U48596; NID:g1354136; PIDN:AAC52596.1; PID:g135
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S. : | : | : | : | : : | : : SLQAVAPTSCLENSSLEHTVHREKTGKGLSATRLSASSEDISDRLAGVSVGLPSSTTTEQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 SRCDDSFGGGGNSGNAVIPSDETVFTPVEDKCRLDVNTELNSSIEDLLEASMPSSDTTVT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SQAHSLTSLAKTWAARGSRSR---EPSP 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KR---RSKARKKKKKSSKSLAHAGVALAKPLPRTPEQESCTIPVQEDESPLGAPYVRNT 193
                                                                                                                                                                                                                                                                       POAFVPCKIPS------RDSDQL-RKFSLQFQRNCSEH------RDSDQL 217
                                                                                                                                                                                                                                                                                                                                   PLPTHPFPYSRLPHPFPFHPLQPWKPHPLESFLGKLACVDSQKPLPDPHLSKLA----- 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                        --CVDS-----PKPLPGPH----LEPSC-LSRGAHEKFSVEEYLVHALQGSVSS-- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 FKSEVAVLSPEKAENDDTYKDDVNHNQKCKEKMEÄEEEEALÄIAMÄMSAŠQDALPIVPQL 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTEDNEGVLLTEKLKP-----VDYEYREEVHWATHQLRLGRGSFGEVHRMEDKQTGF 424
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                                                                                                                                                                                                              POFTKPLKEPGLGQLCFKQLGEGLRPALPRSELHKLISPLQ--CLNHVWKLHHPQDGGPL 251
                                                                                                                                                                                                                                                                                                                                                                                            ---SPVFTQSRPPPSSNIHRPKPSRPVP------GSTSKLGDATKSSMTLDLGSA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 YKLEAVEKSPVFCGKWEILNDVITKGTAKEGSEAGPAAISIIAQAECENSQEFS-----
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                                                                                                                              PKPAVQTKGRPHSQCLNSSPLSHA--QLMFPAPSAPCSSAPSVP---DIS-
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C,Superfamily: protein kinase homology
C,Keywords: ATP; phosphotransferase; protein kinase
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les 165; Conservative
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mitogen-activated protein kinase kinase (EC 2.7.-.-) - human C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C;Accession: JE039 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C;Accession: JE030 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
B;Mang, X.; Diener, X.; Tan, T.; Yao, Z.
B;Ochem. Biophys. Res. Commun. 253, 33-37, 1998
A;Title: MAPKKK6, a novel mitogen-activated protein kinase kinase kinase, that associate A;Reference number: JE0363; MUID:99092374; PMID:9875215 31; Gaps 6.7%; Score 336; DB 2; Length 1288; 24.0%; Pred. No. 5.2e-08; tive 92; Mismatches 276; Indels 194; Length 1288; Query Match Best Local Similarity 24.0%; Matches 177; Conservative

OY 332 SVEEYLWHALQGSVSSQAHSLTSLAKTWAARGSRSREPSPKTEDNEGVLLTEKLKPVDY 391 Db 80 TVEDLL-A-RANHISNTAKHPYGQRDGSILLAWVTPQNG 119 QY 332 EXRESVHANTHQLALGRGSFGEVHRMEDKQTGFQCAKKKYRLEVFRAEL 441	C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C; Accession: A96591 R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000	A, Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A., Lin, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A, Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A, Reference number: A86141; MuID:21016719; PMID:11130712 A, Accession: A96591 A, Status: preliminary A, Molecule type: DNA A, Residues: 1651 < STO> A, Residues: UNIPROT:09F236; GB: AB005173; NID: G9857521; PIDN: AAG00876.1: GSPDB:GN	Genetics: Gene: 124C10.7 Map position: 1 Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase Ouery Match Best Local Similarity 26.1%; Pred. No. 8e-08; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 116; Gaps 18; Matches 132; Conservative 69; Mismatches 188; Indels 18; Matches 132; Conservative 69; Mismatches 188; Indels 18; Matches 132; Conservative 69; Mismatches 188; Indels 18; Matches 132; Conservative 69; Mismatches 188; Indel
QY 149 KSSKSLAHAGVALAKPLPRTPEQESCTIPVQEDESPLGAPVVRNTPOPTKPLKEPGL 205 10 EDSKELRLIGMKLGCLLARKGCVEKMQYYMVUGFYLGAQILANDP	: ; VGMYKVHPPMPSSI. YKEPRHPPPNQANY -SSPRHAP	923 723 976 783 1025	RESULT 7 441253 Kinace-related transforming protein (EC 2.7.1) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: A41253 R;Miyoshi, J; Higashi, T.; Mukai, H.; Ohuchi, T.; Kakunaga, T. A;Itle: Structure and transforming potential of the human cot oncogene encoding a putath A;Title: Structure and transforming potential of the human cot oncogene encoding a putath A;Reference number: A41253; MUID:91304400; PMID:2072910 A;Recension: A41253 A;Status: preliminary; not compared with conceptual translation A;Residues: 1-415 AMIY> A;Residues: 1-415 AMIY> A;Residues: 1-415 AMIY> C;Reywords: phosphotransferase F;136-388/Domain: protein kinase homology <kin> Query Match Guery Match Beet Local Similarity 27.7%; Pred, No. 2.70-08; Matches 104; Conservative 65; Mismatches 136; Indels 70; Gaps 13;</kin>

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A;Molecule type: DNA
A;Residues: 149-1478 <TRI>
A;Cross-references: EMBL:D10389; DDBJ:D90446
R;Miosga, T.; Schaaff-Gerstenschlaeger, I.; Baur, A.; Boles; E.; Chalwatzis, N.; Fournie
Submitted to the Protein Sequence Database, September 1995
A;Reference number: S56855
                                                                                                                                                                                                                                   Residues: 1-1478 <MIW>
;Cross-references: EMBL:Z49370; NID:g1008269; PIDN:CAA89389.1; PID:g1008270; MIPS:YJL09
                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 602-959,'R',961,'R',963-1085,'V',1087,'SLLIAHT',1092-1094,'RMD',1101,'TV',11
A;Cross-references: EMBL:M88604; NID:g172073; PIDN:AAA21179.1; PID:g172074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Description: phosphotransferase, protein kinase, involved in cell proliferation C;Superfamily: protein kinase homology C;Superfamily: phosphoprotein; phosphotransferase; serine/threonine-specific protein k;F;1173-1440/Domain: protein kinase homology «KIN» F;1181-1189/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SPKNVASSR 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1138 KRONTKMWGTRMVEVTENH--MVSINKAKNSKGEYK-EFAWMKGEM-IGKGSFGAVYLCL 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TEDNEGVLLTEKLKPVDYEYREEVHWATHQLRLGRGSFGEVHRME 418
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C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C.Accession: T34356
R.Bradshaw, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 FPYSRLPHPFPFHPLQPWKPHPLESFLGKLACVDSQKPLPDPHLSKLACVDSPKPLPGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466 NIFMELLEGGSLGQLVKEQGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 LEPSCLSRGAHEKFSVEEYLVHALQGS---VSSSQAHSLTSLAKTWAARGSRSREPSPK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 DKQTGFQCAVKKVRLEVFRAE--------ELMACAGLTSPRIVPLYGAVREGPWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGSHAALCDFGHAVCLQPDGLGKSLLTGDYI PGTETHMAPEVV - LGRSCDAKVDVWSSCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.4%; Score 325; DB 2; Length 1478;
28.7%; Pred. No. 1.9e-07;
Live 53; Mismatches 163; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         585 MMLHMLNGCHPWTQFFRGPLCLKIA---SEPPPVREIPPSCAPLTAQ 628
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A; Description: The sequence of C. elegans cosmid T19A5.
A; Reference number: Z21512
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                                                                                                                                                                                                                                                                                               R;Cusick, M.E.
submitted to the EMBL Data Library, March 1992
A;Reference number: 827437
AAccession: 830794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: SGD:BCK1; SLK1; SSP31
A;Cross-references: SGD:S0003631; MIPS:YJL095w
A;Map position: 10L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1043 FPRANLDKPITEGIASPTSPKSLDSLL
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Matches 117; Conserv
                                                                                                                                                                                                             A; Molecule type: DNA
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                                                                                                                                                                               A;Accession: S56872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein kinase BCK1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein J0906; protein kinase SLK1; protein kinase SSP31; protein VJI
C;Species: Saccharomyces cerevisiae
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 16-Aug-2004
C;Accession: S20117; S50298; S22285; S19061; J01432; S56872; S30794; J01118
R;Costigan, C.; Gehrung, S.; Snyder, M.
Mol. Cell. Biol. 12, 1162-1178, 1992
A;Title: A synthetic lethal screen identifies SLK1, a novel protein kinase homolog impli
A;Reference number: S20117; MUID:92186847; PMID:1545797
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A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-58, I'. 60-263, P'.265-278, I'.,280-702, S',707-708, KP',714, VITWTE',715-79
A,Cross-references: EMBL:X60227; NID:g3414; PIDN:CAA42788.1; PID:g3415
A,Experimental source: strain EG123
R,Irie, K., Araki, H, Oshima, Y.
Gene 108, 139-144, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Sequence and function analysis of a 9.74 kb fragment of Saccharomyces cerevisia
A;Reference number: S50295; MUID:95176706; PMID:7871887
A;Accession: S50298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: A new protein kinase, SSP31, modulating the SMP3 gene-product involved in plasm
A;Reference number: JQ1432; MUID:92104496; PMID:1840547
A;Accession: JQ1432
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A;Reference number: $19061
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A Residues: 1-1478 AMIO>
A Residues: 1-1478 AMIO>
A Residues: 1-1478 AMIO>
A CROSS-references: EMBL:X77923; NID:g640004; PIDN:CAA54896.1; PID:g640009
A CROSS-references: EMBL:X77923; NID:g640004; PIDN:CAA54896.1; PID:g640009
B Lee, K.S.; Levin, D.E.
Mol. Cell. Biol. 12, 112-182,
A Title: Dominant mutations in a gene encoding a putative protein kinase (BCK1) bypass that the commer: S22285; MulD:92107166; PMID:1729597
A; Reference number: S22285
A; Molecule type: DNA
A; Residues: 1-58, 17, 60-1478 ALES>
A; Cross-references: EMBL:X60227
A; Experimental source: strain EG123
B; Levin, D.E.
Submitted to the EMBL Data Library, June 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-1478 <COS>
A;Cross-references: UNIPROT:Q01389; EMBL:M84389
A;Experimental source: strain S288C
A;Experimental source: strain S288C
F;Miosga, T.; Boles, E.; Schaaff-Gerstenschlaeger, I.; Schmitt, S.; Zimmermann, F.K.
Yeast 10, 1481-1488, 1994
                                                                                                                                                                                                                                      716
   GKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFFRGPLCL 606
                                                                                                                      657
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                                                                                                                                                                                                                                                                                                                                                                                                               -----FPEKSIQNNSLC 397
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                                    230 AKSM-----KGTPYWMAPEVILQTGHSFSADIWSVGCTVIEMVTGKAPWSQQYK--
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40;

Gaps

Indels 305; Length

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A;Molecule type: DNA
A;Residues: 1-883 «STO»
Afross: references: UNIPROT:Q9CAD5; GB:AE005173; NID:g6456172; PIDN:AAF09160.1; GSPDB:GR
C;Genetics:
A;Gene: F2457.11
A;Map position: 1
                                                                                                                                                                                     106 KQYSQSESLDQIPNNVAHATEGKMARVCWKGKRRSKARKKKKKSSKSLAHAGVALAKPL 165
                                                                                                                                                                                                           Query Match 6.2%; Score 313.5; DB 2; Best Local Similarity 20.7%; Pred. No. 3.6e-07; Matches 202; Conservative 121; Mismatches 350;
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Arabidopsis thaliana
C,Species: Arabidopsis thaliana
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Dacession: Age62
R,Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ruthers, B.; Hudrar, L.
Nature 408, 816-820, 2000
A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizoo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A,Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Muthors: Salzberg, S.L.; Schwartz, J.C.; Davis, R.W.
A; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Riffler: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: A96662
                  A,Residues: 1-653 <BRA>
A,Cross-references: UNIPROT:Q22553; EMBL:U53153; PIDN:AAC69038.1; GSPDB:GN00023; CESP:T1
A,Experimental source: strain Bristol N2; clone T19A5
                                                                                                                                                                                    20;
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                                                                                                                                                                                                                                                                                 476
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                                                                                                                                                                                                                                                                                                                                                                                                         537 HAVCLOPDGLGKSLLTGDYIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPW 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 ATSSLPQSHTASSGGATTITLGSPNGSPTSSLARTQ-----SMVSPSGQRSGSA-- 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              821 RDTLSSGVHSWS-SQAEARSSSWNMVLARGRPTDTPSYFNGVKVQIQSLNGEHLHIREFH 879
                                                                                                                                                                                                                                                                                GFQCAVKKVRLEVFRAE - - - - ELMACAGLTSPRIVPLYGAVREGPWVNI FMELLEGGS
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                                                                                                                                                                                    Gaps
                                                                                                                                                                                    148;
                                                                 C;Genetics:
A;Gene: CESP:T19A5.2
A;Map position: 5
A;Introns: 26/3; 101/3; 157/1; 209/3; 272/3; 305/2; 373/3; 635/3
                                                                                                                                                    Length 653;
                                                                                                                                                                                  Indels
                                                                                                                                                 1 6.3%; Score 319; DB 2; L. Similarity 24.3%; Pred. No. 1.5e-07; 16; Conservative 78; Mismatches 228;
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A;Molecule type: DNA
A:Residues: 1-653 <BRA>
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Matches 146;
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680 816 PSWLPLPKPHGATSIPDNTGAEPDFATASVSSGSSVGDIPSDSLLSPLASDCENGNRTPV 174 ---HVWKLHHPQ-----DGG 249 NISSRDQSMHSNKNSAEMFKPVPNKNRILSASPRRRPLGTHVKNLQIPQRDLVLCSAPDS 234 302 LLSSPSRSPMRSFIPDQVSNHGLLISKPYSDVSLLGSGQCSSPGSGYNSGNNSIGGDMAT 294 ----KLACVDSPKPLPGPHLEPSCLSRGAHEKFSVEEYLVHALQGSVSSSQAHSLTSLA 357 KTWAARGSRSREPSPKTEDNE-----GVLLTEKLKPVDYEY-------REE 396 P--RAGGSTTGSPTRRLDDNRQQSHRLPLPPLLISNTCPFSPTYSAATSPSVPRSPARAE 391 440 500 510 558 561 559 TETHWAPEVVL-GRSCDAKVDVWSSCCMMLHMLNGCHPWTQFFRGPLCLKIASEPPVRE 617 702 725 760 ------CPISPVGSPIFHSHSPHI----SGRRSPSPISS--PHALSGSSTPL 765 TGCGGAIPFHHQRQTTVN-FLH------EGIGSSRSPGSGGNFYTNSFFQEPSRQ 813 817 SOSSRDTLSSGVH-SWSSQAEARSS-SWNWVLARGRPTDTPSYFNGVKVQIQSLNGEHLH 874 PRTP-----EQESCTIPVQEDESPLGAPYVRNTPQFTKPLKEPGLGQLCFKQLGEGLR 392 ATVSPGSRWKKGRL-LGMGSFGHVYLGFNSESGEMCAMKEVTLCSDDPKSRESAQQLGQE | | | | : : | | | | | | | SGLAYLHAKNITVHRDIKGANILVDPHG-RVKVADFGMAKHITAQSGPLS-----FKG SPYNMAPEVIKUSNGSNLAVDIWSLGCTVLEMATTKPPWSQYEGVPAMFKIGNS-KELPD R -- KATVPEQELQQLEIELFLNSLSQPFSLEEQEQILSCLSIDSLS -- LSDDSEKNPSKA QLFWPQSRCSPECSPVPSPRM-------TSPGPSSRIQSGAVTPLH V-----HWATHQLRLGRGSFGEVHRMEDKQTGFQCAVKKVRL-----EVFRAEE ISVLSRLRHQNIVQYYGSETVDDKLYIYLEYVSGGSIYKLLQEYGQFGENAIRNYTQQIL EGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHA--VCLQPDGLGKSLLTGDYIPG 618 IPPSCAPLTAQAIQEGLRKEPIHRVSAABL--------GGKVNRALQ----TLHAQPRELSPRAPGPRP 703 AEETTGRAPKLOPPLPP--EPPEPNKSPPLTLSKEESGMWEPLPLSSLEPAPARNPSSPE PLPLPTHPFPYSRLPHPFPFHPLQPWKPHPLESFLGKLACVDSQKPLPDPHLS----LMACAGLTSPRIVPLYGAVREGPWVNI FMELLEGGSLGQLVKEQGCLPEDRALYYLGQAL 681 TWRSLDIGHARS-----LPCLDSEDATNYQQKGLKHGSGFSISQSPRNMS----••• ----QVGGLKSPWRGEYKEPRHPPPNQANYHQ----.. PA-LPRSELH----.. 992 191 셤 à à

A; Status: preliminary

433 LE-VFRAEELMACAGLTSPRIVPLYGAVREGPWVNIFMELLEGGSLGQLV :	Db 395 QHEGRFPEQRAKFYIAELVLALEHLHKHDIIYRDLKPENILLDADG-HIALCDFGL 449 Qy 542 QPDGLGKSLLTGDYIPGTETHMAPEVVL-GRSCDAKVDVWSSCCMMLHMLNGCHPWTQFF 600 bb 450 SKANLSANATTNIFC-GTTEYLAPEVLLEDKGYTKQVDFWSLGVLVFEMCCGWSPFY 505 Qy 601 RGPLCLKIASEPPPVREIPPSCAPLTAQAIQEG-LRKEPIHRVSAAELG 648 bb 506APDVQQMTNIAFGKVRFPKGVLSSEGRSFVRGLLNRNPNHRLG 549 Qy 649 GKVNRALQQVGGLKSPWRGEYKEPPHPPPNQANYHQTLHAQPRELSPRAPGRRPAEETTG 708 bb 550 AVADTTELKEHPFFADINWDLLSKK	RESULT 13 protein kinase, p21-activated (BC 2.7.1) - human NiAlternate names; protein kinase PAK65; S6/H4 kinase C;Se61es; Homo sapiens (man) C;Deccies; Homo sapiens (man) C;Deccies; Homo sapiens (man) C;Deccies; Homo sapiens (man) C;Deccies; Homo sapiens (man) C;Deccies; Homo sapiens (man) C;Deccies; Homo sapiens (man) C;Deccession: S58682 S55289; S55289; S55389; S55389; S5744; S618, M; Knause, U.J.; Bagrodia, S.; Ambrose, D.; Bokoch, G.M.; Chernoff, J. Submitted to the EMBL Data Library, April 1995 A;Deccription: Human p21-activated protein kinases regulate actin organization in mammal A;Reference number: S5868 A;Molecule type: NDA A;Residues: 1-525 48ED A;Residues: 1-525 48ED A;Residues: 1-525 48ED A;Residues: 1-525 48ED A;Residues: 1-525 48ED A;Reference number: S55289; MUID:95265037; PMID:7744004 A;Reference number: S55289; MUID:95265037; PMID:7744004 A;Reference number: S55289; MUID:95066037; PMID:774004 A;Residues: YEERTQOXSMIEL', 31-89, T', 91-149, T', 151-224, T', 226-328, T', 310-338, 340-525 A;Wolccule type: mRNA A;Residues: YEERTQOXSMIEL', 31-89, T', 91-149, T', 151-224, T', 226-328, T', 310-338, 340-525 A;Wolccule type: protein A;Residues: 402-418 4MA> A;Residues: 402-418 4MA> A;Residues: 402-418 4MA> A;Residues: 6A-180119 PMID:95606211; PMID:756080 A;Connence: erratum A;Residues: 1-30 4MA> A;Residues: 1-30 4MA> A;Residues: 1-30 4MA> A;Residues: 1-30 4MA> A;Residues: 1-30 4MA> A;Residues: 1-30 4MA> A;Reference number: A57441; MUID:95403344; PMID:7673144 A;Rolecule type: number: A57441; MUID:95403344; PMID:7673144 A;Rolecule type: protein
Db 814 QDRSRSSPRTPPHVFWDNNGSIQPGYNWNKDNQPVLSDHVSQQLLSEHLK 863 Qy 875 IRBFHRVKVGDIATGISS 892 ::	RESULT 12 S55694 Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Bate: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004 C;Accession: S55694; T38040 R;Jin, M.; Fujita, M.; Culley, B.M.; Apolinario, E.; Yamamoto, M.; Maundrell, K.; Hoffma Genetics 140, 457-467, 1995 A;Title: sckl, a high copy number suppressor of defects in the cAMP-dependent protein ki A;Reference number: S55694; MUID:9612027; PMID:7498728 A;Reterence number: S55694 A;Status: preliminary A;Molecule type: DINA A;Residues: 1.696 culn> A;Residues: 1.696 culn> A;Residues: 1.696 culn> A;Reference number: Z21764 A;Reference number: Z21764 A;Reference number: Z21764 A;Reference number: Z21764 A;Reference number: Z21764 A;Reference number: Z21764 A;Reference number: Z1764 A;Reference number: Z1764 A;Reference number: Z1764 A;Reference number: Z1764 A;Reference number: Z1764 A;Reference number: Z21764 A;R	A General Schill SPDB:SPACIB9.02C A Introns: 80(1); 311/1; 633/2 A Introns: 80(3); 311/1; 633/2 A Introns: 80(3); 311/1; 633/2 C Superiamily: procein kinase homology C Superiamily: procein kinase homology kINS C Superiamily: procein kinase homology kINS C Superiamily: procein kinase homology kINS C Superiamily: procein kinase homology kINS C Superiamily: procein kinase ATP-binding motif Query Match Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:5% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; Best Local Similarity 21:6% Pred. No. 5.6e-07; B

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probable MEK kinase MAP3Ka, 84794-81452 (imported] - Arabidopsis thaliana probable MEK kinase MAP3Ka, 84794-81452 (imported] - Arabidopsis thaliana (c;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G96575
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. A;Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: G96575
A;Accession: G96575
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C;Genetics:
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                                                                                 250 GLLRKDPAERLPAEE ---AERALRLVGAGGAPPGRG----PRTGAPPSGAFAPTVVA--
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                                                         EGLRKEPIHRVSAAELGGKVNRALQQVG-GLKSPWRGEYKEPRHPPPNQANYHQTLHAQP
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26.4%;
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Best Local Similarity
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A; Residues: 1-608 <STO>
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A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                         ELIINEILVMKELKNPNIVNFLDSYLVGDELFVVMEYLAGGSLTDVVTETACMDEAQIAA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 VCRECLQALEFLHANQVIHRDIKSDNVLLGMEGS-VKLTDFGFCAQITPEQSKRSTWV-- 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 TVYDVATDGGRPW--IVMELVRGLSLADLLDAEGPLEPRRAALIGAEVLAALRAAHAAGV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCDAKVDVWSSCCMMLHMLNGCHPWTQFFRGPLCLKIASEPPPVREIPPSCAPLTAQAIQ 631
                                                                                                                                                                                                                                                                                                                                    139 LHRDVKPANVLLANDG-RVVLTDFGIA---RVEGSEALTMTGEVV-GSPEFLAPERALGR
                                                                                                                                                                                                                                                             380 VLLTEKLKPVDYEYREEVHWATHQLRLGRGSFGEVHRMEDKQTGFQCAVKKVRLEVFRAE
                                                                                                                                                                                                                                                                                                                                                                                        EL----MACAGLTSPRIVPLYGAVREGPWVNIFMELLEGGSLGQLVKEQGCLPEDRALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 495 YLGOALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVCLQPDGLGKSLLTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YIPGTETHMAPEVVLGRSCDAKVDVWSSCCMMLHMLNGCHPWTQFFRGPL--CLKIASEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGRGSFGEVHRMEDKQTGFQCAVKKVRL-----EVFR----AEELMACAGLTSPRIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHGDVKADNVLLSSDGSHAALCDFGHAVCLQPDGLGKSLLTGDYIPGTETHMAPEVVLGR
A;Residues: 197-216;402,'S',404-409 <BEN>
A;Experimental source: placenta
C;Superfamily: protein kinase homology
C;Keywords: APP; autophosphorylation; phosphoprotein; phosphotransferase;
F;247-501/Domain: protein kinase homology <KIN>
F;255-263/Region: protein kinase APP-binding motif
F;197,402/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                          Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%; Score 305; DB 2; Length 55: 31.7%; Pred. No. 5.4e-07; ive 37; Mismatches 135; Indels
                                                                                                                                                                                              Indels
                                                                                                                                                                                              54; Mismatches 160;
                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPVREIPPSCAPLTAQAIQEGLRKEPIHRVSAAEL 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPELQNPEKLSPIFRDFLNRCLEMDVEKRGSAKEL 495
                                                                                                                                                                              4.9e-07
                                                                                                                                                        6.0%; Score 305.5; 28.1%; Pred. No. 4.9
                                                                                                                                                                                              94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity 31.7% 106; Conservative
                                                                                                                                                                            Local Similarity
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Best Local 9
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                                                                                                                                                          Query Match
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Matches
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